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Description

BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND USES THEREOF

BACKGROUND OF INVENTION

FIELD OF THE INVENTION

[0001] The present invention relates to a group of bioinformatically detectable novel genes, here identified as "genomic address messenger"or "GAM"genes, which are believed to be related to the micro RNA (miRNA) group of genes.

DESCRIPTION OF PRIOR ART

[0002] Over 300 small noncoding RNA"s, termed Micro RNA"s (miRNA"s), have been identified to date in animals and plants (*1-8*). The MIR genes, code for ~70-120nt long non-protein-coding RNA sequences, that are the precursors of the ~22 nt miRNA sequences, which in some cases, specifically inhibit translation of target genes, by complementary binding to their untranslated regions

(UTR) (*9–13*). The first two MIR genes discovered, Lin-4 and Let-7, were found in the nematode *Ceanorhabditis elegans*, and shown to be involved in developmental timing (*14, 15*), hence originally called Short Temporal RNA (stRNA) (*16*). The ~22 nt sequences inhibit translation of two respective target genes, Lin-14 and Lin-41, by complementary binding to their 3" untranslated regions (UTR) (*14, 17*). Later studies by three separate groups (*1–3*) identified several precursor and mature miRNA"s, some of them in clusters (*1*), expressed as sequences found in size fractionated (<80nt) total RNA, in a wide spectrum of species, including *C. elegans*, *Drosophila melanogaster*, *Homo sapiens*, as well as plants. More recently, additional miRNA"s from human (mir-91 to mir-121 (*6*)), mouse (mir-122 to mir-155 (*4*)) and plants (mir-156 to mir-171 (*5*)), have been reported. Furthermore, Llave *et al* identified in *Arabidopsis thaliana* 125 sequences, 21-24 nucleotides in length and presumably miRNAs (*8*). Each of the MIR genes is transcribed and processed to an ~80 nt-long hairpin shaped miRNA precursor, which is then processed by an enzyme called Dicer, to yield the mature ~22 nt-long single stranded miRNA. Such small RNAs will inhibit translation of target genes by complementary binding to sites in the

3" or 5" untranslated regions (*18*). Their structural similarity to the two well-studied miRNA"s in *C. elegans*, Lin-4 and Let-7, supports the belief that MIR genes code for specific translation inhibitors of target genes. However, determining the targets of the miRNAs is more complicated than just searching for antisense complementarity, because bulges and loops, disrupting perfect complementarity, are not only tolerated, but seem to be the rule in the postulated binding between the miRNA"s and their target UTR"s(*19*). Target-gene binding sites of most reported miRNA"s, except of Lin-4 and Let-7, have not been found, and therefore the specific functionality of these genes is still unknown. Using a computational approach, Rhoades *et al* (*19*), predicted targets for 14 *A. thaliana* miRNA"s by identifying their near complementarity to the predicted targets. However, using the same approach was not helpful in identifying miRNA targets in *C. elegans* and *D. melanogaster*, raising the possibility that the near-perfect complementarity appears to be specific to plants (*19*).

[0003] Based on the striking homology of the newly discovered MIR genes to their well-studied predecessors Lin-4 and Let-7, the new MIR genes are believed to have a similar basic function as that of Lin-4 and Let-7: modulation of

target genes by complimentary binding to the UTR of these target genes, with special emphasis on modulation of developmental control processes. This is despite the fact that the above mentioned recent studies did not find target genes to which the newly discovered MIR genes complementarily bind. While existing evidence suggests that the number of regulatory RNA genes "may turn out to be very large, numbering in the hundreds or even thousands in each genome", detecting such genes is challenging (Ruvkun G., "Perspective: Glimpses of a tiny RNA world", Science 294 ,779 (2001)).

[0004] The ability to detect novel miRNA genes is limited by the methodologies used to detect such genes. All miRNA genes identified so far either present a visibly discernable whole body phenotype, as do Lin-4 and Let-7 (Wightman et. al., Cell 75, 855 (1993); Reinhart et al., Nature 403, 901 (2000)), or produce significant enough quantities of RNA so as to be detected by the standard biochemical genomic techniques, as do the 93 recently detected miRNA genes. Since a limited number clones were sequenced by the researchers discovering these genes, 300 by Bartel and 100 by Tuschl (Bartel et. al., Science 294 ,858 (2001); Tuschl et. al., Science 294 ,853 (2001)), the RNA genes

found can not be much rarer than 1% of all RNA genes. The recently detected miRNA genes therefore represent the more prevalent among the miRNA gene family.

[0005] Current methodology has therefore been unable to detect RNA genes which either do not present a visually discernable whole body phenotype, or are rare (e.g. rarer than 0.1% of all RNA genes), and therefore do not produce significant enough quantities of RNA so as to be detected by standard biochemical technique.

SUMMARY OF INVENTION

[0006] The present invention relates to a novel group of regulatory, non-protein coding genes, which are functional in specifically inhibiting translation of other genes, some of which are known to be involved in various diseases. Each gene in this novel group of genes, here identified as "GAM"or "Genomic Address Messengers", specifically inhibits translation of one of more other "target" genes by means of complimentary hybridization of a segment of the RNA transcript encoded by GAM, to an inhibitor site located in an untranslated region (UTR) of the mRNA of the one or more "target" genes.

[0007] In various preferred embodiments, the present invention seeks to provide improved method and system for specific

modulation of expression of specific known "target" genes involved in significant human diseases, and improved method and system for detection of expression of these target genes.

[0008] Accordingly, the invention provides several substantially pure DNAs (e.g., genomic DNA, cDNA or synthetic DNA) each encoding a novel gene of the GAM group of gene, vectors comprising the DNAs, probes comprising the DNAs, a method and system for selectively modulating translation of known "target" genes utilizing the vectors, and a method and system for detecting expression of known "target" genes utilizing the probe.

[0009] By "substantially pure DNA" is meant DNA that is free of the genes which, in the naturally-occurring genome of the organism from which the DNA of the invention is derived, flank the genes discovered and isolated by the present invention. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote at a site other than its natural site; or which exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion)

independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence.

[0010] "Inhibiting translation" is defined as the ability to prevent synthesis of a specific protein encoded by a respective gene, by means of inhibiting the translation of the mRNA of this gene. "Translation inhibiter site" is defined as the minimal DNA sequence sufficient to inhibit translation.

[0011] There is thus provided in accordance with a preferred embodiment of the present invention a bioinformatically detectable novel gene encoding substantially pure DNA wherein: RNA encoded by the bioinformatically detectable novel gene is about 18 to about 24 nucleotides in length, and originates from an RNA precursor, which RNA precursor is about 50 to about 120 nucleotides in length, a nucleotide sequence of a first half of the RNA precursor is a partial inversed-reversed sequence of a nucleotide sequence of a second half thereof, a nucleotide sequence of the RNA encoded by the novel gene is a partial inversed-reversed sequence of a nucleotide sequence of a binding site associated with at least one target gene, the novel gene cannot be detected by either of the following: a visually discernable whole body phenotype, and detection

of 99.9% of RNA species shorter than 25 nucleotides expressed in a tissue sample, and a function of the novel gene is bioinformatically deducible.

[0012] There is further provided in accordance with another preferred embodiment of the present invention a bioinformatically detectable novel gene encoding substantially pure DNA wherein: RNA encoded by the bioninformatically detectable novel gene includes a plurality of RNA sections, each of the RNA sections being about 50 to about 120 nucleotides in length, and including an RNA segment, which RNA segment is about 18 to about 24 nucleotides in length, a nucleotide sequence of a first half of each of the RNA sections encoded by the novel gene is a partial inversed-reversed sequence of nucleotide sequence of a second half thereof, a nucleotide sequence of each of the RNA segments encoded by the novel gene is a partial inversed-reversed sequence of the nucleotide sequence of a binding site associated with at least one target gene, and a function of the novel gene is bioinformatically deducible from the following data elements: the nucleotide sequence of the RNA encoded by the novel gene, a nucleotide sequence of the at least one target gene, and function of the at least one target gene.

[0013] There is still further provided in accordance with another preferred embodiment of the present invention a bioinformatically detectable novel gene encoding substantially pure DNA wherein: RNA encoded by the bioinformatically detectable novel gene is about 18 to about 24 nucleotides in length, and originates from an RNA precursor, which RNA precursor is about 50 to about 120 nucleotides in length, a nucleotide sequence of a first half of the RNA precursor is a partial inversed-reversed sequence of a nucleotide sequence of a second half thereof, a nucleotide sequence of the RNA encoded by the novel gene is a partial inversed-reversed sequence of a nucleotide sequence of a binding site associated with at least one target gene, a function of the novel gene is modulation of expression of the at least one target gene, and the at least one target gene does not encode a protein.

[0014] There is additionaly provided in accordance with another preferred embodiment of the present invention A bioinformatically detectable novel gene encoding substantially pure DNA wherein: the bioinformatically detectable novel gene does not encode a protein, RNA encoded by the bioinformatically detectable novel gene is maternally transferred by a cell to at least one daughter cell of the

cell, a function of the novel gene includes modulation of a cell type of the daughter cell, and the modulation is bioinformatically deducible.

[0015] There is moreover provided in accordance with another preferred embodiment of the present invention a bioinformatically detectable novel gene encoding substantially pure DNA wherein: the bioinformatically detectable novel gene does not encode a protein, a function of the novel gene is promotion of expression of the at lease one target gene, and the at least one target gene is bioinformatically deducible.

[0016] Further in accordance with a preferred embodiment of the present invention the function of the novel gene is bioinformatically deducible from the following data elements: the nucleotide sequence of the RNA encoded by the bioinformatically detectable novel gene, a nucleotide sequence of the at least one target gene, and a function of the at least one target gene.

[0017] Still further in accordance with a preferred embodiment of the present invention the RNA encoded by the novel gene complementarily binds the binding site associated with the at least one target gene, thereby modulating expression of the at least one target gene.

[0018] Additionally in accordance with a preferred embodiment of the present invention the binding site associated with at least one target gene is located in an untranslated region of RNA encoded by the at least one target gene.

[0019] Moreover in accordance with a preferred embodiment of the present invention the function of the novel gene is selective inhibition of translation of the at least one target gene, which selective inhibition includes complementary hybridization of the RNA encoded by the novel gene to the binding site.

[0020] Further in accordance with a preferred embodiment of the present invention the invention includes a vector including the DNA.

[0021] Still further in accordance with a preferred embodiment of the present invention the invention includes a method of selectively inhibiting translation of at least one gene, including introducing the vector.

[0022] Moreover in accordance with a preferred embodiment of the present invention the introducing includes utilizing RNAi pathway.

[0023] Additionally in accordance with a preferred embodiment of the present invention the invention includes a gene expression inhibition system including: the vector, and a

vector inserter, functional to insert the vector into a cell, thereby selectively inhibiting translation of at least one gene.

[0024] Further in accordance with a preferred embodiment of the present invention the invention includes a probe including the DNA.

[0025] Still further in accordance with a preferred embodiment of the present invention the invention includes a method of selectively detecting expression of at least one gene, including using the probe.

[0026] Additionally in accordance with a preferred embodiment of the present invention the invention includes a gene expression detection system including: the probe, and a gene expression detector functional to selectively detect expression of at least one gene.

Brief Description of Drawings

[0027] Fig.1 is a simplified diagram illustrating the genomic differentiation enigma that the present invention addresses;

[0028] Figs. 2 through 4 are schematic diagrams which when taken together provide an analogy that illustrates a conceptual model of the present invention, addressing the genomic differentiation enigma;

[0029] Figs. 5A and 5B are schematic diagrams, which when

taken together illustrate a "genomic records" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma;

[0030] Fig. 6 is a schematic diagram illustrating a "genomically programmed cell differentiation" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma;

[0031] Fig. 7 is a schematic diagram illustrating a "genomically programmed cell-specific protein expression modulation" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma;

[0032] Reference is now made to Fig. 8, which is a simplified diagram describing each of a plurality of novel bioinformatically detected genes of the present invention, referred to here as Genomic Address Messenger (GAM) genes, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art. GAM is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM was detected is described hereinabove with reference to Figs. 2-8. GAM GENE and GAM TARGET GENE are human genes contained in the human genome. GAM GENE encodes a GAM PRECURSOR RNA.

Similar to other miRNA genes, and unlike most ordinary genes, GAM PRECURSOR RNA does not encode a protein. GAM PRECURSOR RNA folds onto itself, forming GAM FOLDED PRECURSOR RNA, which has a two-dimensional ?hairpin structure?. As is well known in the art, this ?hairpin structure?, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof. By ?inversed-reversed? is meant a sequence which is reversed and wherein each nucleotide is replaced by a complementary nucleotide, as is well known in the art (e.g. ATGGC is the inversed-reversed sequence of GCCAT). An enzyme complex designated DICER COMPLEX, ?dices? the GAM FOLDED PRECURSOR RNA into GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, ?dicing? of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. GAM TARGET GENE encodes a corresponding messenger RNA, GAM TARGET RNA. GAM TARGET RNA comprises three regions, as is

typical of mRNA of a protein coding gene: a 5? untranslated region, a protein coding region and a 3? untranslated region, designated 5?UTR, PROTEIN CODING and 3?UTR respectively. GAM RNA binds complementarily to one or more target binding sites located in untranslated regions of GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting ? GAM RNA may have a different number of target binding sites in untranslated regions of a GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3?UTR region, this is meant as an example only ? these target binding sites may be located in the 3?UTR region, the 5?UTR region, or in both 3?UTR and 5?UTR regions. The complementary binding of GAM RNA to target binding sites on GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM TARGET RNA into GAM TARGET PROTEIN. GAM TARGET PROTEIN is therefore outlined by a broken line. It is appreciated that GAM TARGET GENE in fact represents a plurality of GAM target genes. The mRNA of each one of this plurality of GAM target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM RNA, and which when bound by GAM RNA causes inhibition of translation of respective one or more GAM target proteins. It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM GENE on one or more GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., ?Perspective: Glimpses of a tiny RNA

world?, Science 294 ,779 (2001)). It is yet further appreciated that specific functions, and accordingly utilities, of GAM correlate with, and may be deduced from, the identity of the target genes which GAM binds and inhibits, and the function of these target genes, as elaborated hereinbelow. Nucleotide sequences of the GAM PRECURSOR RNA, and of the ?diced? GAM RNA, and a schematic representation of the secondary folding of GAM FOLDED PRECURSOR RNA of each of the plurality of GAM GENEs described by Fig. 8 are further described hereinbelow with reference to Table 1. Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on , and schematic representation of the complementarity of each of these target binding sites to GAM RNA are described hereinbelow with reference to Table 2.

[0033] Fig. 9 is a simplified block diagram illustrating a bioinformatic gene detection system capable of detecting genes of the novel group of genes of the present invention, which system is constructed and operative in accordance with a preferred embodiment of the present invention;

[0034] Fig. 10 is a simplified flowchart illustrating operation of a mechanism for training of a computer system to recog-

nize the novel genes of the present invention, which mechanism is constructed and operative in accordance with a preferred embodiment of the present invention;

[0035] Fig. 11A is a simplified block diagram of a non-coding genomic sequence detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0036] Fig. 11B is a simplified flowchart illustrating operation of a non-coding genomic sequence detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0037] Fig. 12A is a simplified block diagram of a hairpin detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0038] Fig. 12B is a simplified flowchart illustrating operation of a hairpin detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0039] Fig. 13A is a simplified block diagram of a dicer-cut location detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0040] Fig. 13B is a simplified flowchart illustrating training of a dicer-cut location detector constructed and operative in accordance with a preferred embodiment of the present

invention;

[0041] Fig. 13C is a simplified flowchart illustrating operation of a dicer-cut location detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0042] Fig. 14A is a simplified block diagram of a target-gene binding-site detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0043] Fig. 14B is a simplified flowchart illustrating operation of a target-gene binding-site detector constructed and operative in accordance with a preferred embodiment of the present invention;

[0044] Fig. 15 is a simplified flowchart illustrating operation of a function & utility analyzer constructed and operative in accordance with a preferred embodiment of the present invention;

[0045] Reference is now made to Fig. 16, which is a simplified diagram describing each of a plurality of novel bioinformatically detected regulatory genes, referred to here as Genomic Record(GR) genes, which encodes an ?operon-like? cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the

function and utility of which at least one target gene is known in the art. GR GENE is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR GENE was detected is described hereinabove with reference to Figs. 6-15. GR GENE encodes GR PRECURSOR RNA, an RNA molecule, typically several hundred nucleotides long. GR PRECURSOR RNA folds spatially, forming GR FOLDED PRECURSOR RNA. It is appreciated that GR FOLDED PRECURSOR RNA comprises a plurality of what is known in the art as ?hairpin? structures. These ?hairpin? structures are due to the fact that the nucleotide sequence of GR PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art. GR FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity into a plurality of separate GAM precursor RNAs, schematically represented by GAM1 PRECURSOR, GAM2 PRECURSOR, GAM3 PRECURSOR, GAM4 PRECURSOR, GAM5 PRECURSOR, GAM6 PRECURSOR, GAM7 PRECURSOR and GAM8 PRECURSOR, each of which GAM precursor RNAs being a hairpin shaped RNA segment, corresponding to

GAM PRECURSOR RNA of Fig. 8. The above mentioned GAM precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, schematically represented as GAM1 RNA, GAM2 RNA, GAM3 RNA, GAM4 RNA, GAM5 RNA, GAM6 RNA, GAM7 RNA and GAM8 RNA respectively, each of which GAM RNAs corresponding to GAM RNA of Fig. 8. GAM1 RNA binds complimentarily to a target binding site located in an untranslated region of GAM1 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1 TARGET RNA into GAM1 TARGET PROTEIN, both of Fig. 8. GAM2 RNA binds complimentarily to a target binding site located in an untranslated region of GAM2 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2 TARGET RNA into GAM2 TARGET PROTEIN, both of Fig. 8. GAM3 RNA binds complimentarily to a target binding site located in an untranslated region of GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM3 TARGET RNA into GAM3 TARGET PROTEIN, both of Fig. 8. GAM4 RNA binds complimentarily to a target binding site located in an untranslated region of GAM4 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4 TARGET RNA into GAM4 TARGET PROTEIN, both of Fig. 8. GAM5 RNA binds complimentarily to a target binding site located in an untranslated region of GAM5 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5 TARGET RNA into GAM5 TARGET PROTEIN, both of Fig. 8. GAM6 RNA binds complimentarily to a target binding site located in an untranslated region of GAM6 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6 TARGET RNA into GAM6 TARGET PROTEIN, both of Fig. 8. GAM7 RNA binds complimentarily to a target binding site located in an untranslated region of GAM7 TARGET RNA, which target binding site corresponds to a target binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7 TARGET RNA into GAM7 TARGET PROTEIN, both of Fig. 8. GAM8 RNA binds complimentarily to a target binding site located in an untranslated region of GAM8 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8 TARGET RNA into GAM8 TARGET PROTEIN, both of Fig. 8. It is appreciated that specific functions, and accordingly utilities, of GR GENE correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the ?operon-like? cluster of GR GENE, schematically represented by GAM1 TARGET PROTEIN through GAM8 TARGET PROTEIN.

[0046] Fig. 17 is a simplified diagram illustrating a mode by which genes of a novel group of operon-like genes of the present invention, modulate expression of other such genes, in a cascading manner;

[0047] Fig. 18 is a block diagram illustrating an overview of a methodology for finding novel genes and novel operon-like genes of the present invention, and their respective functions;

[0048] Fig. 19 is a block diagram illustrating different utilities of novel genes and novel operon-like genes, both of the present invention;

[0049] Figs. 20A and 20B are simplified diagrams, which when taken together illustrate a mode of gene therapy applicable to novel genes of the present invention;

[0050] Fig. 21A is an annotated sequence of EST72223 comprising known miRNA gene MIR98 and novel gene GAM25, both detected by the gene detection system of the present invention;

[0051] Figs. 21B and 21C are pictures of laboratory results demonstrating laboratory confirmation of expression of known gene MIR98 and of novel bioinformatically detected gene GAM25 respectively, both of Fig. 21A, thus validating the bioinformatic gene detection system of the present invention;

[0052] Fig. 21D provides pictures of laboratory results, which when taken together demonstrate further laboratory confirmation of expression of the bioinformatically detected novel gene GAM25 of Fig. 21A, and another novel bioinformatically detected gene GAM26, thus further validating the bioinformatic gene detection system of the present invention;

[0053] Fig. 22A is an annotated sequence of an EST7929020 comprising novel genes GAM24 and GAM26 detected by the gene detection system of the present invention;

[0054] Fig. 22B is a picture of laboratory results, which confirm expression of bioinformatically detected novel genes GAM24 and GAM26 of Fig. 22A, thus further validating the bioinformatic gene detection system of the present invention;

[0055] Fig. 22C is a picture of laboratory results, which confirm endogenous expression of bioinformatically detected novel gene GAM26 of Fig. 22A;

[0056] Fig. 23A is an annotated sequence of an EST1388749 comprising novel gene GAM27 detected by the gene detection system of the present invention;

[0057] Fig. 23B is a picture of laboratory results, which confirm expression of the bioinformatically detected novel gene GAM27 of Fig. 23A;

[0058] Figs. 24A through 1699D are schematic diagrams illustrating sequences, functions and utilities of 1675 specific genes of the novel group of genes of the present invention, detected using the bioinformatic gene detection system described hereinabove with reference to Figs. 8 - 15, 19 and 20 ; and

[0059] Figs. 1700 through 1706 are schematic diagrams illustrating sequences, functions and utilities of 7 specific genes of a group of novel regulatory "operon-like" genes of the present invention, detected using the bioinformatic gene detection system described hereinabove with reference to Figs. 16 and 18 - 20.

Brief Description of Sequences

[0060] A Sequence Listing of genomic sequences of the present invention designated SEQ ID:1 through SEQ ID:97947 is attached to this application, enclosed in computer readable form on CD-ROM. The genomic listing comprises the following nucleotide sequences:Genomic sequences designated SEQ ID:1 through SEQ ID:1675 are nucleotide sequences of 1675 gene precursors of respective novel genes of the present invention;Genomic sequences designated SEQ ID:1676 through SEQ ID:3350 are nucleotide sequences of 1675 genes of the present invention; andGenomic sequences designated SEQ ID:3351 through SEQ ID:97947 are nucleotide sequences of 94597 gene precursors of respective novel genes of the present invention.

Detailed Description

[0061] Reference is now made to Fig. 1 which is a simplified diagram providing a conceptual explanation of a genomic differentiation enigma, which the present invention addresses.

[0062] Fig. 1 depicts different cell types in an organism, such as CARTILAGE CELL, LIVER CELL, FIBROBLAST CELL and BONE CELL all containing identical DNA, and deriving from the initial FERTILIZED EGG CELL, and yet each of these cells expressing different proteins, and hence acquiring different shape and function.

[0063] The present invention proposes that the inevitable conclusion from this constraint is, however, strikingly simple: the coding system used must be modular. It must comprise multiple modules, or records, one for each cell-type, and a mechanism whereby each cell at its inception is instructed which record to open, and behaves according to instructions in that record.

[0064] This modular code concept is somewhat difficult to grasp, since we are strongly habituated to viewing things from an external viewpoint. An architect, for example, looks at a blueprint of a building, which details exactly where each element (block, window, door, electrical switch, etc.) is to be placed relative to all other elements, and then instructs

builders to place these elements in their designated places. This is an external viewpoint: the architect is external to the blueprint, which itself is external to the physical building, and its different elements. The architect may therefore act as an "external organizing agent": seeing the full picture and the relationships between all elements, and being able to instruct from the outside where to place each of them.

[0065] Genomics differentiation coding evidently works differently, without any such external organizing agent: It comprises only one smart block (the first cell), which is the architect and the blueprint, and which continuously duplicates itself, somehow knowing when to manifest itself as a block and when as a window, door, or electrical switch.

[0066] Reference is now made to Figs. 2 through 4 which are schematic diagrams which when taken together provide an analogy that illustrates a conceptual model of the present invention, addressing the genomic differentiation enigma.

[0067] Reference is now made to Fig. 2A. Imagine a very talented chef, capable of preparing any meal provided he is given specific written cooking instructions. This chef is equipped with two items: (a) a thick recipe book, and (b) a

small note with a number scribbled on it. The book comprises multiple pages, each page detailing how to prepare a specific meal. The small note indicates the page to be opened, and therefore the meal to be prepared. The chef looks at the page-number written on the note, opens the recipe book at the appropriate page, and prepares the meal according to the written instructions on this page. As an example, Fig. 2A depicts a CHEF holding a note with the number 12 written on it, he opens the book on page 12, and since that page contains the recipe for preparing BREAD, the CHEF prepares a loaf of BREAD.

[0068] Reference is now made to Fig. 2B, which depicts two identical chefs, CHEF A and CHEF B, holding an identical recipe book. Despite their identity, and the identity of their recipe book, since CHEF A holds a note numbered 12, and therefore opens the book on page 12 and prepares BREAD, whereas CHEF B holds a note numbered 34 and therefore opens the book on page 34 and prepares a PIE.

[0069] Reference is now made to Fig. 3. Imagine the chef of the analogy is also capable of duplicating himself once he has finished preparing the specified meal. The format of the book is such that at the bottom of each page, two numbers are written. When he has finished preparing the meal

specified on that page, the chef is trained to do the following: (i) divide himself into two identical duplicate chefs, (ii) duplicate the recipe book and hand a copy to each of his duplicate chefs, and (iii) write down the two numbers found at the bottom of the page of the meal he prepared, on two small notes, handing one note to each of his two duplicate chefs.

[0070] Each of the two resulting duplicate chefs are now equipped with the same book, and have the same talent to prepare any meal, but since each of them received a different note, they will now prepare different meals.

[0071] Fig. 3 depicts CHEF A holding a recipe book and receiving a note numbered 12. CHEF A therefore opens the book on page 12 and prepares BREAD. When he is finished making bread, CHEF A performs the following actions: (i) divides himself into two duplicate chefs, designated CHEF B and CHEF C, (ii) duplicates his recipe book handing a copy to each of CHEF B and CHEF C, (iii) writes down the numbers found at the bottom of page 12, numbers 34 and 57, on two notes, handing note numbered 34 to CHEF B and note numbered 57 to CHEF C.

[0072] Accordingly, CHEF B receives a note numbered 34 and therefore opens the recipe book on page 34 and prepares

PIE, whereas CHEF C receives a note numbered 57 and therefore opens the book on page 57 and therefore prepares RICE.

[0073] It is appreciated that while CHEF A, CHEF B & CHEF C are identical and hold identical recipe books, they each prepare a different meal. It is also appreciated that the meals prepared by CHEF B and CHEF C are determined CHEF A, and are mediated by the differently numbered notes passed on from CHEF A to CHEF B and CHEF C.

[0074] It is further appreciated that the mechanism illustrated by Fig. 3 enables an unlimited lineage of chefs to divide into duplicate, identical chefs and to determine the meals those duplicate chefs would prepare. For example, having been directed to page 34, when CHEF B divides into duplicate chefs (not shown), he will instruct its two duplicate chefs to prepare meals specified on pages 14 and 93 respectively, according to the numbers at the bottom of page 34 to which he was directed. Similarly, CHEF C will instruct its duplicate chefs to prepare meals specified on pages 21 and 46 respectively, etc.

[0075] Reference is now made to Fig. 4. Imagine that the cooking instructions on each page of the recipe book are written in shorthand format: The main meal-page to which the chef

was directed by the scribbled note, merely contains a list of numbers which direct him to multiple successive pages, each specifying how to prepare an ingredient of that meal.

[0076] As an example, Fig. 4 depicts CHEF A of FIGS 2 and 3, holding a recipe book and a note numbered 12. Accordingly, CHEF A opens the recipe book on page 12, which details the instructions for preparing BREAD. However, the "instructions" on making BREAD found on page 12 comprise only of 3 numbers, 18, 7 and 83, which "refer" CHEF A to pages detailing preparation of the ingredients of BREAD FLOUR, MILK and SALT, respectively.

[0077] As illustrated in Fig. 4, turning from the main "meal page" (e.g. 12) to respective "ingredients pages" (e.g. pages 18, 7 & 83) is mediated by scribbled notes with the page-numbers written on them. In this analogy, the scribbled notes are required for seeking the target pages to be turned to both when turning to main "meal pages" (e.g. page 12), as well as when turning to "ingredient pages" (e.g. pages 18, 7 & 83).

[0078] The chef in the given analogy, schematically depicted in FIGS 2 through 4, represents a cell; the thick recipe book represents the DNA; preparing a meal in the given analogy represents the cell manifesting itself as a specific cell-

type; and ingredients of a meal represent proteins expressed by that cell-type. Like the chef equipped with the thick recipe book in the given analogy, all cells in an organism contain the same DNA and are therefore each potentially capable of manifesting itself as any cell-type, expressing proteins typical of that cell type.

[0079] Reference is now made to Figs. 5A and 5B which are schematic diagrams, which when taken together illustrate a "genomic records" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma.

[0080] The Genomic Records concept asserts that the DNA (the thick recipe book in the illustration) comprises a very large number of Genomic Records (analogous to pages in the recipe book), each containing the instructions for differentiation of a different cell-type, or developmental process. Each Genomic Record is headed by a very short genomic sequence which functions as a "Genomic Address" of that Genomic Record (analogous to the page number in the recipe book). At its inception, in addition to the DNA, each cell also receives a short RNA segment (the scribbled note in the illustration). This short RNA segment binds complementarily to a "Genomic Address" sequence

of one of the Genomic Records, thereby activating that Genomic Record, and accordingly determining the cell"s-fate (analogous to opening the book on the page corresponding to the number on the scribbled note, thereby determining the meal to be prepared).

[0081] Reference is now made to Fig. 5A. Fig 5A illustrates a CELL which comprises a GENOME. The GENOME comprises a plurality of GENOMIC RECORDS, each of which correlates to a specific cell type (for clarity only 6 sample genomic records are shown). Each genomic record comprises genomic instructions on differentiation into a specific cell-type, as further elaborated below with reference to Fig. 7. At cell inception, the CELL receives a maternal short RNA segment, which activates one of the GENOMIC RECORDS, causing the cell to differentiate according to the instructions comprised in that genomic record. As an example, Fig. 5A illustrates reception of a maternal short RNA segment designated A" and outlined by a broken line, which activates the FIBRO genomic record, causing the cell to differentiate into a FIBROBLAST CELL.

[0082] Reference is now made to Fig. 5B, which is a simplified schematic diagram, illustrating cellular differentiation mediated by the "Genomic Records" concept. Fig. 5B depicts

2 cells in an organism, designated CELL A and CELL B, each having a GENOME. It is appreciated that since CELL A and CELL B are cells in the same organism, the GENOME of CELL A is identical to that of CELL B. Despite having an identical GENOME, CELL A differentiates differently from CELL B, due to activation of different genomic records in these two cells. In CELL A the FIBRO GENOMIC RECORD is activated, causing CELL A to differentiate into a FIBROBLAST CELL, whereas in CELL B the BONE GENOMIC RECORD is activated, causing the CELL B to differentiate into a BONE CELL. The cause for activation of different genomic records in these two cells is the different maternal short RNA which they both received: CELL A received a maternal short RNA segment designated A" which activated genomic record FIBRO, whereas CELL B received a maternal short RNA segment designated B" which activated genomic record BONE.

[0083] Reference is now made to Fig. 6 which is a schematic diagram illustrating a "genomically programmed cell differentiation" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma.

[0084] A cell designated CELL A divides into 2 cells designated CELL B and CELL C. CELL A, CELL B and CELL C each com-

prise a GENOME, which GENOME comprises a plurality of GENOMIC RECORDS. It is appreciated that since CELL A, CELL B and CELL C are cells in the same organism, the GENOME of these cells, and the GENOMIC RECORDS comprised therein, are identical.

[0085] As described above with reference to Fig. 5B, at its inception, CELL A receives a maternal short RNA segment, designated A" and marked by a broken line, which activates the FIBRO genomic record, thereby causing CELL A to differentiate into a FIBROBLAST CELL. However, Fig. 6 shows further details of the genomic records: each cell genomic record also comprises two short genomic sequences, referred to here as Daughter Cell Genomic Addresses. Blocks designated B and C are Daughter Cell Genomic Addresses of the FIBRO Genomic Record. At cell division, each parent cell transcribes two short RNA segments, corresponding to the two Daughter Cell Genomic Addresses of the Genomic Record of that parent cell, and transfers one to each of its two daughter cells. CELL A of Fig. 6 transcribes and transfers to its two respective daughter cells, two short RNA segments, outlined by a broken line and designated B" and C", corresponding to daughter cell genomic addresses designated B and C comprised in the

FIBRO genomic record.

[0086] CELL B therefore receives the above mentioned maternal short RNA segment designated B", which binds complementarily to genomic address designated B of genomic record BONE, thereby activating this genomic record, which in turn causes CELL B to differentiate into a BONE CELL. Similarly, CELL C receives the above mentioned maternal short RNA segment designated C", which binds complementarily to genomic address designated C of genomic record CARTIL., thereby activating this genomic record, which in turn causes CELL C to differentiate into a CARTILAGE CELL.

[0087] It is appreciated that the mechanism illustrated by Fig. 6 enables an unlimited lineage of cells to divide into daughter cells containing the same DNA, and to determine the cell-fate of these daughter cells. For example, when CELL B and CELL C divide into their respective daughter cells (not shown), they will transfer short RNA segments designated D" & E", and F" & G" respectively, to their respective daughter cells. The cell fate of each of these daughter cells would be determined by the identity of the maternal short RNA segment they receive, which would determine the genomic record activated.

[0088] Reference is now made to Fig. 7 which is a schematic diagram illustrating a "genomically programmed cell-specific protein expression modulation" concept of the conceptual model of the present invention, addressing the genomic differentiation enigma.

[0089] Cell A receives a maternal short RNA segment designated A", which activates a genomic record designated FIBRO, by anti-sense binding to a binding site "header" of this genomic record, designated A. Genomic record FIBRO encodes 3 short RNA segments, designated 1, 2 and 4 respectively, which modulate expression of target genes designated GENE1, GENE2 and GENE4 respectively. Modulation of expression of these genes results in CELL A differentiating into a FIBROBLAST CELL.

[0090] Reference is now made to Fig. 8 which is a simplified diagram illustrating a mode by which genes of a novel group of genes of the present invention, modulate expression of known target genes.

[0091] The novel genes of the present invention are micro RNA (miRNA)-like, regulatory RNA genes, modulating expression of known target genes. This mode of modulation is common to other known miRNA genes, as described hereinabove with reference to the background of the invention

section.

[0092] GAM GENE and TARGET GENE are two human genes contained in the DNA of the human genome.

[0093] GAM GENE encodes a GAM PRECURSOR RNA. However, similar to other miRNA genes, and unlike most ordinary genes, its RNA, GAM PRECURSOR RNA, does not encode a protein.

[0094] GAM PRECURSOR RNA folds onto itself, forming GAM FOLDED PRECURSOR RNA. As Fig.8 illustrates, GAM FOLDED PRECURSOR RNA forms a "hairpin structure", folding onto itself. As is well known in the art, this "hairpin structure", is typical genes of the miRNA genes, and is due to the fact that nucleotide sequence of the first half of the RNA of a gene in this group is an accurate or partial inversed-reversed sequence of the nucleotide sequence of its second half. By "inversed-reversed"is meant a sequence which is reversed and wherein each nucleotide is replaced by a complimentary nucleotide, as is well known in the art (e.g. ATGGC is the inversed-reversed sequence of GCCAT).

[0095] An enzyme complex, designated DICER COMPLEX, "dices" the GAM FOLDED PRECURSOR RNA into a single stranded RNA segment, about 22 nucleotides long, designated GAM

RNA. As is known in the art, "dicing" of the hairpin structured RNA precursor into shorter RNA segments about 22 nucleotides long by a Dicer type enzyme is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins.

[0096] TARGET GENE encodes a corresponding messenger RNA, designated TARGET RNA. This TARGET RNA comprises 3 regions: a 5" untranslated region, a protein coding region and a 3" untranslated region, designated 5"UTR, PROTEIN CODING and 3"UTR respectively.

[0097] GAM RNA binds complementarily a BINDING SITE, located on the 3"UTR segment of TARGET RNA. This complementarily binding is due to the fact that the nucleotide sequence of GAM RNA is an accurate or partial inversed-reversed sequence of the nucleotide sequence of BINDING SITE.

[0098] The complimentary binding of GAM RNA to BINDING SITE inhibits translation of TARGET RNA into TARGET PROTEIN. TARGET PROTEIN is therefore outlined by a broken line.

[0099] It is appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to GAM genes of the present invention is in fact common to all other miRNA genes. A specific complimen-

tary binding site has been demonstrated only for Lin-4 and Let-7. All the other newly discovered miRNA genes (over 300) are also believed by those skilled in the art to modulate expression of other genes by complimentary binding, although specific complimentary binding sites for these genes have not yet been found (Ruvkun G., "Perspective: Glimpses of a tiny RNA world", Science 294 ,779 (2001)). The present invention discloses a novel group of genes, the GAM genes, belonging to the miRNA genes group, and for which a specific complimentary binding has been determined.

[0100] Reference is now made to Fig. 9 which is a simplified block diagram illustrating a bioinformatic gene detection system capable of detecting genes of the novel group of genes of the present invention, which system is constructed and operative in accordance with a preferred embodiment of the present invention.

[0101] A centerpiece of the present invention is a bioinformatic gene detection engine 100, which is a preferred implementation of a mechanism capable of bioinformatically detecting genes of the novel group of genes of the present invention.

[0102] The function of the bioinformatic gene detection engine

100 is as follows: it receives three types of input, expressed RNA data 102, sequenced DNA data 104, and protein function data 106, performs a complex process of analysis of this data as elaborated below, and based on this analysis produces output of a bioinformatically detected group of novel genes designated 108.

[0103] Expressed RNA data 102 comprises published expressed sequence tags (EST) data, published mRNA data, as well as other sources of published RNA data. Sequenced DNA data 104 comprises alphanumeric data describing sequenced genomic data, which preferably includes annotation data such as location of known protein coding regions relative to the sequenced data. Protein function data 106 comprises scientific publications reporting studies which elucidated physiological function known proteins, and their connection, involvement and possible utility in treatment and diagnosis of various diseases. Expressed RNA data 102, sequenced DNA data 104 may preferably be obtained from data published by the National Center for Bioinformatics (NCBI) at the National Institute of Health (NIH), as well as from various other published data sources. Protein function data 106 may preferably be obtained from any one of numerous relevant published data

sources, such as the Online Mendelian Inherited Disease In Man (OMIM(TM)) database developed by John Hopkins University, and also published by NCBI.

[0104] Prior to actual detection of bioinformatically detected novel genes 108 by the bioinformatic gene detection engine 100, a process of bioinformatic gene detection engine training & validation designated 110 takes place. This process uses the known miRNA genes as a training set (some 200 such genes have been found to date using biological laboratory means), to train the bioinformatic gene detection engine 100 to bioinformatically recognize miRNA-like genes, and their respective potential target binding sites. Bioinformatic gene detection engine training & validation 110 is further describe hereinbelow with reference to Fig. 10.

[0105] The bioinformatic gene detection engine 100 comprises several modules which are preferably activated sequentially, and are described as follows:

[0106] A non-coding genomic sequence detector 112 operative to bioinformatically detect non-protein coding genomic sequences. The non-coding genomic sequence detector 112 is further described hereinbelow with reference to Figs. 11A and 11B.

[0107] A hairpin detector 114 operative to bioinformatically detect genomic "hairpin-shaped" sequences, similar to GAM FOLDED PRECURSOR of Fig. 8. The hairpin detector 114 is further described hereinbelow with reference to Figs. 12A and 12B.

[0108] A dicer-cut location detector 116 operative to bioinformatically detect the location on a hairpin shaped sequence which is enzymatically cut by DICER COMPLEX of Fig. 8. The dicer-cut location detector 116 is further described hereinbelow with reference to Fig. 13A.

[0109] A target-gene binding-site detector 118 operative to bioinformatically detect target genes having binding sites, the nucleotide sequence of which is partially complementary to that of a given genomic sequence, such as a sequence cut by DICER COMPLEX of Fig. 8. The target-gene binding-site detector 118 is further described hereinbelow with reference to Figs. 14A and 14B.

[0110] A function & utility analyzer 120 operative to analyze function and utility of target genes, in order to identify target genes which have a significant clinical function and utility. The function & utility analyzer 120 is further described hereinbelow with reference to Fig. 15.

[0111] Hardware implementation of the bioinformatic gene de-

tection engine 100 is important, since significant computing power is preferably required in order to perform the computation of bioinformatic gene detection engine 100 in reasonable time and cost.

[0112] For example, it is estimated that a using a powerful 8-processor server (e.g. DELL POWEREDGE (TM) 8450, 8 XEON (TM) 550MHz processors, 8 GB RAM), over 6 years (!) of computing time are required to detect all MIR genes in the human EST data, together with their respective binding sites.

[0113] Various computer hardware and software configurations may be utilized in order to address this computation challenge, as is known in the art. A preferred embodiment of the present invention may preferably comprise a hardware configuration, comprising a cluster of one hundred PCs (PENTIUM (TM) IV, 1.7GHz, with 40GB storage each), connected by Ethernet to 7 servers (2-CPU, XEON (TM) 1.2-2.2GHz, with ~200GB storage each), combined with an 8-processor server (8-CPU, Xeon 550Mhz w/ 8GB RAM) connected via 2 HBA fiber-channels to an EMC CLARIION (TM) 100-disks, 3.6 Terabyte storage device. A preferred embodiment of the present invention may also preferably comprise a software configuration which utilizes a com-

mercial database software program, such as MICROSOFT (TM) SQL Server 2000. Using such preferred hardware and software configuration, may reduce computing time required to detect all MIR genes in the human EST data, and their respective binding sites, from 6 years to 45 days.

[0114] It is appreciated that the abovementioned hardware configuration is not meant to be limiting, and is given as an illustration only. The present invention may be implemented in a wide variety of hardware and software configurations.

[0115] The present invention discloses 1675 novel genes of the GAM group of genes, which have been detected bioinformatically, as described hereinbelow with reference to Figs. 24 through 1699, and 7 novel genes of the GR group of genes, which have been detected bioinformatically, as described hereinbelow with reference to Figs. 1700 through 1706. Laboratory confirmation of 4 bioinformatically predicted genes of the GAM group of genes, and 2 bioinformatically predicted genes of the GR group of genes, is described hereinbelow with reference to Figs. 21A through 23.

[0116] Reference is now made to Fig. 10 which is a simplified flowchart illustrating operation of a mechanism for train-

ing of a computer system to recognize the novel genes of the present invention. This mechanism is a preferred implementation of the bioinformatic gene detection engine training & validation 110 described hereinabove with reference to Fig. 9.

[0117] Bioinformatic gene detection engine training & validation 110 of Fig. 9 begins by training the bioinformatic gene detection engine to recognize known miRNA genes, as designated by numeral 122. This training step comprises hairpin detector training & validation 124, further described hereinbelow with reference to Fig. 12 A, dicer-cut location detector training & validation 126, further described hereinbelow with reference to Fig. 13A and 13B, and target-gene binding-site detector training & validation 128, further described hereinbelow with reference to Fig. 14A.

[0118] Next, the bioinformatic gene detection engine 100 is used to bioinformatically detect sample novel genes, as designated by numeral 130. An example of a sample novel gene thus detected is described hereinbelow with reference to Fig. 21.

[0119] Finally, wet lab experiments are preferably conducted in order to validate expression and preferably function the

sample novel genes detected by the bioinformatic gene detection engine 100 in the previous step. An example of wet-lab validation of the abovementioned sample novel gene bioinformatically detected by the system is described hereinbelow with reference to Figs. 22A and 22B.

[0120] Reference is now made to Fig. 11A which is a simplified block diagram of a preferred implementation of the non-coding genomic sequence detector 112 described hereinabove with reference to Fig. 9. Non-protein coding genomic sequence detector 112 of Fig. 9 preferably receives as input at least two types of published genomic data: expressed RNA data 102, including EST data and mRNA data, and sequenced DNA data 104. After its initial training, indicated by numeral 134, and based on the above-mentioned input data, the non-protein coding genomic sequence detector 112 produces as output a plurality of non-protein coding genomic sequences 136. Preferred operation of the non-protein coding genomic sequence detector 112 is described hereinbelow with reference to Fig. 11B.

[0121] Reference is now made to Fig. 11B which is a simplified flowchart illustrating a preferred operation of the non-coding genomic sequence detector 112 of Fig. 9. Detec-

tion of non-protein coding genomic sequences to be further analyzed by the system generally preferably progresses in one of the following two paths.

[0122] A first path for detecting non-protein coding genomic sequences begins by receiving a plurality of known RNA sequences, such as EST data. Each RNA sequence is first compared to all known protein-coding sequences, in order to select only those RNA sequences which are non-protein coding. This can preferably be performed by BLAST comparison of the RNA sequence to known protein coding sequences. The abovementioned BLAST comparison to the DNA preferably also provides the localization of the RNA on the DNA.

[0123] Optionally, an attempt may be made to "expand" the non-protein RNA sequences thus found, by searching for transcription start and end signals, upstream and downstream of location of the RNA on the DNA respectively, as is well known in the art.

[0124] A second path for detecting non-protein coding genomic sequences starts by receiving DNA sequences. The DNA sequences are parsed into non protein coding sequences, based on published DNA annotation data: extracting those DNA sequences which are between known protein coding

sequences. Next, transcription start and end signals are sought. If such signals are found, and depending on their "strength", probable expressed non-protein coding genomic sequences are yielded.

[0125] Reference is now made to Fig. 12A which is a simplified block diagram of a preferred implementation of the hairpin detector 114 described hereinabove with reference to Fig. 9.

[0126] The goal of the hairpin detector 114 is to detect "hairpin" shaped genomic sequences, similar to those of known miRNA genes. As mentioned hereinabove with reference to Fig. 8, a "hairpin" genomic sequence refers to a genomic sequence which "folds onto itself" forming a hairpin like shape, due to the fact that nucleotide sequence of the first half of the nucleotide sequence is an accurate or

[0127] The hairpin detector 114 of Fig. 9 receives as input a plurality of non-protein coding genomic sequences 136 of Fig. 11A, and after a phase of hairpin detector training & validation 124 of Fig. 10, is operative to detect and output "hairpin shaped" sequences found in the input expressed non-protein coding sequences, designated by numeral 138.

[0128] The phase of hairpin detector training & validation 124 is

an iterative process of applying the hairpin detector 114 to known hairpin shaped miRNA genes, calibrating the hairpin detector 114 such that it identifies the training set of known hairpins, as well as sequences which are similar thereto. Preferred operation of the hairpin detector 114 is described hereinbelow with reference to Fig. 12B.

[0129] Reference is now made to Fig. 12B which is a simplified flowchart illustrating a preferred operation of the hairpin detector 114 of Fig. 9.

[0130] A hairpin structure is a two dimensional folding structure, resulting from the nucleotide sequence pattern: the nucleotide sequence of the first half of the hairpin sequence is an inversed-reversed sequence of the second half thereof. Different methodologies are known in the art for detection of various two dimensional and three dimensional hairpin structures.

[0131] In a preferred embodiment of the present invention, the hairpin detector 114 initially calculates possible 2-dimensional (2D) folding patterns of a given one of the non-protein coding genomic sequences 136, preferably using a 2D folding algorithm based on free-energy calculation, such as the Zucker algorithm, as is well known in the art.

[0132] Next, the hairpin detector 114 analyzes the results of the 2D folding, in order to determine the presence, and location of hairpin structures. A 2D folding algorithm typically provides as output a listing of the base-pairing of the 2D folded shape, i.e. a listing of which all two pairs of nucleotides in the sequence which will bond. The goal of this second step, is to asses this base-pairing listing, in order to determine if it describes a hairpin type bonding pattern.

[0133] The hairpin detector 114 then assess those hairpin structures found by the previous step, comparing them to hairpins of known miRNA genes, using various parameters such as length, free-energy, amount and type of mismatches, etc. Only hairpins that bear statistically significant resemblance of the population of hairpins of known miRNAs, according to the abovementioned parameters are accepted.

[0134] Lastly, the hairpin detector 114 attempts to select those hairpin structures which are as stable as the hairpins of know miRNA genes. This may be achieved in various manners. A preferred embodiment of the present invention utilizes the following methodology comprising three steps:

[0135] First, the hairpin detector 114 attempts to group potential hairpins into "families" of closely related hairpins. As is known in the art, a free-energy calculation algorithm, typically provides multiple "versions" each describing a different possible 2D folding pattern for the given genomic sequence, and the free energy of such possible folding. The hairpin detector 114 therefore preferably assesses all hairpins found on all "versions", grouping hairpins which appear in different versions, but which share near identical locations into a common "family" of hairpins. For example, all hairpins in different versions, the center of which is within 7 nucleotides of each other may preferably be grouped to a single "family".

[0136] Next, hairpin "families" are assessed, in order to select only those families which represent hairpins that are as stable as those of known miRNA hairpins. For example, preferably only families which are represented in at least 65% of the free-energy calculation 2D folding versions, are considered stable.

[0137] Finally, an attempt is made to select the most suitable hairpin from each selected family. For example, preferably the hairpin which appears in more versions than other hairpins, and in versions the free-energy of which is

lower, may be selected.

[0138] Reference is now made to Fig. 13A which is a simplified block diagram of a preferred implementation of the dicer-cut location detector 116 described hereinabove with reference to Fig. 9.

[0139] The goal of the dicer-cut location detector 116 is to detect the location in which DICER COMPLEX of Fig. 8, comprising the enzyme Dicer, would "dice" the given hairpin sequence, similar to GAM FOLDED PRECURSOR RNA, yielding GAM RNA both of Fig. 8.

[0140] The dicer-cut location detector 116 of Fig. 9 therefore receives as input a plurality of hairpins on genomic sequences 138 of Fig. 12A, which were calculated by the previous step, and after a phase of dicer-cut location detector training & validation 126 of Fig. 10, is operative to detect a respective plurality of dicer-cut sequences from hairpins 140, one for each hairpin.

[0141] In a preferred embodiment of the present invention, the dicer-cut location detector 116 preferably uses a Support Vector Machine (SVM) trained on the known dicer-cut locations of known miRNA genes, in order to predict dicer-cut locations of novel GAM genes. Dicer-cut location detector training & validation 126, which is further described

hereinbelow with reference to Fig. 13B.

[0142] Reference is now made to Fig. 13B which is a simplified flowchart illustrating a preferred implementation of dicer-cut location detector training & validation 126 of Fig. 13A.

[0143] The general goal of the dicer-cut location detector training & validation 126 is to analyze known hairpin shaped miRNA-precursors and their respective dicer-cut miRNA, in order to determine a common pattern to the dicer-cut location of the known miRNA genes. Once such a common pattern is deduced, it may preferably be used by the dicer cut location detector 116, in detecting the predicted dicer-cut sequences from hairpins 140, from the respective hairpins on genomic sequences 138, all of Fig. 13A.

[0144] First, the dicer-cut location of all known miRNA genes is obtained and studied, so as to train the dicer cut location detector 116: for each of the known miRNA, the location of the miRNA relative to its hairpin-shaped miRNA-precursor is noted.

[0145] The 3" and 5" ends of the dicer-cut location for each of the known miRNA genes is represented relative to , which is known for known miRNA genes, is noted relative to the above, as well as to the nucleotides in each location along the hairpin. Frequency of identity of nucleotides, and nu-

cleotide-pairing, relative to their location in the hairpin, and relative to the known dicer-cut location in the known miRNA genes is analyzed and modeled.

[0146] Different techniques are well known in the art for analysis of existing pattern from a given "training set" of species belonging to a genus, which techniques are then capable, to a certain degree, to detect similar patterns in other species not belonging to the training-set genus. Such techniques include, but are not limited to neural networks, Bayesian networks, Support Vector Machines (SVM), Genetic Algorithms, Markovian modeling, and others, as is well known in the art.

[0147] The dicer-cut location detector module uses standard machine learning techniques (*31*) to predict the 5" and 3" ends of the miRNA excised, or "diced" by the Dicer enzyme from the miRNA hairpin shaped precursor, based on known pairs of miRNA-precursors and their respective resulting miRNAs. The nucleotide sequences of 128 distinct published miRNA were used for training and evaluation of the dicer-cut location detector module (*1, 3*). These included 112 MIR genes for which sequences of both final miRNA and miRNA precursor sequences were published, and 16 MIR genes, for which only the final miRNA se-

quence was published, without the miRNA precursor sequence. In case of the latter, approximations of the precursor hairpin sequences were manually assessed from the DNA sequence in which the MIR was located, using the Zucker-Turner algorithm. The 128 known miRNAs were split into two disjoint sets, used for training and for evaluation respectively.

[0148] Using the abovementioned training set, a Support Vector Machine (SVM) (*32*) predictor was implemented, which tests every possible nucleotide on a hairpin as a candidate for being the 5" end or the 3" end of a miRNA. The training set of the published miRNA precursor sequences was used for training two separate SVM classifiers, one which produces a model for the 5" end of a miRNA relative to its hairpin precursor, and one which produces a similar model for its 3" end. The models take into account the distance of the respective (3" or 5") end of the miRNA from the hairpin"s loop, the nucleotides at its vicinity and the local "bulge" (i.e. base-pair mismatch) structure.

[0149] Performance of the resulting predictor, evaluated on the abovementioned validation set of 64 published miRNAs, was found to be as follows: in 70% of known miRNAs 5"-end location was determined within up to 2 nu-

cleotides.

[0150] Reference is now made to Fig. 13C which is a simplified flowchart illustrating operation of dicer-cut location detector 116 of Fig. 9, constructed and operative in accordance with a preferred embodiment of the present invention.

[0151] The dicer cut location detector 116 is a machine learning computer program module, which is trained on recognizing dicer-cut location of known miRNA genes, and based on this training, is operable to detect dicer cut location of novel GAM FOLDED PRECURSOR RNA. In a preferred embodiment of the present invention, the dicer-cut location module preferably utilizes a Support Vector Machine (SVM) approach, as is well known in the art.

[0152] When assessing a novel GAM precursor, all 19-24 nucleotide long segments comprised in the GAM precursor are initially considered as "potential GAMs", since the dicer-cut location is initially unknown.

[0153] For each such potential GAM, its 3" end is scored by the 3" end recognition classifier, and its 5" end is scored by the 5" end recognition classifier.

[0154] Scores of the abovementioned two classifiers are integrated, yielding an integrated score for each "potential

GAM".

[0155] The integrated score is then evaluated as follows: (a) the "potential GAM" having the highest score is taken to be the most probably GAM, and (b) if the integrated score of this "potential GAM" is higher than a pre-defined threshold, then the potential GAM is accepted as the PREDICTED GAM.

[0156] Reference is now made to Fig. 14A which is a simplified block diagram of a preferred implementation of the target-gene binding-site detector 118 described hereinabove with reference to Fig. 9. The goal of the target-gene binding-site detector 118 is to detect a BINDING SITE of Fig. 8, located in an untranslated region of the RNA of a known gene, the nucleotide sequence of which BINDING SITE is at least partially complementary to that of a GAM RNA of Fig. 8, thereby determining that the above-mentioned known gene is a target gene of GAM of Fig. 8.

[0157] The target-gene binding-site detector 118 of Fig. 9 therefore receives as input a plurality of dicer-cut sequences from hairpins 140 of Fig. 13A which were calculated by the previous step, and a plurality of potential target gene sequences 142 which derive sequence DNA data 104 of Fig. 9, and after a phase of target-gene binding-

site detector training & validation 128 of Fig. 10, is operative to detect target-genes having binding site/s 144 the nucleotide sequence of which is at least partially complementary to that of each of the plurality of dicer-cut sequences from hairpins 140. Preferred operation of the target-gene binding-site detector is further described hereinbelow with reference to Fig. 14B.

[0158] Reference is now made to Fig. 14B which is a simplified flowchart illustrating a preferred operation of the target-gene binding-site detector 118 of Fig. 9. In a preferred embodiment of the present invention, the target-gene binding-site detector 118 first performs a BLAST comparison of the nucleotide sequence of each of the plurality of dicer-cut sequences from hairpins 140, to the potential target gene sequences 142, in order to find crude potential matches. Blast results are then filtered to results which are similar to those of known binding sites (e.g. binding sites of miRNA genes Lin-4 and Let-7 to target genes Lin-14, Lin-41, Lin 28 etc.). Next the binding site is expanded, checking if nucleotide sequenced immediately adjacent to the binding site found by BLAST, may improve the match. Suitable binding sites, then are computed for free-energy and spatial structure. The results are ana-

lyzed, selecting only those binding sites, which have free-energy and spatial structure similar to that of known binding sites.

[0159] Reference is now made to Fig. 15 which is a simplified flowchart illustrating a preferred operation of the function & utility analyzer 120 described hereinabove with reference to Fig. 9. The goal of the function & utility analyzer 120 is to determine if a potential target gene is in fact a valid clinically useful target gene. Since a potential novel GAM gene binding a binding site in the UTR of a target gene is understood to inhibit expression of that target gene, and if that target gene is shown to have a valid clinical utility, then in such a case it follows that the potential novel gene itself also has a valid useful function which is the opposite of that of the target gene.

[0160] The function & utility analyzer 120 preferably receives as input a plurality of potential novel target genes having binding-site/s 144, generated by the target-gene binding-site detector 118, both of Fig. 14A. Each potential gene, is evaluated as follows:

[0161] First the system first checks to see if the function of the potential target gene is scientifically well established. Preferably, this can be achieved bioinformatically by

searching various published data sources presenting information on known function of proteins. Many such data sources exist and are published as is well known in the art.

[0162] Next, for those target genes the function of which is scientifically known and is well documented, the system then checks if scientific research data exists which links them to known diseases. For example, a preferred embodiment of the present invention utilizes the OMIM(TM) database published by NCBI, which summarizes research publications relating to genes which have been shown to be associated with diseases.

[0163] Finally, the specific possible utility of the target gene is evaluated. While this process too may be facilitated by bioinformatic means, it might require human evaluation of published scientific research regarding the target gene, in order to determine the utility of the target gene to the diagnosis and or treatment of specific disease. Only potential novel genes, the target-genes of which have passed all three examinations, are accepted as novel genes.

[0164] Reference is now made to FIG. 16, which is a simplified diagram describing a novel bioinformatically detected group of regulatory genes, referred to here as Genomic

Record (GR) genes, that encode an "operon-like" cluster of novel miRNA-like genes, each modulating expression of a plurality of target genes, the function and utility of which target genes is known.

[0165] GR GENE (Genomic Record Gene) is gene of a novel, bioinformatically detected group of regulatory, non protein coding, RNA genes. The method by which GR is detected is described hereinabove with reference to FIGS. 6-15.

[0166] GR GENE encodes an RNA molecule, typically several hundred nucleotides long, designated GR PRECURSOR RNA.

[0167] GR PRECURSOR RNA folds spatially, as illustrated by GR FOLDED PRECURSOR RNA, into a plurality of what is known in the art as "hair-pin" structures. The nucleotide sequence of GR PRECURSOR RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, thereby causing formation of a plurality of "hairpin" structures, as is well known in the art.

[0168] GR FOLDED PRECURSOR RNA is naturally processed by cellular enzymatic activity, into 3 separate hairpin shaped RNA segments, each corresponding to GAM PRECURSOR RNA of Fig. 8, designated GAM1 PRECURSOR, GAM2 PRE-

CURSOR and GAM3 PRECURSOR respectively.

[0169] The above mentioned GAM precursors, are diced by Dicer of FIG. 8, yielding short RNA segments of about 22 nucleotides in length, each corresponding to GAM RNA of FIG. 8, designated GAM1, GAM2 and GAM3 respectively.

[0170] GAM1, GAM2 and GAM3 each bind complementarily to binding sites located in untranslated regions of respective target genes, designated GAM1-TARGET RNA, GAM2-TARGET RNA and GAM3-TARGET RNA respectively. This binding inhibits translation of the respective target proteins designated GAM1-TARGET PROTEIN, GAM2-TARGET PROTEIN and GAM3-TARGET PROTEIN respectively.

[0171] The structure of GAM genes comprised in a GR GENE, and their mode of modulation of expression of their respective target genes is described hereinabove with reference to Fig. 8. The bioinformatic approach to detection of GAM genes comprised in a GR GENE is described hereinabove with reference to Figs. 9 through 15. The present invention discloses 147 novel genes of the GR group of genes, which have been detected bioinformatically, as described hereinbelow with reference to Figs. 551 through 697. Laboratory confirmation of 3 genes of the GR group of

genes is described hereinbelow with reference to Figs. 21A through 23.

[0172] In summary, the current invention discloses a very large number of novel GR genes, each of which encodes a plurality of GAM genes, which in turn may modulate expression of a plurality of target proteins. It is appreciated therefore that the function of GR genes is in fact similar to that of the Genomic Records concept of the present invention addressing the differentiation enigma, described hereinabove with reference to Fig. 7.

[0173] Reference is now made to Fig. 17 which is a simplified diagram illustrating a mode by which genes of a novel group of operon-like genes, described hereinabove with reference to Fig. 16 of the present invention, modulate expression of other such genes, in a cascading manner.

[0174] GR1 GENE and GR2 GENE are two genes of the novel group of operon-like genes designated GR of Fig. 16. As is typical of genes of the GR group of genes, GR1 and GR2 each encode a long RNA precursor, which in turn folds into a folded RNA precursor comprising multiple hairpin shapes, and is cut into respective separate hairpin shaped RNA segments, each of which RNA segments being diced to yield a gene of a group of genes designated GAM of Fig.

8. In this manner GR1 yields GAM1, GAM2 and GAM3, and GR2 yields GAM4, GAM5 and GAM6.

[0175] As Fig. 17 shows, GAM 3 which derives from GR1, binds a binding site located adjacent to GR2 GENE, thus modulating expression of GR2, thereby invoking expression of GAM4, GAM5 and GAM6 which derive from GR2.

[0176] It is appreciated that the mode of modulation of expression presented by Fig. 17 enables an unlimited "cascading effect" in which a GR gene comprises multiple GAM genes, each of which may modulate expression of other GR genes, each such GR gene comprising additional GAM genes, etc., whereby eventually certain GAM genes modulate expression of target proteins. This mechanism is in accord with the conceptual model of the present invention addressing the differentiation enigma, described hereinabove with specific reference to Figs. 6 and 7.

[0177] Reference is now made to Fig. 18 which is a block diagram illustrating an overview of a methodology for finding novel genes and operon-like genes of the present invention, and their respective functions.

[0178] According to a preferred embodiment of the present invention, the methodology to finding novel genes of the present invention and their function comprises of the fol-

lowing major steps:

[0179] First, genes of the novel group of genes of the present invention, referred to here as GAM genes, are located and their function elicited by detecting target proteins they bind and the function of those target proteins, as described hereinabove with reference to Figs. 9 through 15.

[0180] Next, genes of a novel group of operon-like genes of the present invention, referred to here as GR genes, are located, by locating clusters of proximally located GAM genes, based on the previous step.

[0181] Consequently, the hierarchy of GR and GAM genes is elicited: binding sites for non-protein-binding GAM genes comprised in each GR gene found, are sought adjacent to other GR genes. When found, such a binding site indicates that the connection between the GAM and the GR the expression of which it modulates, and thus the hierarchy of the GR genes and the GAM genes they comprise.

[0182] Lastly, the function of GR genes and GAM genes which are "high" in the hierarchy, i.e. GAM genes which modulate expression of other GR genes rather than directly modulating expression of target proteins, may be deduced. A preferred approach is as follows: The function of protein-modulating GAM genes is deducible from the proteins

which they modulate, provided that the function of these target proteins are known. The function of "higher" GAM genes may be deduced by comparing the function of protein-modulating GAM genes, with the hierarchical relationships by which the "higher" GAM genes are connected to the protein-modulating GAM genes. For example, given a group of several protein-modulating GAM genes, which collectively cause a protein expression pattern typical of a certain cell-type, then a "higher" GAM gene is sought which modulates expression of GR genes which perhaps modulate expression of other genes which eventually modulate expression of the given group of protein-modulating GAM genes. The "higher" GAM gene found in this manner, is taken to be responsible for differentiation of that cell-type, as per the conceptual model of the invention described hereinabove with reference to Fig. 6.

[0183] Reference is now made to Fig. 19 which is a block diagram illustrating different utilities of genes of the novel group of genes of the present invention referred to here as GAM genes and GR genes.

[0184] The present invention discloses a first plurality of novel genes referred to here as GAM genes, and a second plurality of operon-like genes referred to here as GR genes,

each of the GR genes encoding a plurality of GAM genes. The present invention further discloses a very large number of known target-genes, which are bound by, and the expression of which is modulated by each of the novel genes of the present invention. Published scientific data referenced by the present invention provides specific, substantial, and credible evidence that the abovementioned target genes modulated by novel genes of the present invention, are associated with various diseases. Specific novel genes of the present invention, target genes thereof and diseases associated therewith, are described hereinbelow with reference to Figs. 23 through 30,022. It is therefore appreciated that a function of GAM genes and GR genes of the present invention is modulation of expression of target genes related to known diseases, and that therefore utilities of novel genes of the present invention include diagnosis and treatment of the abovementioned diseases. Fig. 19 describes various types of diagnostic and therapeutic utilities of novel genes of the present invention.

[0185] A utility of novel genes of the present invention is detection of GAM genes and of GR genes. It is appreciated that since GAM genes and GR genes modulate expression of

disease related target genes, that detection of expression of GAM genes in clinical scenarios associated with said diseases is a specific, substantial and credible utility. Diagnosis of novel genes of the present invention may preferably be implemented by RNA expression detection techniques, including but not limited to biochips, as is well known in the art. Diagnosis of expression of genes of the present invention may be useful for research purposes, in order to further understand the connection between the novel genes of the present invention and the abovementioned related diseases, for disease diagnosis and prevention purposes, and for monitoring disease progress.

[0186] Another utility of novel genes of the present invention is anti-GAM gene therapy, a mode of therapy which allows up regulation of a disease related target-gene of a novel GAM gene of the present invention, by lowering levels of the novel GAM gene which naturally inhibits expression of that target gene. This mode of therapy is particularly useful with respect to target genes which have been shown to be under-expressed in association with a specific disease. Anti-GAM gene therapy is further discussed hereinbelow with reference to Figs. 20A and 20B.

[0187] A further utility of novel genes of the present invention is GAM replacement therapy, a mode of therapy which achieves down regulation of a disease related target-gene of a novel GAM gene of the present invention, by raising levels of the GAM gene which naturally inhibits expression of that target gene. This mode of therapy is particularly useful with respect to target genes which have been shown to be over-expressed in association with a specific disease. GAM replacement therapy involves introduction of supplementary GAM gene products into a cell, or stimulation of a cell to produce excess GAM gene products. GAM replacement therapy may preferably be achieved by transfecting cells with an artificial DNA molecule encoding a GAM gene, which causes the cells to produce the GAM gene product, as is well known in the art.

[0188] Yet a further utility of novel genes of the present invention is modified GAM therapy. Disease conditions are likely to exist, in which a mutation in a binding site of a GAM gene prevents natural GAM gene to effectively bind inhibit a disease related target-gene, causing up regulation of that target gene, and thereby contributing to the disease pathology. In such conditions, a modified GAM gene is designed which effectively binds the mutated GAM bind-

ing site, i.e. is an effective anti-sense of the mutated GAM binding site, and is introduced in disease effected cells. Modified GAM therapy is preferably achieved by transfecting cells with an artificial DNA molecule encoding the modified GAM gene, which causes the cells to produce the modified GAM gene product, as is well known in the art.

[0189] An additional utility of novel genes of the present invention is induced cellular differentiation therapy. As aspect of the present invention is finding genes which determine cellular differentiation, as described hereinabove with reference to Fig. 18. Induced cellular differentiation therapy comprises transfection of cell with such GAM genes thereby determining their differentiation as desired. It is appreciated that this approach may be widely applicable, inter alia as a means for auto transplantation harvesting cells of one cell-type from a patient, modifying their differentiation as desired, and then transplanting them back into the patient. It is further appreciated that this approach may also be utilized to modify cell differentiation in vivo, by transfecting cells in a genetically diseased tissue with a cell-differentiation determining GAM gene, thus stimulating these cells to differentiate appropriately.

[0190] Reference is now made to Figs. 20A and 20B, simplified

diagrams which when taken together illustrate anti-GAM gene therapy mentioned hereinabove with reference to Fig. 19. A utility of novel genes of the present invention is anti-GAM gene therapy, a mode of therapy which allows up regulation of a disease related target-gene of a novel GAM gene of the present invention, by lowering levels of the novel GAM gene which naturally inhibits expression of that target gene. Fig. 20A shows a normal GAM gene, inhibiting translation of a target gene of GAM gene, by binding to a BINDING SITE found in an untranslated region of TARGET RNA, as described hereinabove with reference to Fig. 8.

[0191] Fig. 20B shows an example of anti-GAM gene therapy. ANTI-GAM RNA is short artificial RNA molecule the sequence of which is an anti-sense of GAM RNA. Anti-GAM treatment comprises transfecting diseased cells with ANTI-GAM RNA, or with a DNA encoding thereof. The ANTI-GAM RNA binds the natural GAM RNA, thereby preventing binding of natural GAM RNA to its BINDING SITE. This prevents natural translation inhibition of TARGET RNA by GAM RNA, thereby up regulating expression of TARGET PROTEIN.

[0192] It is appreciated that anti-GAM gene therapy is particu-

larly useful with respect to target genes which have been shown to be under-expressed in association with a specific disease.

[0193] Reference is now made to Fig. 21A which is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention. Fig. 21A shows the nucleotide sequence of a known human non-protein coding EST (Expressed Sequence Tag), identified as EST72223. It is appreciated that the sequence of this EST comprises sequences of one known miRNA gene, identified as MIR98, and of one novel GAM gene, referred to here as GAM25, detected by the bioinformatic gene detection system of the present invention, described hereinabove with reference to Fig. 9.

[0194] Reference is now made to Figs. 21B and 21C that are pictures of laboratory results, which when taken together demonstrate laboratory confirmation of expression of the bioinformatically detected novel gene of Fig. 21A. Reference is now made to Fig. 21B which is a Northern blot analysis of MIR-98 and EST72223 transcripts. MIR-98 and EST72223 were reacted with MIR-98 and GAM25 probes as indicated in the figure. It is appreciated that the probes of both MIR-98 and GAM24 reacted with EST72223, indi-

cating that EST72223 contains the sequences of MIR-98 and of GAM25. It is further appreciated that the probe of GAM25 does not cross-react with MIR-98.

[0195] Reference is now made to Fig. 21C. A Northern blot analysis of EST72223 and MIR-98 transfections were performed, subsequently marking RNA by the MIR-98 and GAM25 probes . Left, Northern reacted with MIR-98, Right, Northern reacted with GAM25. The molecular Sizes of EST72223, MIR-98 and GAM25 are indicated by arrows. Hela are control cells that have not been introduced to exogenous RNA. EST and MIR-98 Transfections are RNA obtained from Hela transfected with EST72223 and MIR-98, respectively. MIR-98 and EST are the transcripts used for the transfection experiment. The results indicate that EST72223, when transfected into Hela cells, is cut yielding known miRNA gene MIR-98 and novel miRNA gene GAM25.

[0196] Reference is now made to Fig. 21D, which is a Northern blot of a lisate experiment with MIR-98 and GAM25. Northern blot analysis of hairpins in EST72223 . Left, Northern reacted with predicted Mir-98 hairpin probe, Right, Northern reacted with predicted GAM25 hairpin probe. The molecular size of EST Is indicated by arrow.

The molecular sizes of Mir-98 and GAM25 are 80nt and 100nt, respectively as indicated by arrows. The 22nt molecular marker is indicated by arrow. 1-Hela lysate; 2-EST incubated 4h with Hela lysate; 3-EST without lysate; 4-Mir transcript incubated 4h with Hela lysate; 5-Mir transcript incubated overnight with Hela lysate; 6- Mir transcript without lysate; 7-RNA extracted from Hela cells following transfection with Mir transcript.

[0197] Technical methods used in experiments, the results of which are depicted in Figs. 21B, 21C and 21D are as follows:

[0198] *Transcript preparations:* Transcripts were prepared of EST72223(TIGR) and of MIR98 and predicted GAM4 within it, and of EST7929020(IMAGE) and of predicted GAM3 within it.. Transcripts were prepared by m ^{7}G(5')ppp(5')G-capping reaction by using mMessage mMachine kit (Ambion) according to the manufacture"s protocol. Briefly, PCR products amplified with specific primers contain T7 promoter at the 5" end and T3 promoter at the 3"end were prepared from each DNA. The purified PCR products were transcribed with T7 polymerase. Transcript products were 725nt (EST72223), 102nt (MIR98), 125nt (GAM4) and 70nt (GAM3)

long.EST72223 was PCR amplified with T7-EST 72223 forward primer:5"-TAATACGACTCACTATAGGCCCTTATTAGAGGATTCTGCT-3" and T3-EST72223 reverse primer: 5"-AATTAACCCTCACTAAAGGTTTTTTTTTCCTGAGACAGAGT-3".MIR98 was PCR amplified using EST72223 as a template with T7MIR98 forward primer: 5-"TAATACGACTCACTATAGGGTGAGGTAGTAAGTTGTATTGTT-3"and T3MIR98 reverse primer: 5"-AATTAACCCTCACTAAAGGGAAAGTAGTAAGTTGTATAGTT-3".GAM4 was PCR amplified using EST72223 as a template with GAM4 forward primer: 5"-GAGGCAGGAGAATTGCTTGA- 3" and T3-EST72223 reverse primer:5"-AATTAACCCTCACTAAAGGCCTGAGACAGAGTCTTGCTC-3".GAM3 was PCR amplified using EST7929020 as a template with T7-GAM3 forward primer: 5"-TAATACGACTCACTATAGGGTCAGAGTGAACAGGCAACC-3" and T3-GAM3 reverse primer:5"-AATTAACCCTCACTAAAGGGTCAGATGAGTAGGTTGCGAA -3".

[0199] *Transfection procedure:* Capped RNA transcripts were incubated at 30Â°C in supplemented Hela S100 obtained from

4C Biotech, Seneffe, Belgium. The Hela S100 was supplemented by dialysis to a final concentration of 20mM Hepes, 100mM KCl, 2.5mM $MgCl_2$, 0.5mM DTT, 20% glycerol and protease inhibitor cocktail tablets (Complete mini Roche Molecular Biochemicals) and kept at 4Â°C for one month. After addition of all components, final concentrations were 100mM capped target RNA, 2mM ATP, 0.2mM GTP, 500U/ml RNasin, 30?g/ml creatine kinase, 25mM creatine phosphate, 2.5mM DTT and 50% S100 extract. Cleavage reaction was stopped at different time points (0, 0.5, 1, 4, 24h) by the addition of 8 volumes of proteinase K buffer (200Mm Tris-Hcl, pH 7.5, 25m M EDTA, 300mM NaCl, and 2% SDS) and incubated at 65Â°C for 15min. Proteinase K, dissolved in 50mM Tris-HCl, pH 8, 5m M $CaCl_2$, and 50% glycerol, was added to a final concentration of 0.6 mg/ml. Samples were subjected to phenol/chloroform extraction. Pellets were dissolved in water and kept frozen. Samples were analyzed after addition of two volumes TBE-Urea buffer (1xTBE, 7M urea) on a TBE-Urea PAGE gel.

[0200] *Target RNA cleavage assay*: Digoxigenin (DIG) labeled antisense transcripts was prepared from purified PCR product of MIR98 by using a DIG RNA labeling kit with T3 poly-

merase (Roche Molecular Biochemicals) according to the manufacturer"s protocol. PCR primers are detailed above. Labeled transcript was 102nt long.Digoxigenin (DIG) labeled PCR was prepared for GAM4 by using a DIG PCR labeling kit (Roche Molecular Biochemicals) according to the manufacture"s protocol. PCR primers are detailed above. Labeled PCR was 145bp long.3"-DIG-tailed oligo ssDNA antisense probes, containing DIG-dUTP and dATP at an average tail length of 50 nucleotides were prepared with the DIG Oligonucleotide Labeling Kit (Roche Molecular Biochemicals) from 100pmole oligonucleotides. Labeled predicted "correct"GAM3 oligonucleotide is 5"-GAGTAGGTTGCGAAAATTTTCTCC-3" and labeled "incorrect"GAM3 oligonucleotide is 5"-CCCATTTTGTAGGTTGCCTGTTCA-3", and predicted "correct"GAM4 oligonucleotide is 5"-CTTCCTGGGTTCAAGCAATT-3", while labeled "incorrect"GAM4 oligonucleotide is 5"-. CTGAGACA-GAGTCTTGCTCTG-3". Labeled oligo probes were 24nt long.

[0201] *Northern analysis:* RNA samples were boiled for 3 min before loading on a segmented, top 6%, bottom 13% polyacrylamide gel, containing 7M urea and 1xTBE. Gels were

run in 1xTBE at a constant voltage of 250V and then transferred onto a positively charged nylon membrane (Biodyne PLUS 0.45?m, Pall) and UV cross-linked. Hybridization was performed overnight with DIG-labeled probes at 42^0C in DIG Easy-Hyb buffer (Roche). Membranes were washed twice with 2xSSC and 0.1% SDS for 10 min. at 42^0C and then washed twice with 0.5xSSC and 0.1% SDS for 5 min at 42^0C. The membrane was then developed by using a DIG luminescent detection kit (Roche) using anti-DIG and CSPD reaction, according to the manufacturer"s protocol.

[0202] It is appreciated that the data presented in Figs. 21A, 21B, 21C and 21D, when taken together validate the function of the bioinformatic gene detection engine 100 of Fig. 9. Fig. 21A shows a novel GAM gene bioinformatically detected by the bioinformatic gene detection engine 100, and Figs. 21B, 21C and 21D show laboratory confirmation of the expression of this novel gene. This is in accord with the engine training and validation methodology described hereinabove with reference to Fig. 10.

[0203] Reference is now made to Fig. 22A which is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention. Fig.

22A shows the nucleotide sequence of a known human non-protein coding EST (Expressed Sequence Tag), identified as EST 7929020. It is appreciated that the sequence of this EST comprises sequences of two novel GAM genes, referred to here as GAM24 and GAM26, detected by the bioinformatic gene detection system of the present invention, described hereinabove with reference to Fig. 9.

[0204] Reference is now made to Fig. 22B which presents pictures of laboratory results, that demonstrate laboratory confirmation of expression of the bioinformatically detected novel gene of Fig. 22A. Northern blot analysis of hairpins in EST7929020. Left, Northern reacted with predicted GAM26 hairpin probe, Right, Northern reacted with predicted GAM24 hairpin probe. The molecular size of EST is indicated by arrow. The molecular sizes of GAM24 and GAM26 are 60nt, as indicated by arrow. The 22nt molecular marker is indicated by arrow. 1-Hela lysate; 2- EST incubated 4h with Hela lysate ; 3- EST incubated overnight with Hela lysate; 4-EST without lysate; 5-GAM transcript; 6- GAM 22nt marker;7-GAM PCR probe; 8-RNA from control Hela cells; 9-RNA extracted from Hela cells following transfection with EST.

[0205] Reference is now made to Fig. 22C which is a picture of a

Northern blot confirming Endogenous expression of bioinformatically detected gene GAM25 of Fig. 22A from in Hela cells. Northern was reacted with a predicted GAM26 hairpin probe. The molecular size of EST7929020 is indicated. The molecular sizes of GAM26 is 58nt, as indicated. A 19nt DNA oligo molecular marker is indicated. Endogenous expression of GAM26 in Hela total RNA fraction and in S-100 fraction is indicated by arrows. 1-GAM26 transcript; 2- GAM25 DNA oligo marker; 3-RNA from control Hela cells; 4-RNA extracted from Hela cells following transfection with EST; 5- RNA extracted from S-100 Hela lysate.

[0206] Reference is now made to Fig. 23A which is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention. Fig. 23A shows the nucleotide sequence of a known human non-protein coding EST (Expressed Sequence Tag), identified as EST 1388749. It is appreciated that the sequence of this EST comprises sequence of a novel GAM gene, referred to here as GAM27, detected by the bioinformatic gene detection system of the present invention, described hereinabove with reference to Fig. 9.

[0207] Reference is now made to Fig. 23B which is a picture of

Northern blot analysis, confirming expression of novel bioinformatically detected gene GAM26, and natural processing thereof from EST1388749. Northern reacted with predicted GAM27 hairpin probe. The molecular size of EST is indicated by arrow. The molecular sizes of GAM27 is 130nt, as indicated by arrow. The 22nt molecular marker is indicated by arrow. 1-Hela lysate; 2-EST incubated 4h with Hela lysate; 3- EST incubated overnight with Hela lysate; 4-EST without lysate; 5-GAM transcript; 6- GAM 22nt marker; 7-GAM PCR probe.

[0208] Fig. 8 further provides a conceptual description of a novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 25 (GAM25) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0209] GAM25 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM25 was detected is described hereinabove with reference to Figs. 2-8.

[0210] GAM25 gene, herein designated GAM GENE, and GAM25 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0211] GAM25 gene, herein designated GAM GENE, encodes a GAM25 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM25 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM25 precursor RNA is designated SEQ ID:1, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1 is located at position 464492 relative to contig NT_011799.10, on chromosome X.

[0212] GAM25 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM25 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0213] An enzyme complex designated DICER COMPLEX, dices the GAM25 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, into GAM25 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM25 RNA is designated SEQ ID:2, and is provided hereinbelow with reference to the sequence listing part.

[0214] GAM25 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM25 target RNA, herein designated GAM TARGET RNA. GAM25 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0215] GAM25 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM25 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM25 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM25 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM25 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0216] The complementary binding of GAM25 RNA, herein designated GAM RNA, to target binding sites on GAM25 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM25 target RNA, herein designated GAM TARGET RNA, into GAM25 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0217] It is appreciated that GAM25 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM25 target genes. The mRNA of each one of this plurality of GAM25 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM25 RNA, herein designated GAM RNA, and which when bound by GAM25 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM25 target proteins.

[0218] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM25 gene, herein designated GAM GENE, on one or more GAM25 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not

yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0219] It is yet further appreciated that specific functions, and accordingly utilities, of GAM25 correlate with, and may be deduced from, the identity of the target genes which GAM25 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0220] Nucleotide sequences of the GAM25 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM25 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM25 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM25 are further described hereinbelow with reference to Table Table1.

[0221] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM25 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0222] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

27 (GAM27) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0223] GAM27 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM27 was detected is described hereinabove with reference to Figs. 2-8.

[0224] GAM27 gene, herein designated GAM GENE, and GAM27 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0225] GAM27 gene, herein designated GAM GENE, encodes a GAM27 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM27 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM27 precursor RNA is designated SEQ ID:511, and is provided hereinbelow with reference to the sequence listing part.

[0226] GAM27 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM27 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0227] An enzyme complex designated DICER COMPLEX, dices the GAM27 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM27 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM27 RNA is designated SEQ ID:2187, and is provided hereinbelow with reference to the sequence listing part.

[0228] GAM27 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM27 target RNA, herein designated GAM TARGET RNA. GAM27 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding re-

gion and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0229] GAM27 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM27 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM27 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM27 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM27 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0230] The complementary binding of GAM27 RNA, herein desig-

nated GAM RNA, to target binding sites on GAM27 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM27 target RNA, herein designated GAM TARGET RNA, into GAM27 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0231] It is appreciated that GAM27 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM27 target genes. The mRNA of each one of this plurality of GAM27 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM27 RNA, herein designated GAM RNA, and which when bound by GAM27 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM27 target proteins.

[0232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM27 gene, herein designated GAM GENE, on one or more GAM27 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As

mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0233] It is yet further appreciated that specific functions, and accordingly utilities, of GAM27 correlate with, and may be deduced from, the identity of the target genes which GAM27 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0234] Nucleotide sequences of the GAM27 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM27 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM27 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM27 are further described hereinbelow with reference to Table Table1.

[0235] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM27 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0236] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 28 (GAM28) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0237] GAM28 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM28 was detected is described hereinabove with reference to Figs. 2-8.

[0238] GAM28 gene, herein designated GAM GENE, and GAM28 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0239] GAM28 gene, herein designated GAM GENE, encodes a GAM28 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM28 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nu-

cleotide sequence identical or highly similar to the nucleotide sequence of GAM28 precursor RNA is designated SEQ ID:1, and is provided hereinbelow with reference to the sequence listing part.

[0240] GAM28 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM28 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0241] An enzyme complex designated DICER COMPLEX, dices the GAM28 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM28 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM28 RNA is

designated SEQ ID:1674, and is provided hereinbelow with reference to the sequence listing part.

[0242] GAM28 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM28 target RNA, herein designated GAM TARGET RNA. GAM28 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0243] GAM28 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM28 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM28 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM28 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM28 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0244] The complementary binding of GAM28 RNA, herein designated GAM RNA, to target binding sites on GAM28 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM28 target RNA, herein designated GAM TARGET RNA, into GAM28 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0245] It is appreciated that GAM28 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM28 target genes. The mRNA of each one of this plurality of GAM28 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM28 RNA, herein designated GAM RNA, and which when bound by GAM28 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM28 target proteins.

[0246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM28 gene, herein designated GAM GENE, on one or more GAM28 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0247] It is yet further appreciated that specific functions, and accordingly utilities, of GAM28 correlate with, and may be deduced from, the identity of the target genes which GAM28 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0248] Nucleotide sequences of the GAM28 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM28 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM28 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM28 are further described hereinbelow with reference to Table Table1.

[0249] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM28 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0250] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 29 (GAM29) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0251] GAM29 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM29 was detected is described hereinabove with reference to Figs. 2-8.

[0252] GAM29 gene, herein designated GAM GENE, and GAM29 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0253] GAM29 gene, herein designated GAM GENE, encodes a GAM29 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM29 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM29 precursor RNA is designated SEQ ID:2, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2 is located at position 5411280 relative to contig NT_005334.11, on chromosome 2.

[0254] GAM29 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM29 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[0255] An enzyme complex designated DICER COMPLEX, dices the GAM29 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM29 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM29 RNA is designated SEQ ID:1675, and is provided hereinbelow with reference to the sequence listing part.

[0256] GAM29 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM29 target RNA, herein designated GAM TARGET RNA. GAM29 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0257] GAM29 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM29 target RNA, herein desig-

nated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM29 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM29 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM29 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0258] The complementary binding of GAM29 RNA, herein designated GAM RNA, to target binding sites on GAM29 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM29 target RNA, herein designated GAM TARGET RNA, into GAM29 target protein, herein desig-

nated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0259] It is appreciated that GAM29 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM29 target genes. The mRNA of each one of this plurality of GAM29 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM29 RNA, herein designated GAM RNA, and which when bound by GAM29 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM29 target proteins.

[0260] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM29 gene, herein designated GAM GENE, on one or more GAM29 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those

skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0261] It is yet further appreciated that specific functions, and accordingly utilities, of GAM29 correlate with, and may be deduced from, the identity of the target genes which GAM29 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0262] Nucleotide sequences of the GAM29 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM29 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM29 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM29 are further described hereinbelow with reference to Table Table1.

[0263] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM29 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0264] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 30 (GAM30) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0265] GAM30 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM30 was detected is described hereinabove with reference to Figs. 2-8.

[0266] GAM30 gene, herein designated GAM GENE, and GAM30 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0267] GAM30 gene, herein designated GAM GENE, encodes a GAM30 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM30 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM30 precursor RNA is designated SEQ ID:3, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:3 is located at position 2349674 relative to contig

NT_021907.13, on chromosome 1.

[0268] GAM30 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM30 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0269] An enzyme complex designated DICER COMPLEX, dices the GAM30 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM30 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM30 RNA is designated SEQ ID:1676, and is provided hereinbelow with reference to the sequence listing part.

[0270] GAM30 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM30 target RNA, herein designated GAM TARGET RNA. GAM30 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0271] GAM30 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM30 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM30 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM30 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM30 target RNA, herein designated GAM TARGET RNA. It is further

appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0272] The complementary binding of GAM30 RNA, herein designated GAM RNA, to target binding sites on GAM30 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM30 target RNA, herein designated GAM TARGET RNA, into GAM30 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0273] It is appreciated that GAM30 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM30 target genes. The mRNA of each one of this plurality of GAM30 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM30 RNA, herein designated GAM RNA, and which when bound by GAM30 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM30 target proteins.

[0274] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM30 gene, herein designated GAM GENE, on one or more GAM30 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0275] It is yet further appreciated that specific functions, and accordingly utilities, of GAM30 correlate with, and may be deduced from, the identity of the target genes which GAM30 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0276] Nucleotide sequences of the GAM30 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM30 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM30 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM30 are further described hereinbelow with reference to Table Table1.

[0277] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM30 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0278] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 31 (GAM31) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0279] GAM31 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM31 was detected is described hereinabove with reference to Figs. 2-8.

[0280] GAM31 gene, herein designated GAM GENE, and GAM31 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0281] GAM31 gene, herein designated GAM GENE, encodes a GAM31 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM31 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM31 precursor RNA is designated SEQ ID:4, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:4 is located at position 3434852 relative to contig NT_009714.13, on chromosome 12.

[0282] GAM31 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98678, which mouse homolog is detected in mouse EST accession BG288438.1.

[0283] GAM31 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM31 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0284] An enzyme complex designated DICER COMPLEX, dices the GAM31 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM31 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM31 RNA is designated SEQ ID:1677, and is provided hereinbelow with reference to the sequence listing part.

[0285] GAM31 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM31 target RNA, herein designated GAM TARGET RNA. GAM31 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0286] GAM31 RNA, herein designated GAM RNA, binds comple-

mentarily to one or more target binding sites located in untranslated regions of GAM31 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM31 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM31 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM31 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0287] The complementary binding of GAM31 RNA, herein designated GAM RNA, to target binding sites on GAM31 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits

translation of GAM31 target RNA, herein designated GAM TARGET RNA, into GAM31 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0288] It is appreciated that GAM31 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM31 target genes. The mRNA of each one of this plurality of GAM31 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM31 RNA, herein designated GAM RNA, and which when bound by GAM31 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM31 target proteins.

[0289] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM31 gene, herein designated GAM GENE, on one or more GAM31 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known

miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0290] It is yet further appreciated that specific functions, and accordingly utilities, of GAM31 correlate with, and may be deduced from, the identity of the target genes which GAM31 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0291] Nucleotide sequences of the GAM31 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM31 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM31 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM31 are further described hereinbelow with reference to Table Table1.

[0292] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM31 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0293] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 32 (GAM32) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0294] GAM32 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM32 was detected is described hereinabove with reference to Figs. 2-8.

[0295] GAM32 gene, herein designated GAM GENE, and GAM32 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0296] GAM32 gene, herein designated GAM GENE, encodes a GAM32 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM32 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM32 precursor RNA is designated SEQ ID:5, and is provided hereinbelow with reference to

the sequence listing part. Nucleotide sequence SEQ ID:5 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[0297] GAM32 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM32 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0298] An enzyme complex designated DICER COMPLEX, dices the GAM32 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM32 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM32 RNA is designated SEQ ID:1678, and is provided hereinbelow with

reference to the sequence listing part.

[0299] GAM32 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM32 target RNA, herein designated GAM TARGET RNA. GAM32 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0300] GAM32 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM32 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM32 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM32 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM32 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0301] The complementary binding of GAM32 RNA, herein designated GAM RNA, to target binding sites on GAM32 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM32 target RNA, herein designated GAM TARGET RNA, into GAM32 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0302] It is appreciated that GAM32 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM32 target genes. The mRNA of each one of this plurality of GAM32 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM32 RNA, herein designated GAM RNA, and which when bound by GAM32 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM32 tar-

get proteins.

[0303] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM32 gene, herein designated GAM GENE, on one or more GAM32 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0304] It is yet further appreciated that specific functions, and accordingly utilities, of GAM32 correlate with, and may be deduced from, the identity of the target genes which GAM32 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0305] Nucleotide sequences of the GAM32 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM32 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM32 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM32 are further described hereinbelow with reference to Table Table1.

[0306] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM32 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0307] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 33 (GAM33) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0308] GAM33 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM33 was detected is described hereinabove with reference to Figs. 2-8.

[0309] GAM33 gene, herein designated GAM GENE, and GAM33

target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0310] GAM33 gene, herein designated GAM GENE, encodes a GAM33 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM33 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM33 precursor RNA is designated SEQ ID:6, and is provided hereinbelow with reference to the sequence listing part.

[0311] GAM33 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM33 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0312] An enzyme complex designated DICER COMPLEX, dices the GAM33 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, into GAM33 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM33 RNA is designated SEQ ID:1679, and is provided hereinbelow with reference to the sequence listing part.

[0313] GAM33 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM33 target RNA, herein designated GAM TARGET RNA. GAM33 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0314] GAM33 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM33 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM33 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM33 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM33 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0315] The complementary binding of GAM33 RNA, herein designated GAM RNA, to target binding sites on GAM33 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM33 target RNA, herein designated GAM TARGET RNA, into GAM33 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0316] It is appreciated that GAM33 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM33 target genes. The mRNA of each one of this plurality of GAM33 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM33 RNA, herein designated GAM RNA, and which when bound by GAM33 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM33 target proteins.

[0317] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM33 gene, herein designated GAM GENE, on one or more GAM33 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not

yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0318] It is yet further appreciated that specific functions, and accordingly utilities, of GAM33 correlate with, and may be deduced from, the identity of the target genes which GAM33 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0319] Nucleotide sequences of the GAM33 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM33 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM33 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM33 are further described hereinbelow with reference to Table Table1.

[0320] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM33 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0321] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

34 (GAM34) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0322] GAM34 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM34 was detected is described hereinabove with reference to Figs. 2-8.

[0323] GAM34 gene, herein designated GAM GENE, and GAM34 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0324] GAM34 gene, herein designated GAM GENE, encodes a GAM34 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM34 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM34 precursor RNA is designated SEQ ID:7, and is provided hereinbelow with reference to the sequence listing part.

[0325] GAM34 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM34 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0326] An enzyme complex designated DICER COMPLEX, dices the GAM34 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM34 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM34 RNA is designated SEQ ID:1680, and is provided hereinbelow with reference to the sequence listing part.

[0327] GAM34 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM34 target RNA, herein designated GAM TARGET RNA. GAM34 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding re-

gion and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0328] GAM34 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM34 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM34 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM34 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM34 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0329] The complementary binding of GAM34 RNA, herein desig-

nated GAM RNA, to target binding sites on GAM34 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM34 target RNA, herein designated GAM TARGET RNA, into GAM34 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0330] It is appreciated that GAM34 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM34 target genes. The mRNA of each one of this plurality of GAM34 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM34 RNA, herein designated GAM RNA, and which when bound by GAM34 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM34 target proteins.

[0331] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM34 gene, herein designated GAM GENE, on one or more GAM34 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As

mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0332] It is yet further appreciated that specific functions, and accordingly utilities, of GAM34 correlate with, and may be deduced from, the identity of the target genes which GAM34 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0333] Nucleotide sequences of the GAM34 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM34 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM34 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM34 are further described hereinbelow with reference to Table Table1.

[0334] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM34 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0335] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 35 (GAM35) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0336] GAM35 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM35 was detected is described hereinabove with reference to Figs. 2-8.

[0337] GAM35 gene, herein designated GAM GENE, and GAM35 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0338] GAM35 gene, herein designated GAM GENE, encodes a GAM35 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM35 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nu-

cleotide sequence identical or highly similar to the nucleotide sequence of GAM35 precursor RNA is designated SEQ ID:8, and is provided hereinbelow with reference to the sequence listing part.

[0339] GAM35 has 5 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[0340] SEQ ID:99544 detected in mouse EST Accession BF141241.1.

[0341] SEQ ID:98081 detected in mouse EST Accession AI019032.1.

[0342] SEQ ID:98082 detected in mouse EST Accession AA611182.1.

[0343] SEQ ID:98158 detected in mouse EST Accession BE850845.1.

[0344] SEQ ID:98159 detected in mouse EST Accession BF452989.1.

[0345] GAM35 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM35 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0346] An enzyme complex designated DICER COMPLEX, dices the GAM35 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM35 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM35 RNA is designated SEQ ID:1681, and is provided hereinbelow with reference to the sequence listing part.

[0347] GAM35 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM35 target RNA, herein designated GAM TARGET RNA. GAM35 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding re-

gion and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0348] GAM35 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM35 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM35 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM35 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM35 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0349] The complementary binding of GAM35 RNA, herein desig-

nated GAM RNA, to target binding sites on GAM35 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM35 target RNA, herein designated GAM TARGET RNA, into GAM35 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0350] It is appreciated that GAM35 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM35 target genes. The mRNA of each one of this plurality of GAM35 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM35 RNA, herein designated GAM RNA, and which when bound by GAM35 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM35 target proteins.

[0351] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM35 gene, herein designated GAM GENE, on one or more GAM35 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As

mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0352] It is yet further appreciated that specific functions, and accordingly utilities, of GAM35 correlate with, and may be deduced from, the identity of the target genes which GAM35 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0353] Nucleotide sequences of the GAM35 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM35 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM35 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM35 are further described hereinbelow with reference to Table Table1.

[0354] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM35 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0355] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 36 (GAM36) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0356] GAM36 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM36 was detected is described hereinabove with reference to Figs. 2-8.

[0357] GAM36 gene, herein designated GAM GENE, and GAM36 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0358] GAM36 gene, herein designated GAM GENE, encodes a GAM36 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM36 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nu-

cleotide sequence identical or highly similar to the nucleotide sequence of GAM36 precursor RNA is designated SEQ ID:9, and is provided hereinbelow with reference to the sequence listing part.

[0359] GAM36 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99445, which mouse homolog is detected in mouse EST accession BI246688.1.

[0360] GAM36 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM36 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0361] An enzyme complex designated DICER COMPLEX, dices the GAM36 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM36 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA seg-

ment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM36 RNA is designated SEQ ID:1682, and is provided hereinbelow with reference to the sequence listing part.

[0362] GAM36 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM36 target RNA, herein designated GAM TARGET RNA. GAM36 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0363] GAM36 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM36 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM36 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM36 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM36 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0364] The complementary binding of GAM36 RNA, herein designated GAM RNA, to target binding sites on GAM36 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM36 target RNA, herein designated GAM TARGET RNA, into GAM36 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0365] It is appreciated that GAM36 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM36 target genes. The mRNA of each one of this plu-

rality of GAM36 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM36 RNA, herein designated GAM RNA, and which when bound by GAM36 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM36 target proteins.

[0366] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM36 gene, herein designated GAM GENE, on one or more GAM36 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0367] It is yet further appreciated that specific functions, and accordingly utilities, of GAM36 correlate with, and may be deduced from, the identity of the target genes which GAM36 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0368] Nucleotide sequences of the GAM36 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM36 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM36 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM36 are further described hereinbelow with reference to Table Table1.

[0369] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM36 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0370] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 37 (GAM37) gene, which modulates expression of respective target genes thereof, the function and utility of which

target genes is known in the art.

[0371] GAM37 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM37 was detected is described hereinabove with reference to Figs. 2-8.

[0372] GAM37 gene, herein designated GAM GENE, and GAM37 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0373] GAM37 gene, herein designated GAM GENE, encodes a GAM37 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM37 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM37 precursor RNA is designated SEQ ID:10, and is provided hereinbelow with reference to the sequence listing part.

[0374] GAM37 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM37 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0375] An enzyme complex designated DICER COMPLEX, dices the GAM37 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM37 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM37 RNA is designated SEQ ID:1683, and is provided hereinbelow with reference to the sequence listing part.

[0376] GAM37 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM37 target RNA, herein designated GAM TARGET RNA. GAM37 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0377] GAM37 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM37 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM37 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM37 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM37 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0378] The complementary binding of GAM37 RNA, herein designated GAM RNA, to target binding sites on GAM37 target RNA, herein designated GAM TARGET RNA, such as BIND-

ING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM37 target RNA, herein designated GAM TARGET RNA, into GAM37 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0379] It is appreciated that GAM37 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM37 target genes. The mRNA of each one of this plurality of GAM37 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM37 RNA, herein designated GAM RNA, and which when bound by GAM37 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM37 target proteins.

[0380] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM37 gene, herein designated GAM GENE, on one or more GAM37 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site

has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0381] It is yet further appreciated that specific functions, and accordingly utilities, of GAM37 correlate with, and may be deduced from, the identity of the target genes which GAM37 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0382] Nucleotide sequences of the GAM37 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM37 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM37 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM37 are further described hereinbelow with reference to Table Table1.

[0383] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM37 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0384] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 38 (GAM38) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0385] GAM38 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM38 was detected is described hereinabove with reference to Figs. 2-8.

[0386] GAM38 gene, herein designated GAM GENE, and GAM38 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0387] GAM38 gene, herein designated GAM GENE, encodes a GAM38 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM38 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM38 precursor RNA is designated

SEQ ID:11, and is provided hereinbelow with reference to the sequence listing part.

[0388] GAM38 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM38 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0389] An enzyme complex designated DICER COMPLEX, dices the GAM38 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM38 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM38 RNA is designated SEQ ID:1684, and is provided hereinbelow with reference to the sequence listing part.

[0390] GAM38 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM38 target RNA, herein designated GAM TARGET RNA. GAM38 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0391] GAM38 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM38 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM38 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM38 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM38 tar-

get RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0392] The complementary binding of GAM38 RNA, herein designated GAM RNA, to target binding sites on GAM38 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM38 target RNA, herein designated GAM TARGET RNA, into GAM38 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0393] It is appreciated that GAM38 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM38 target genes. The mRNA of each one of this plurality of GAM38 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM38 RNA, herein designated GAM RNA, and which when bound by GAM38 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM38 target proteins.

[0394] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM38 gene, herein designated GAM GENE, on one or more GAM38 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0395] It is yet further appreciated that specific functions, and accordingly utilities, of GAM38 correlate with, and may be deduced from, the identity of the target genes which GAM38 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0396] Nucleotide sequences of the GAM38 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM38 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM38 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM38 are further described hereinbelow with reference to Table Table1.

[0397] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM38 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0398] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 39 (GAM39) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0399] GAM39 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM39 was detected is described hereinabove with reference to Figs. 2-8.

[0400] GAM39 gene, herein designated GAM GENE, and GAM39 target gene, herein designated GAM TARGET GENE, are

human genes contained in the human genome.

[0401] GAM39 gene, herein designated GAM GENE, encodes a GAM39 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM39 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM39 precursor RNA is designated SEQ ID:12, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:12 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[0402] GAM39 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM39 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0403] An enzyme complex designated DICER COMPLEX, dices

the GAM39 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM39 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM39 RNA is designated SEQ ID:1685, and is provided hereinbelow with reference to the sequence listing part.

[0404] GAM39 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM39 target RNA, herein designated GAM TARGET RNA. GAM39 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0405] GAM39 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM39 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM39

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM39 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM39 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0406] The complementary binding of GAM39 RNA, herein designated GAM RNA, to target binding sites on GAM39 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM39 target RNA, herein designated GAM TARGET RNA, into GAM39 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0407] It is appreciated that GAM39 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM39 target genes. The mRNA of each one of this plurality of GAM39 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM39 RNA, herein designated GAM RNA, and which when bound by GAM39 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM39 target proteins.

[0408] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM39 gene, herein designated GAM GENE, on one or more GAM39 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complemen-

tary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0409] It is yet further appreciated that specific functions, and accordingly utilities, of GAM39 correlate with, and may be deduced from, the identity of the target genes which GAM39 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0410] Nucleotide sequences of the GAM39 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM39 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM39 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM39 are further described hereinbelow with reference to Table Table1.

[0411] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM39 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0412] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 40 (GAM40) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0413] GAM40 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM40 was detected is described hereinabove with reference to Figs. 2-8.

[0414] GAM40 gene, herein designated GAM GENE, and GAM40 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0415] GAM40 gene, herein designated GAM GENE, encodes a GAM40 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM40 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM40 precursor RNA is designated SEQ ID:13, and is provided hereinbelow with reference to the sequence listing part.

[0416] GAM40 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM40 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0417] An enzyme complex designated DICER COMPLEX, dices the GAM40 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM40 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM40 RNA is designated SEQ ID:1686, and is provided hereinbelow with reference to the sequence listing part.

[0418] GAM40 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM40 target RNA, herein designated GAM TARGET RNA. GAM40 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein

coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0419] GAM40 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM40 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM40 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM40 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM40 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0420] The complementary binding of GAM40 RNA, herein designated GAM RNA, to target binding sites on GAM40 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM40 target RNA, herein designated GAM TARGET RNA, into GAM40 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0421] It is appreciated that GAM40 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM40 target genes. The mRNA of each one of this plurality of GAM40 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM40 RNA, herein designated GAM RNA, and which when bound by GAM40 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM40 target proteins.

[0422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM40 gene, herein designated GAM GENE, on one or more GAM40 target gene, herein designated GAM TARGET

GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0423] It is yet further appreciated that specific functions, and accordingly utilities, of GAM40 correlate with, and may be deduced from, the identity of the target genes which GAM40 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0424] Nucleotide sequences of the GAM40 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM40 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM40 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM40 are further described hereinbelow with reference to Table Table1.

[0425] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM40 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0426] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 41 (GAM41) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0427] GAM41 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM41 was detected is described hereinabove with reference to Figs. 2-8.

[0428] GAM41 gene, herein designated GAM GENE, and GAM41 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0429] GAM41 gene, herein designated GAM GENE, encodes a GAM41 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM41 precursor RNA, herein designated

GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM41 precursor RNA is designated SEQ ID:14, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:14 is located at position 10846648 relative to contig NT_006576.11, on chromosome 5.

[0430] GAM41 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM41 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0431] An enzyme complex designated DICER COMPLEX, dices the GAM41 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM41 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is

catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM41 RNA is designated SEQ ID:1687, and is provided hereinbelow with reference to the sequence listing part.

[0432] GAM41 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM41 target RNA, herein designated GAM TARGET RNA. GAM41 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0433] GAM41 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM41 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM41 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM41 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM41 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0434] The complementary binding of GAM41 RNA, herein designated GAM RNA, to target binding sites on GAM41 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM41 target RNA, herein designated GAM TARGET RNA, into GAM41 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0435] It is appreciated that GAM41 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM41 target genes. The mRNA of each one of this plurality of GAM41 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM41 RNA, herein designated GAM RNA, and which when bound by GAM41 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM41 target proteins.

[0436] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM41 gene, herein designated GAM GENE, on one or more GAM41 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0437] It is yet further appreciated that specific functions, and accordingly utilities, of GAM41 correlate with, and may be

deduced from, the identity of the target genes which GAM41 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0438] Nucleotide sequences of the GAM41 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM41 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM41 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM41 are further described hereinbelow with reference to Table Table1.

[0439] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM41 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0440] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 42 (GAM42) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0441] GAM42 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM42 was detected is described hereinabove with reference to Figs. 2-8.

[0442] GAM42 gene, herein designated GAM GENE, and GAM42 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0443] GAM42 gene, herein designated GAM GENE, encodes a GAM42 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM42 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM42 precursor RNA is designated SEQ ID:15, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:15 is located at position 2183835 relative to contig NT_034383.2, on chromosome 1.

[0444] GAM42 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM42 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0445] An enzyme complex designated DICER COMPLEX, dices the GAM42 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM42 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM42 RNA is designated SEQ ID:1688, and is provided hereinbelow with reference to the sequence listing part.

[0446] GAM42 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM42 target RNA, herein designated GAM TARGET RNA. GAM42 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0447] GAM42 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM42 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM42 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM42 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM42 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0448] The complementary binding of GAM42 RNA, herein designated GAM RNA, to target binding sites on GAM42 target RNA, herein designated GAM TARGET RNA, such as BIND-

ING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM42 target RNA, herein designated GAM TARGET RNA, into GAM42 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0449] It is appreciated that GAM42 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM42 target genes. The mRNA of each one of this plurality of GAM42 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM42 RNA, herein designated GAM RNA, and which when bound by GAM42 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM42 target proteins.

[0450] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM42 gene, herein designated GAM GENE, on one or more GAM42 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site

has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0451] It is yet further appreciated that specific functions, and accordingly utilities, of GAM42 correlate with, and may be deduced from, the identity of the target genes which GAM42 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0452] Nucleotide sequences of the GAM42 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM42 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM42 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM42 are further described hereinbelow with reference to Table Table1.

[0453] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM42 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0454] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 43 (GAM43) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0455] GAM43 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM43 was detected is described hereinabove with reference to Figs. 2-8.

[0456] GAM43 gene, herein designated GAM GENE, and GAM43 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0457] GAM43 gene, herein designated GAM GENE, encodes a GAM43 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM43 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM43 precursor RNA is designated

SEQ ID:16, and is provided hereinbelow with reference to the sequence listing part.

[0458] GAM43 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM43 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0459] An enzyme complex designated DICER COMPLEX, dices the GAM43 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM43 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM43 RNA is designated SEQ ID:1689, and is provided hereinbelow with reference to the sequence listing part.

[0460] GAM43 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM43 target RNA, herein designated GAM TARGET RNA. GAM43 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0461] GAM43 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM43 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM43 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM43 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM43 tar-

get RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0462] The complementary binding of GAM43 RNA, herein designated GAM RNA, to target binding sites on GAM43 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM43 target RNA, herein designated GAM TARGET RNA, into GAM43 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0463] It is appreciated that GAM43 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM43 target genes. The mRNA of each one of this plurality of GAM43 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM43 RNA, herein designated GAM RNA, and which when bound by GAM43 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM43 target proteins.

[0464] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM43 gene, herein designated GAM GENE, on one or more GAM43 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0465] It is yet further appreciated that specific functions, and accordingly utilities, of GAM43 correlate with, and may be deduced from, the identity of the target genes which GAM43 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0466] Nucleotide sequences of the GAM43 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM43 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM43 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM43 are further described hereinbelow with reference to Table Table1.

[0467] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM43 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0468] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 44 (GAM44) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0469] GAM44 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM44 was detected is described hereinabove with reference to Figs. 2-8.

[0470] GAM44 gene, herein designated GAM GENE, and GAM44 target gene, herein designated GAM TARGET GENE, are

human genes contained in the human genome.

[0471] GAM44 gene, herein designated GAM GENE, encodes a GAM44 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM44 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM44 precursor RNA is designated SEQ ID:17, and is provided hereinbelow with reference to the sequence listing part.

[0472] GAM44 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM44 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0473] An enzyme complex designated DICER COMPLEX, dices the GAM44 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM44 RNA, herein desig-

nated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM44 RNA is designated SEQ ID:1690, and is provided hereinbelow with reference to the sequence listing part.

[0474] GAM44 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM44 target RNA, herein designated GAM TARGET RNA. GAM44 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0475] GAM44 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM44 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM44 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM44 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM44 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0476] The complementary binding of GAM44 RNA, herein designated GAM RNA, to target binding sites on GAM44 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM44 target RNA, herein designated GAM TARGET RNA, into GAM44 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0477] It is appreciated that GAM44 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM44 target genes. The mRNA of each one of this plurality of GAM44 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM44 RNA, herein designated GAM RNA, and which when bound by GAM44 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM44 target proteins.

[0478] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM44 gene, herein designated GAM GENE, on one or more GAM44 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny

RNA world, Science 294,779 (2001)).

[0479] It is yet further appreciated that specific functions, and accordingly utilities, of GAM44 correlate with, and may be deduced from, the identity of the target genes which GAM44 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0480] Nucleotide sequences of the GAM44 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM44 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM44 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM44 are further described hereinbelow with reference to Table Table1.

[0481] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM44 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0482] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 45 (GAM45) gene, which modulates expression of respec-

tive target genes thereof, the function and utility of which target genes is known in the art.

[0483] GAM45 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM45 was detected is described hereinabove with reference to Figs. 2-8.

[0484] GAM45 gene, herein designated GAM GENE, and GAM45 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0485] GAM45 gene, herein designated GAM GENE, encodes a GAM45 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM45 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM45 precursor RNA is designated SEQ ID:18, and is provided hereinbelow with reference to the sequence listing part.

[0486] GAM45 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM45 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0487] An enzyme complex designated DICER COMPLEX, dices the GAM45 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM45 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM45 RNA is designated SEQ ID:1691, and is provided hereinbelow with reference to the sequence listing part.

[0488] GAM45 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM45 target RNA, herein designated GAM TARGET RNA. GAM45 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PRO-

TEIN CODING and 3UTR respectively.

[0489] GAM45 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM45 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM45 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM45 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM45 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0490] The complementary binding of GAM45 RNA, herein designated GAM RNA, to target binding sites on GAM45 target

RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM45 target RNA, herein designated GAM TARGET RNA, into GAM45 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0491] It is appreciated that GAM45 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM45 target genes. The mRNA of each one of this plurality of GAM45 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM45 RNA, herein designated GAM RNA, and which when bound by GAM45 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM45 target proteins.

[0492] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM45 gene, herein designated GAM GENE, on one or more GAM45 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background

section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0493] It is yet further appreciated that specific functions, and accordingly utilities, of GAM45 correlate with, and may be deduced from, the identity of the target genes which GAM45 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0494] Nucleotide sequences of the GAM45 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM45 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM45 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM45 are further described hereinbelow with reference to Table Table1.

[0495] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM45 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0496] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 46 (GAM46) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0497] GAM46 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM46 was detected is described hereinabove with reference to Figs. 2-8.

[0498] GAM46 gene, herein designated GAM GENE, and GAM46 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0499] GAM46 gene, herein designated GAM GENE, encodes a GAM46 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM46 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM46 precursor RNA is designated SEQ ID:19, and is provided hereinbelow with reference to the sequence listing part.

[0500] GAM46 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM46 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0501] An enzyme complex designated DICER COMPLEX, dices the GAM46 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM46 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM46 RNA is designated SEQ ID:1692, and is provided hereinbelow with

reference to the sequence listing part.

[0502] GAM46 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM46 target RNA, herein designated GAM TARGET RNA. GAM46 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0503] GAM46 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM46 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM46 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM46 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM46 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0504] The complementary binding of GAM46 RNA, herein designated GAM RNA, to target binding sites on GAM46 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM46 target RNA, herein designated GAM TARGET RNA, into GAM46 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0505] It is appreciated that GAM46 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM46 target genes. The mRNA of each one of this plurality of GAM46 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM46 RNA, herein designated GAM RNA, and which when bound by GAM46 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM46 tar-

get proteins.

[0506] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM46 gene, herein designated GAM GENE, on one or more GAM46 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0507] It is yet further appreciated that specific functions, and accordingly utilities, of GAM46 correlate with, and may be deduced from, the identity of the target genes which GAM46 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0508] Nucleotide sequences of the GAM46 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM46 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM46 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM46 are further described hereinbelow with reference to Table Table1.

[0509] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM46 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0510] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 47 (GAM47) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0511] GAM47 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM47 was detected is described hereinabove with reference to Figs. 2-8.

[0512] GAM47 gene, herein designated GAM GENE, and GAM47

target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0513] GAM47 gene, herein designated GAM GENE, encodes a GAM47 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM47 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM47 precursor RNA is designated SEQ ID:20, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:20 is located at position 4851374 relative to contig NT_022517.13, on chromosome 3.

[0514] GAM47 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM47 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0515] An enzyme complex designated DICER COMPLEX, dices the GAM47 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM47 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM47 RNA is designated SEQ ID:1693, and is provided hereinbelow with reference to the sequence listing part.

[0516] GAM47 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM47 target RNA, herein designated GAM TARGET RNA. GAM47 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0517] GAM47 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM47 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM47 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM47 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM47 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0518] The complementary binding of GAM47 RNA, herein designated GAM RNA, to target binding sites on GAM47 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM47 target RNA, herein designated GAM TARGET RNA, into GAM47 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is there-

fore outlined by a broken line.

[0519] It is appreciated that GAM47 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM47 target genes. The mRNA of each one of this plurality of GAM47 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM47 RNA, herein designated GAM RNA, and which when bound by GAM47 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM47 target proteins.

[0520] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM47 gene, herein designated GAM GENE, on one or more GAM47 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes

by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0521] It is yet further appreciated that specific functions, and accordingly utilities, of GAM47 correlate with, and may be deduced from, the identity of the target genes which GAM47 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0522] Nucleotide sequences of the GAM47 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM47 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM47 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM47 are further described hereinbelow with reference to Table Table1.

[0523] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM47 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0524] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 48 (GAM48) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0525] GAM48 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM48 was detected is described hereinabove with reference to Figs. 2-8.

[0526] GAM48 gene, herein designated GAM GENE, and GAM48 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0527] GAM48 gene, herein designated GAM GENE, encodes a GAM48 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM48 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM48 precursor RNA is designated SEQ ID:21, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:21 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[0528] GAM48 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM48 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0529] An enzyme complex designated DICER COMPLEX, dices the GAM48 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM48 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM48 RNA is designated SEQ ID:1694, and is provided hereinbelow with reference to the sequence listing part.

[0530] GAM48 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM48

target RNA, herein designated GAM TARGET RNA. GAM48 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0531] GAM48 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM48 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM48 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM48 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM48 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites

in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0532] The complementary binding of GAM48 RNA, herein designated GAM RNA, to target binding sites on GAM48 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM48 target RNA, herein designated GAM TARGET RNA, into GAM48 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0533] It is appreciated that GAM48 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM48 target genes. The mRNA of each one of this plurality of GAM48 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM48 RNA, herein designated GAM RNA, and which when bound by GAM48 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM48 target proteins.

[0534] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM48 gene, herein designated GAM GENE, on one or more GAM48 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0535] It is yet further appreciated that specific functions, and accordingly utilities, of GAM48 correlate with, and may be deduced from, the identity of the target genes which GAM48 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0536] Nucleotide sequences of the GAM48 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM48 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM48 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM48 are further described hereinbelow with reference to Table Table1.

[0537] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM48 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0538] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 49 (GAM49) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0539] GAM49 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM49 was detected is described hereinabove with reference to Figs. 2-8.

[0540] GAM49 gene, herein designated GAM GENE, and GAM49 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0541] GAM49 gene, herein designated GAM GENE, encodes a

GAM49 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM49 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM49 precursor RNA is designated SEQ ID:22, and is provided hereinbelow with reference to the sequence listing part.

[0542] GAM49 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM49 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0543] An enzyme complex designated DICER COMPLEX, dices the GAM49 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM49 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured

RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM49 RNA is designated SEQ ID:1695, and is provided hereinbelow with reference to the sequence listing part.

[0544] GAM49 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM49 target RNA, herein designated GAM TARGET RNA. GAM49 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0545] GAM49 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM49 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM49 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM49 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM49 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0546] The complementary binding of GAM49 RNA, herein designated GAM RNA, to target binding sites on GAM49 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM49 target RNA, herein designated GAM TARGET RNA, into GAM49 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0547] It is appreciated that GAM49 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM49 target genes. The mRNA of each one of this plurality of GAM49 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM49 RNA, herein designated GAM RNA, and which when bound by GAM49 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM49 target proteins.

[0548] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM49 gene, herein designated GAM GENE, on one or more GAM49 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0549] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM49 correlate with, and may be deduced from, the identity of the target genes which GAM49 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0550] Nucleotide sequences of the GAM49 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM49 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM49 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM49 are further described hereinbelow with reference to Table Table1.

[0551] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM49 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0552] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 50 (GAM50) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0553] GAM50 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM50 was detected is described hereinabove with reference to Figs. 2-8.

[0554] GAM50 gene, herein designated GAM GENE, and GAM50 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0555] GAM50 gene, herein designated GAM GENE, encodes a GAM50 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM50 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM50 precursor RNA is designated SEQ ID:23, and is provided hereinbelow with reference to the sequence listing part.

[0556] GAM50 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM50 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0557] An enzyme complex designated DICER COMPLEX, dices the GAM50 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM50 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM50 RNA is designated SEQ ID:1696, and is provided hereinbelow with reference to the sequence listing part.

[0558] GAM50 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM50 target RNA, herein designated GAM TARGET RNA. GAM50 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0559] GAM50 RNA, herein designated GAM RNA, binds comple-

mentarily to one or more target binding sites located in untranslated regions of GAM50 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM50 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM50 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM50 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0560] The complementary binding of GAM50 RNA, herein designated GAM RNA, to target binding sites on GAM50 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits

translation of GAM50 target RNA, herein designated GAM TARGET RNA, into GAM50 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0561] It is appreciated that GAM50 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM50 target genes. The mRNA of each one of this plurality of GAM50 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM50 RNA, herein designated GAM RNA, and which when bound by GAM50 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM50 target proteins.

[0562] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM50 gene, herein designated GAM GENE, on one or more GAM50 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known

miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0563] It is yet further appreciated that specific functions, and accordingly utilities, of GAM50 correlate with, and may be deduced from, the identity of the target genes which GAM50 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0564] Nucleotide sequences of the GAM50 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM50 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM50 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM50 are further described hereinbelow with reference to Table Table1.

[0565] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM50 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0566] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 51 (GAM51) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0567] GAM51 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM51 was detected is described hereinabove with reference to Figs. 2-8.

[0568] GAM51 gene, herein designated GAM GENE, and GAM51 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0569] GAM51 gene, herein designated GAM GENE, encodes a GAM51 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM51 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM51 precursor RNA is designated SEQ ID:24, and is provided hereinbelow with reference to

the sequence listing part. Nucleotide sequence SEQ ID:24 is located at position 26456349 relative to contig NT_007819.11, on chromosome 7.

[0570] GAM51 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM51 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0571] An enzyme complex designated DICER COMPLEX, dices the GAM51 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM51 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM51 RNA is designated SEQ ID:1697, and is provided hereinbelow with

reference to the sequence listing part.

[0572] GAM51 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM51 target RNA, herein designated GAM TARGET RNA. GAM51 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0573] GAM51 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM51 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM51 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM51 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM51 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0574] The complementary binding of GAM51 RNA, herein designated GAM RNA, to target binding sites on GAM51 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM51 target RNA, herein designated GAM TARGET RNA, into GAM51 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0575] It is appreciated that GAM51 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM51 target genes. The mRNA of each one of this plurality of GAM51 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM51 RNA, herein designated GAM RNA, and which when bound by GAM51 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM51 tar-

get proteins.

[0576] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM51 gene, herein designated GAM GENE, on one or more GAM51 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0577] It is yet further appreciated that specific functions, and accordingly utilities, of GAM51 correlate with, and may be deduced from, the identity of the target genes which GAM51 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0578] Nucleotide sequences of the GAM51 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM51 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM51 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM51 are further described hereinbelow with reference to Table Table1.

[0579] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM51 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0580] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 52 (GAM52) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0581] GAM52 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM52 was detected is described hereinabove with reference to Figs. 2-8.

[0582] GAM52 gene, herein designated GAM GENE, and GAM52

target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0583] GAM52 gene, herein designated GAM GENE, encodes a GAM52 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM52 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM52 precursor RNA is designated SEQ ID:25, and is provided hereinbelow with reference to the sequence listing part.

[0584] GAM52 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM52 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0585] An enzyme complex designated DICER COMPLEX, dices the GAM52 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, into GAM52 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM52 RNA is designated SEQ ID:1698, and is provided hereinbelow with reference to the sequence listing part.

[0586] GAM52 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM52 target RNA, herein designated GAM TARGET RNA. GAM52 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0587] GAM52 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM52 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM52 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM52 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM52 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0588] The complementary binding of GAM52 RNA, herein designated GAM RNA, to target binding sites on GAM52 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM52 target RNA, herein designated GAM TARGET RNA, into GAM52 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0589] It is appreciated that GAM52 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM52 target genes. The mRNA of each one of this plurality of GAM52 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM52 RNA, herein designated GAM RNA, and which when bound by GAM52 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM52 target proteins.

[0590] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM52 gene, herein designated GAM GENE, on one or more GAM52 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not

yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0591] It is yet further appreciated that specific functions, and accordingly utilities, of GAM52 correlate with, and may be deduced from, the identity of the target genes which GAM52 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0592] Nucleotide sequences of the GAM52 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM52 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM52 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM52 are further described hereinbelow with reference to Table Table1.

[0593] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM52 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0594] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

53 (GAM53) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0595] GAM53 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM53 was detected is described hereinabove with reference to Figs. 2-8.

[0596] GAM53 gene, herein designated GAM GENE, and GAM53 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0597] GAM53 gene, herein designated GAM GENE, encodes a GAM53 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM53 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM53 precursor RNA is designated SEQ ID:27, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:27 is located at position 174354 relative to contig NT_007819.11, on chromosome 7.

[0598] GAM53 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM53 folded precur-

sor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0599] An enzyme complex designated DICER COMPLEX, dices the GAM53 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM53 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM53 RNA is designated SEQ ID:1703, and is provided hereinbelow with reference to the sequence listing part.

[0600] GAM53 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM53 target RNA, herein designated GAM TARGET RNA. GAM53 target RNA, herein designated GAM TARGET RNA, com-

prises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0601] GAM53 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM53 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM53 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM53 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM53 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[0602] The complementary binding of GAM53 RNA, herein designated GAM RNA, to target binding sites on GAM53 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM53 target RNA, herein designated GAM TARGET RNA, into GAM53 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0603] It is appreciated that GAM53 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM53 target genes. The mRNA of each one of this plurality of GAM53 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM53 RNA, herein designated GAM RNA, and which when bound by GAM53 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM53 target proteins.

[0604] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM53 gene, herein designated GAM GENE, on one or

more GAM53 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0605] It is yet further appreciated that specific functions, and accordingly utilities, of GAM53 correlate with, and may be deduced from, the identity of the target genes which GAM53 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0606] Nucleotide sequences of the GAM53 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM53 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM53 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM53 are further described

hereinbelow with reference to Table Table1.

[0607] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM53 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0608] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 54 (GAM54) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0609] GAM54 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM54 was detected is described hereinabove with reference to Figs. 2-8.

[0610] GAM54 gene, herein designated GAM GENE, and GAM54 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0611] GAM54 gene, herein designated GAM GENE, encodes a GAM54 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM54 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM54 precursor RNA is designated SEQ ID:28, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:28 is located at position 6275175 relative to contig NT_034383.2, on chromosome 1.

[0612] GAM54 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[0613] SEQ ID:99552 detected in mouse EST Accession BG242574.1.

[0614] SEQ ID:99553 detected in mouse EST Accession AW413196.1.

[0615] SEQ ID:99554 detected in mouse EST Accession AI316374.1.

[0616] SEQ ID:99555 detected in mouse EST Accession AA684283.1.

[0617] SEQ ID:99556 detected in mouse EST Accession AA168500.1.

[0618] SEQ ID:99557 detected in mouse EST Accession AA017943.1.

[0619] SEQ ID:99558 detected in mouse EST Accession AA122754.1.

[0620] SEQ ID:99559 detected in mouse EST Accession BI148579.1.

[0621] GAM54 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM54 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0622] An enzyme complex designated DICER COMPLEX, dices the GAM54 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM54 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme

called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM54 RNA is designated SEQ ID:1704, and is provided hereinbelow with reference to the sequence listing part.

[0623] GAM54 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM54 target RNA, herein designated GAM TARGET RNA. GAM54 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0624] GAM54 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM54 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM54 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM54 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM54 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0625] The complementary binding of GAM54 RNA, herein designated GAM RNA, to target binding sites on GAM54 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM54 target RNA, herein designated GAM TARGET RNA, into GAM54 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0626] It is appreciated that GAM54 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM54 target genes. The mRNA of each one of this plurality of GAM54 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM54 RNA,

herein designated GAM RNA, and which when bound by GAM54 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM54 target proteins.

[0627] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM54 gene, herein designated GAM GENE, on one or more GAM54 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0628] It is yet further appreciated that specific functions, and accordingly utilities, of GAM54 correlate with, and may be deduced from, the identity of the target genes which

GAM54 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0629] Nucleotide sequences of the GAM54 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM54 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM54 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM54 are further described hereinbelow with reference to Table Table1.

[0630] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM54 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0631] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 55 (GAM55) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0632] GAM55 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM55 was detected is described hereinabove with reference to Figs. 2-8.

[0633] GAM55 gene, herein designated GAM GENE, and GAM55 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0634] GAM55 gene, herein designated GAM GENE, encodes a GAM55 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM55 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM55 precursor RNA is designated SEQ ID:29, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:29 is located at position 2978630 relative to contig NT_007933.10, on chromosome 7.

[0635] GAM55 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM55 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0636] An enzyme complex designated DICER COMPLEX, dices the GAM55 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM55 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM55 RNA is designated SEQ ID:1705, and is provided hereinbelow with reference to the sequence listing part.

[0637] GAM55 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM55 target RNA, herein designated GAM TARGET RNA. GAM55 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0638] GAM55 RNA, herein designated GAM RNA, binds comple-

mentarily to one or more target binding sites located in untranslated regions of GAM55 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM55 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM55 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM55 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0639] The complementary binding of GAM55 RNA, herein designated GAM RNA, to target binding sites on GAM55 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits

translation of GAM55 target RNA, herein designated GAM TARGET RNA, into GAM55 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0640] It is appreciated that GAM55 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM55 target genes. The mRNA of each one of this plurality of GAM55 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM55 RNA, herein designated GAM RNA, and which when bound by GAM55 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM55 target proteins.

[0641] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM55 gene, herein designated GAM GENE, on one or more GAM55 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known

miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0642] It is yet further appreciated that specific functions, and accordingly utilities, of GAM55 correlate with, and may be deduced from, the identity of the target genes which GAM55 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0643] Nucleotide sequences of the GAM55 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM55 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM55 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM55 are further described hereinbelow with reference to Table Table1.

[0644] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM55 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0645] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 56 (GAM56) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0646] GAM56 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM56 was detected is described hereinabove with reference to Figs. 2-8.

[0647] GAM56 gene, herein designated GAM GENE, and GAM56 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0648] GAM56 gene, herein designated GAM GENE, encodes a GAM56 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM56 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM56 precursor RNA is designated SEQ ID:30, and is provided hereinbelow with reference to

the sequence listing part. Nucleotide sequence SEQ ID:30 is located at position 3890949 relative to contig NT_033944.3, on chromosome 6.

[0649] GAM56 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM56 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0650] An enzyme complex designated DICER COMPLEX, dices the GAM56 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM56 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM56 RNA is designated SEQ ID:1706, and is provided hereinbelow with

reference to the sequence listing part.

[0651] GAM56 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM56 target RNA, herein designated GAM TARGET RNA. GAM56 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0652] GAM56 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM56 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM56 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM56 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM56 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0653] The complementary binding of GAM56 RNA, herein designated GAM RNA, to target binding sites on GAM56 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM56 target RNA, herein designated GAM TARGET RNA, into GAM56 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0654] It is appreciated that GAM56 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM56 target genes. The mRNA of each one of this plurality of GAM56 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM56 RNA, herein designated GAM RNA, and which when bound by GAM56 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM56 tar-

get proteins.

[0655] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM56 gene, herein designated GAM GENE, on one or more GAM56 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0656] It is yet further appreciated that specific functions, and accordingly utilities, of GAM56 correlate with, and may be deduced from, the identity of the target genes which GAM56 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0657] Nucleotide sequences of the GAM56 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM56 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM56 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM56 are further described hereinbelow with reference to Table Table1.

[0658] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM56 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0659] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 57 (GAM57) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0660] GAM57 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM57 was detected is described hereinabove with reference to Figs. 2-8.

[0661] GAM57 gene, herein designated GAM GENE, and GAM57

target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0662] GAM57 gene, herein designated GAM GENE, encodes a GAM57 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM57 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM57 precursor RNA is designated SEQ ID:31, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:31 is located at position 1011391 relative to contig NT_033050.3, on chromosome 3.

[0663] GAM57 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM57 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0664] An enzyme complex designated DICER COMPLEX, dices the GAM57 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM57 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM57 RNA is designated SEQ ID:1707, and is provided hereinbelow with reference to the sequence listing part.

[0665] GAM57 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM57 target RNA, herein designated GAM TARGET RNA. GAM57 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0666] GAM57 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM57 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM57 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM57 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM57 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0667] The complementary binding of GAM57 RNA, herein designated GAM RNA, to target binding sites on GAM57 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM57 target RNA, herein designated GAM TARGET RNA, into GAM57 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is there-

fore outlined by a broken line.

[0668] It is appreciated that GAM57 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM57 target genes. The mRNA of each one of this plurality of GAM57 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM57 RNA, herein designated GAM RNA, and which when bound by GAM57 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM57 target proteins.

[0669] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM57 gene, herein designated GAM GENE, on one or more GAM57 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes

by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0670] It is yet further appreciated that specific functions, and accordingly utilities, of GAM57 correlate with, and may be deduced from, the identity of the target genes which GAM57 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0671] Nucleotide sequences of the GAM57 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM57 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM57 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM57 are further described hereinbelow with reference to Table Table1.

[0672] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM57 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0673] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 58 (GAM58) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0674] GAM58 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM58 was detected is described hereinabove with reference to Figs. 2-8.

[0675] GAM58 gene, herein designated GAM GENE, and GAM58 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0676] GAM58 gene, herein designated GAM GENE, encodes a GAM58 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM58 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM58 precursor RNA is designated SEQ ID:32, and is provided hereinbelow with reference to the sequence listing part.

[0677] GAM58 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM58 folded precur-

sor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0678] An enzyme complex designated DICER COMPLEX, dices the GAM58 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM58 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM58 RNA is designated SEQ ID:1708, and is provided hereinbelow with reference to the sequence listing part.

[0679] GAM58 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM58 target RNA, herein designated GAM TARGET RNA. GAM58 target RNA, herein designated GAM TARGET RNA, com-

prises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0680] GAM58 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM58 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM58 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM58 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM58 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[0681] The complementary binding of GAM58 RNA, herein designated GAM RNA, to target binding sites on GAM58 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM58 target RNA, herein designated GAM TARGET RNA, into GAM58 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0682] It is appreciated that GAM58 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM58 target genes. The mRNA of each one of this plurality of GAM58 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM58 RNA, herein designated GAM RNA, and which when bound by GAM58 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM58 target proteins.

[0683] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM58 gene, herein designated GAM GENE, on one or

more GAM58 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0684] It is yet further appreciated that specific functions, and accordingly utilities, of GAM58 correlate with, and may be deduced from, the identity of the target genes which GAM58 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0685] Nucleotide sequences of the GAM58 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM58 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM58 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM58 are further described

hereinbelow with reference to Table Table1.

[0686] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM58 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0687] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 59 (GAM59) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0688] GAM59 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM59 was detected is described hereinabove with reference to Figs. 2-8.

[0689] GAM59 gene, herein designated GAM GENE, and GAM59 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0690] GAM59 gene, herein designated GAM GENE, encodes a GAM59 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM59 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM59 precursor RNA is designated SEQ ID:33, and is provided hereinbelow with reference to the sequence listing part.

[0691] GAM59 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM59 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0692] An enzyme complex designated DICER COMPLEX, dices the GAM59 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM59 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme

called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM59 RNA is designated SEQ ID:1709, and is provided hereinbelow with reference to the sequence listing part.

[0693] GAM59 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM59 target RNA, herein designated GAM TARGET RNA. GAM59 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0694] GAM59 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM59 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM59 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM59 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM59 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0695] The complementary binding of GAM59 RNA, herein designated GAM RNA, to target binding sites on GAM59 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM59 target RNA, herein designated GAM TARGET RNA, into GAM59 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0696] It is appreciated that GAM59 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM59 target genes. The mRNA of each one of this plurality of GAM59 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM59 RNA,

herein designated GAM RNA, and which when bound by GAM59 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM59 target proteins.

[0697] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM59 gene, herein designated GAM GENE, on one or more GAM59 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0698] It is yet further appreciated that specific functions, and accordingly utilities, of GAM59 correlate with, and may be deduced from, the identity of the target genes which

GAM59 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0699] Nucleotide sequences of the GAM59 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM59 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM59 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM59 are further described hereinbelow with reference to Table Table1.

[0700] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM59 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0701] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 60 (GAM60) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0702] GAM60 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM60 was detected is described hereinabove with reference to Figs. 2-8.

[0703] GAM60 gene, herein designated GAM GENE, and GAM60 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0704] GAM60 gene, herein designated GAM GENE, encodes a GAM60 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM60 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM60 precursor RNA is designated SEQ ID:34, and is provided hereinbelow with reference to the sequence listing part.

[0705] GAM60 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM60 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[0706] An enzyme complex designated DICER COMPLEX, dices the GAM60 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM60 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 96%) nucleotide sequence of GAM60 RNA is designated SEQ ID:1710, and is provided hereinbelow with reference to the sequence listing part.

[0707] GAM60 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM60 target RNA, herein designated GAM TARGET RNA. GAM60 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0708] GAM60 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM60 target RNA, herein desig-

nated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM60 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM60 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM60 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0709] The complementary binding of GAM60 RNA, herein designated GAM RNA, to target binding sites on GAM60 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM60 target RNA, herein designated GAM TARGET RNA, into GAM60 target protein, herein desig-

nated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0710] It is appreciated that GAM60 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM60 target genes. The mRNA of each one of this plurality of GAM60 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM60 RNA, herein designated GAM RNA, and which when bound by GAM60 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM60 target proteins.

[0711] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM60 gene, herein designated GAM GENE, on one or more GAM60 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those

skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0712] It is yet further appreciated that specific functions, and accordingly utilities, of GAM60 correlate with, and may be deduced from, the identity of the target genes which GAM60 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0713] Nucleotide sequences of the GAM60 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM60 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM60 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM60 are further described hereinbelow with reference to Table Table1.

[0714] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM60 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0715] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 61 (GAM61) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0716] GAM61 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM61 was detected is described hereinabove with reference to Figs. 2-8.

[0717] GAM61 gene, herein designated GAM GENE, and GAM61 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0718] GAM61 gene, herein designated GAM GENE, encodes a GAM61 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM61 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM61 precursor RNA is designated SEQ ID:35, and is provided hereinbelow with reference to the sequence listing part.

[0719] GAM61 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM61 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0720] An enzyme complex designated DICER COMPLEX, dices the GAM61 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM61 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM61 RNA is designated SEQ ID:1711, and is provided hereinbelow with reference to the sequence listing part.

[0721] GAM61 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM61 target RNA, herein designated GAM TARGET RNA. GAM61

target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0722] GAM61 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM61 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM61 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM61 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM61 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0723] The complementary binding of GAM61 RNA, herein designated GAM RNA, to target binding sites on GAM61 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM61 target RNA, herein designated GAM TARGET RNA, into GAM61 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0724] It is appreciated that GAM61 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM61 target genes. The mRNA of each one of this plurality of GAM61 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM61 RNA, herein designated GAM RNA, and which when bound by GAM61 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM61 target proteins.

[0725] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM61 gene, herein designated GAM GENE, on one or more GAM61 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0726] It is yet further appreciated that specific functions, and accordingly utilities, of GAM61 correlate with, and may be deduced from, the identity of the target genes which GAM61 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0727] Nucleotide sequences of the GAM61 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM61 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM61 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM61 are further described hereinbelow with reference to Table Table1.

[0728] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM61 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0729] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 62 (GAM62) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0730] GAM62 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM62 was detected is described hereinabove with reference to Figs. 2-8.

[0731] GAM62 gene, herein designated GAM GENE, and GAM62 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0732] GAM62 gene, herein designated GAM GENE, encodes a GAM62 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM62 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM62 precursor RNA is designated SEQ ID:36, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:36 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[0733] GAM62 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM62 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0734] An enzyme complex designated DICER COMPLEX, dices the GAM62 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM62 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA seg-

ment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM62 RNA is designated SEQ ID:1712, and is provided hereinbelow with reference to the sequence listing part.

[0735] GAM62 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM62 target RNA, herein designated GAM TARGET RNA. GAM62 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0736] GAM62 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM62 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM62 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM62 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM62 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0737] The complementary binding of GAM62 RNA, herein designated GAM RNA, to target binding sites on GAM62 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM62 target RNA, herein designated GAM TARGET RNA, into GAM62 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0738] It is appreciated that GAM62 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM62 target genes. The mRNA of each one of this plu-

rality of GAM62 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM62 RNA, herein designated GAM RNA, and which when bound by GAM62 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM62 target proteins.

[0739] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM62 gene, herein designated GAM GENE, on one or more GAM62 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0740] It is yet further appreciated that specific functions, and accordingly utilities, of GAM62 correlate with, and may be deduced from, the identity of the target genes which GAM62 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0741] Nucleotide sequences of the GAM62 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM62 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM62 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM62 are further described hereinbelow with reference to Table Table1.

[0742] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM62 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0743] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 63 (GAM63) gene, which modulates expression of respective target genes thereof, the function and utility of which

target genes is known in the art.

[0744] GAM63 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM63 was detected is described hereinabove with reference to Figs. 2-8.

[0745] GAM63 gene, herein designated GAM GENE, and GAM63 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0746] GAM63 gene, herein designated GAM GENE, encodes a GAM63 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM63 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM63 precursor RNA is designated SEQ ID:37, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:37 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[0747] GAM63 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse

EST's in which these homologs were detected are:

[0748] SEQ ID:99532 detected in mouse EST Accession BG807850.1.

[0749] SEQ ID:99533 detected in mouse EST Accession BG805970.1.

[0750] SEQ ID:99534 detected in mouse EST Accession AW208601.1.

[0751] SEQ ID:99536 detected in mouse EST Accession AA671455.1.

[0752] SEQ ID:99537 detected in mouse EST Accession BE691413.1.

[0753] SEQ ID:99538 detected in mouse EST Accession BE691447.1.

[0754] SEQ ID:99539 detected in mouse EST Accession BG145596.1.

[0755] SEQ ID:99540 detected in mouse EST Accession BE692802.1.

[0756] SEQ ID:99525 detected in mouse EST Accession BB610842.1.

[0757] SEQ ID:99526 detected in mouse EST Accession BB609859.1.

[0758] SEQ ID:99527 detected in mouse EST Accession AA144533.1.

[0759] SEQ ID:99528 detected in mouse EST Accession AW824753.1.

[0760] SEQ ID:99529 detected in mouse EST Accession BE943987.1.

[0761] SEQ ID:99530 detected in mouse EST Accession BG808025.1.

[0762] SEQ ID:99531 detected in mouse EST Accession BG808010.1.

[0763] GAM63 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM63 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0764] An enzyme complex designated DICER COMPLEX, dices the GAM63 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM63 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured

RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM63 RNA is designated SEQ ID:1713, and is provided hereinbelow with reference to the sequence listing part.

[0765] GAM63 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM63 target RNA, herein designated GAM TARGET RNA. GAM63 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0766] GAM63 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM63 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM63 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM63 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM63 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0767] The complementary binding of GAM63 RNA, herein designated GAM RNA, to target binding sites on GAM63 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM63 target RNA, herein designated GAM TARGET RNA, into GAM63 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0768] It is appreciated that GAM63 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM63 target genes. The mRNA of each one of this plurality of GAM63 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM63 RNA, herein designated GAM RNA, and which when bound by GAM63 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM63 target proteins.

[0769] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM63 gene, herein designated GAM GENE, on one or more GAM63 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0770] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM63 correlate with, and may be deduced from, the identity of the target genes which GAM63 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0771] Nucleotide sequences of the GAM63 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM63 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM63 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM63 are further described hereinbelow with reference to Table Table1.

[0772] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM63 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0773] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 64 (GAM64) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0774] GAM64 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM64 was detected is described hereinabove with reference to Figs. 2-8.

[0775] GAM64 gene, herein designated GAM GENE, and GAM64 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0776] GAM64 gene, herein designated GAM GENE, encodes a GAM64 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM64 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM64 precursor RNA is designated SEQ ID:38, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:38 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[0777] GAM64 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM64 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0778] An enzyme complex designated DICER COMPLEX, dices the GAM64 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM64 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM64 RNA is designated SEQ ID:1714, and is provided hereinbelow with reference to the sequence listing part.

[0779] GAM64 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM64 target RNA, herein designated GAM TARGET RNA. GAM64 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PRO-

TEIN CODING and 3UTR respectively.

[0780] GAM64 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM64 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM64 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM64 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM64 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0781] The complementary binding of GAM64 RNA, herein designated GAM RNA, to target binding sites on GAM64 target

RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM64 target RNA, herein designated GAM TARGET RNA, into GAM64 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0782] It is appreciated that GAM64 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM64 target genes. The mRNA of each one of this plurality of GAM64 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM64 RNA, herein designated GAM RNA, and which when bound by GAM64 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM64 target proteins.

[0783] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM64 gene, herein designated GAM GENE, on one or more GAM64 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background

section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0784] It is yet further appreciated that specific functions, and accordingly utilities, of GAM64 correlate with, and may be deduced from, the identity of the target genes which GAM64 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0785] Nucleotide sequences of the GAM64 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM64 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM64 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM64 are further described hereinbelow with reference to Table Table1.

[0786] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM64 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0787] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 65 (GAM65) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0788] GAM65 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM65 was detected is described hereinabove with reference to Figs. 2-8.

[0789] GAM65 gene, herein designated GAM GENE, and GAM65 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0790] GAM65 gene, herein designated GAM GENE, encodes a GAM65 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM65 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM65 precursor RNA is designated SEQ ID:39, and is provided hereinbelow with reference to the sequence listing part.

[0791] GAM65 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM65 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[0792] An enzyme complex designated DICER COMPLEX, dices the GAM65 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM65 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM65 RNA is designated SEQ ID:1715, and is provided hereinbelow with

reference to the sequence listing part.

[0793] GAM65 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM65 target RNA, herein designated GAM TARGET RNA. GAM65 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[0794] GAM65 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM65 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM65 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM65 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM65 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[0795] The complementary binding of GAM65 RNA, herein designated GAM RNA, to target binding sites on GAM65 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM65 target RNA, herein designated GAM TARGET RNA, into GAM65 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[0796] It is appreciated that GAM65 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM65 target genes. The mRNA of each one of this plurality of GAM65 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM65 RNA, herein designated GAM RNA, and which when bound by GAM65 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM65 tar-

get proteins.

[0797] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM65 gene, herein designated GAM GENE, on one or more GAM65 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[0798] It is yet further appreciated that specific functions, and accordingly utilities, of GAM65 correlate with, and may be deduced from, the identity of the target genes which GAM65 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[0799] Nucleotide sequences of the GAM65 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM65 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM65 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM65 are further described hereinbelow with reference to Table Table1.

[0800] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM65 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[0801] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 66 (GAM66) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[0802] GAM66 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM66 was detected is described hereinabove with reference to Figs. 2-8.

[0803] GAM66 gene, herein designated GAM GENE, and GAM66

target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[0804] GAM66 gene, herein designated GAM GENE, encodes a GAM66 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM66 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM66 precursor RNA is designated SEQ ID:40, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:40 is located at position 10696101 relative to contig NT_008046.11, on chromosome 8.

[0805] GAM66 has 214 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[0806] SEQ ID:99068 detected in mouse EST Accession AW558312.1.

[0807] SEQ ID:99069 detected in mouse EST Accession AW546283.1.

[0808] SEQ ID:99070 detected in mouse EST Accession

AW215867.1.

[0809] SEQ ID:99071 detected in mouse EST Accession AW558561.1.

[0810] SEQ ID:99072 detected in mouse EST Accession AA560843.1.

[0811] SEQ ID:99073 detected in mouse EST Accession BB291600.2.

[0812] SEQ ID:99074 detected in mouse EST Accession BF321445.1.

[0813] SEQ ID:99075 detected in mouse EST Accession AW553446.1.

[0814] SEQ ID:99076 detected in mouse EST Accession AW212847.1.

[0815] SEQ ID:99077 detected in mouse EST Accession BF133895.1.

[0816] SEQ ID:99078 detected in mouse EST Accession BF148881.1.

[0817] SEQ ID:99079 detected in mouse EST Accession BF319652.1.

[0818] SEQ ID:99080 detected in mouse EST Accession AA560598.1.

[0819] SEQ ID:99081 detected in mouse EST Accession W15034.1.

[0820] SEQ ID:99082 detected in mouse EST Accession BI106007.1.

[0821] SEQ ID:99083 detected in mouse EST Accession AW413436.1.

[0822] SEQ ID:99084 detected in mouse EST Accession BI077804.1.

[0823] SEQ ID:99085 detected in mouse EST Accession AA517208.1.

[0824] SEQ ID:99086 detected in mouse EST Accession BI692725.1.

[0825] SEQ ID:99092 detected in mouse EST Accession BE912032.1.

[0826] SEQ ID:99093 detected in mouse EST Accession BG966426.1.

[0827] SEQ ID:99094 detected in mouse EST Accession AW538045.1.

[0828] SEQ ID:99095 detected in mouse EST Accession BF540152.1.

[0829] SEQ ID:99096 detected in mouse EST Accession BF721954.1.

[0830] SEQ ID:99097 detected in mouse EST Accession AV222177.2.

[0831] SEQ ID:99098 detected in mouse EST Accession

AI788811.1.

[0832] SEQ ID:99099 detected in mouse EST Accession AI646043.1.

[0833] SEQ ID:99100 detected in mouse EST Accession BI153792.1.

[0834] SEQ ID:99101 detected in mouse EST Accession BF301044.1.

[0835] SEQ ID:99102 detected in mouse EST Accession BE572604.1.

[0836] SEQ ID:99103 detected in mouse EST Accession BB189705.1.

[0837] SEQ ID:99105 detected in mouse EST Accession AW681308.1.

[0838] SEQ ID:99106 detected in mouse EST Accession BG171980.1.

[0839] SEQ ID:99845 detected in mouse EST Accession AA267316.1.

[0840] SEQ ID:99846 detected in mouse EST Accession BF451344.1.

[0841] SEQ ID:99847 detected in mouse EST Accession BB675917.1.

[0842] SEQ ID:99848 detected in mouse EST Accession BB673870.1.

[0843] SEQ ID:99849 detected in mouse EST Accession AA561346.1.

[0844] SEQ ID:99850 detected in mouse EST Accession BG229702.1.

[0845] SEQ ID:99851 detected in mouse EST Accession AA794417.1.

[0846] SEQ ID:99852 detected in mouse EST Accession W57260.1.

[0847] SEQ ID:99853 detected in mouse EST Accession AA216911.1.

[0848] SEQ ID:99854 detected in mouse EST Accession AA166066.1.

[0849] SEQ ID:99855 detected in mouse EST Accession AW990662.1.

[0850] SEQ ID:99856 detected in mouse EST Accession AW987286.1.

[0851] SEQ ID:99857 detected in mouse EST Accession BB733657.1.

[0852] SEQ ID:99858 detected in mouse EST Accession AA271319.1.

[0853] SEQ ID:99859 detected in mouse EST Accession AA407008.1.

[0854] SEQ ID:99860 detected in mouse EST Accession

BB686892.1.

[0855] SEQ ID:99861 detected in mouse EST Accession AW228870.1.

[0856] SEQ ID:99862 detected in mouse EST Accession BB712520.1.

[0857] SEQ ID:99863 detected in mouse EST Accession BB674546.1.

[0858] SEQ ID:99864 detected in mouse EST Accession BB676683.1.

[0859] SEQ ID:99865 detected in mouse EST Accession BB727137.1.

[0860] SEQ ID:99866 detected in mouse EST Accession BF450684.1.

[0861] SEQ ID:99867 detected in mouse EST Accession BB710474.1.

[0862] SEQ ID:99868 detected in mouse EST Accession BF450382.1.

[0863] SEQ ID:99869 detected in mouse EST Accession AI227404.1.

[0864] SEQ ID:99870 detected in mouse EST Accession BB684227.1.

[0865] SEQ ID:99871 detected in mouse EST Accession AW322177.1.

[0866] SEQ ID:99872 detected in mouse EST Accession BB761932.1.

[0867] SEQ ID:99873 detected in mouse EST Accession BE283847.1.

[0868] SEQ ID:99874 detected in mouse EST Accession BF319909.1.

[0869] SEQ ID:99875 detected in mouse EST Accession AI852094.1.

[0870] SEQ ID:99876 detected in mouse EST Accession BE197581.1.

[0871] SEQ ID:99877 detected in mouse EST Accession AI007313.1.

[0872] SEQ ID:99878 detected in mouse EST Accession AI183017.1.

[0873] SEQ ID:99879 detected in mouse EST Accession AA688511.1.

[0874] SEQ ID:99880 detected in mouse EST Accession AL034859.1.

[0875] SEQ ID:99881 detected in mouse EST Accession BE335207.1.

[0876] SEQ ID:99882 detected in mouse EST Accession AA117196.1.

[0877] SEQ ID:99883 detected in mouse EST Accession

W84301.1.

[0878] SEQ ID:99884 detected in mouse EST Accession AA462159.1.

[0879] SEQ ID:99885 detected in mouse EST Accession AI326947.1.

[0880] SEQ ID:99886 detected in mouse EST Accession AW123202.1.

[0881] SEQ ID:99887 detected in mouse EST Accession BB757430.1.

[0882] SEQ ID:99888 detected in mouse EST Accession BE334642.1.

[0883] SEQ ID:99889 detected in mouse EST Accession BF780391.1.

[0884] SEQ ID:99890 detected in mouse EST Accession AW542604.1.

[0885] SEQ ID:99891 detected in mouse EST Accession AA118144.1.

[0886] SEQ ID:99892 detected in mouse EST Accession AA759821.1.

[0887] SEQ ID:99893 detected in mouse EST Accession AA139140.1.

[0888] SEQ ID:99894 detected in mouse EST Accession BF721903.1.

[0889] SEQ ID:99895 detected in mouse EST Accession BE377838.1.

[0890] SEQ ID:99896 detected in mouse EST Accession BG093728.1.

[0891] SEQ ID:99897 detected in mouse EST Accession AI596439.1.

[0892] SEQ ID:99898 detected in mouse EST Accession AW545293.1.

[0893] SEQ ID:99899 detected in mouse EST Accession BF098965.1.

[0894] SEQ ID:99900 detected in mouse EST Accession BE200086.1.

[0895] SEQ ID:99901 detected in mouse EST Accession AU021070.1.

[0896] SEQ ID:99902 detected in mouse EST Accession BF225531.1.

[0897] SEQ ID:99903 detected in mouse EST Accession BG919635.1.

[0898] SEQ ID:99904 detected in mouse EST Accession BI466395.1.

[0899] SEQ ID:99905 detected in mouse EST Accession AW413441.1.

[0900] SEQ ID:99906 detected in mouse EST Accession

AA434838.1.

[0901] SEQ ID:99907 detected in mouse EST Accession BG063770.1.

[0902] SEQ ID:99908 detected in mouse EST Accession BE334348.1.

[0903] SEQ ID:99909 detected in mouse EST Accession C78518.1.

[0904] SEQ ID:99910 detected in mouse EST Accession BF320443.1.

[0905] SEQ ID:99911 detected in mouse EST Accession BI651688.1.

[0906] SEQ ID:99912 detected in mouse EST Accession BG277852.1.

[0907] SEQ ID:99913 detected in mouse EST Accession W70725.1.

[0908] SEQ ID:99914 detected in mouse EST Accession BF227358.1.

[0909] SEQ ID:99915 detected in mouse EST Accession AW764038.1.

[0910] SEQ ID:99916 detected in mouse EST Accession AW228118.1.

[0911] SEQ ID:99917 detected in mouse EST Accession AA050116.1.

[0912] SEQ ID:99918 detected in mouse EST Accession AA863935.1.

[0913] SEQ ID:99919 detected in mouse EST Accession AA690541.1.

[0914] SEQ ID:99920 detected in mouse EST Accession BE374735.1.

[0915] SEQ ID:99921 detected in mouse EST Accession BB744784.1.

[0916] SEQ ID:99922 detected in mouse EST Accession BE335188.1.

[0917] SEQ ID:99923 detected in mouse EST Accession BI438144.1.

[0918] SEQ ID:99924 detected in mouse EST Accession AW321045.1.

[0919] SEQ ID:99925 detected in mouse EST Accession BB680938.1.

[0920] SEQ ID:99926 detected in mouse EST Accession BF012238.1.

[0921] SEQ ID:99927 detected in mouse EST Accession AA655917.1.

[0922] SEQ ID:99928 detected in mouse EST Accession BG868291.1.

[0923] SEQ ID:99929 detected in mouse EST Accession

AA536898.1.

[0924] SEQ ID:99930 detected in mouse EST Accession AA117197.1.

[0925] SEQ ID:99931 detected in mouse EST Accession AA497794.1.

[0926] SEQ ID:99932 detected in mouse EST Accession AW823185.1.

[0927] SEQ ID:99933 detected in mouse EST Accession BI690011.1.

[0928] SEQ ID:99934 detected in mouse EST Accession BF118059.1.

[0929] SEQ ID:99935 detected in mouse EST Accession AA499168.1.

[0930] SEQ ID:99936 detected in mouse EST Accession AL118347.1.

[0931] SEQ ID:99937 detected in mouse EST Accession BB757112.1.

[0932] SEQ ID:99938 detected in mouse EST Accession AA607770.1.

[0933] SEQ ID:99939 detected in mouse EST Accession AI226413.1.

[0934] SEQ ID:99940 detected in mouse EST Accession AW209995.1.

[0935] SEQ ID:99941 detected in mouse EST Accession BE306625.1.

[0936] SEQ ID:99942 detected in mouse EST Accession AA222621.1.

[0937] SEQ ID:99943 detected in mouse EST Accession W66681.1.

[0938] SEQ ID:99944 detected in mouse EST Accession AA596527.1.

[0939] SEQ ID:99945 detected in mouse EST Accession AW909511.1.

[0940] SEQ ID:99946 detected in mouse EST Accession BE625520.1.

[0941] SEQ ID:99947 detected in mouse EST Accession BG063771.1.

[0942] SEQ ID:99948 detected in mouse EST Accession AA008270.1.

[0943] SEQ ID:99949 detected in mouse EST Accession BI851591.1.

[0944] SEQ ID:99950 detected in mouse EST Accession AW540818.1.

[0945] SEQ ID:99951 detected in mouse EST Accession W89434.1.

[0946] SEQ ID:99952 detected in mouse EST Accession

AA574848.1.

[0947] SEQ ID:99953 detected in mouse EST Accession AI593680.1.

[0948] SEQ ID:99954 detected in mouse EST Accession BI645538.1.

[0949] SEQ ID:99955 detected in mouse EST Accession AA797916.1.

[0950] SEQ ID:99956 detected in mouse EST Accession BE627600.1.

[0951] SEQ ID:99957 detected in mouse EST Accession BI793662.1.

[0952] SEQ ID:99958 detected in mouse EST Accession AW555286.1.

[0953] SEQ ID:99959 detected in mouse EST Accession BE553673.1.

[0954] SEQ ID:99960 detected in mouse EST Accession AW538411.1.

[0955] SEQ ID:99961 detected in mouse EST Accession AA117944.1.

[0956] SEQ ID:99962 detected in mouse EST Accession AW764182.1.

[0957] SEQ ID:99963 detected in mouse EST Accession AW539487.1.

[0958] SEQ ID:99964 detected in mouse EST Accession BF148729.1.

[0959] SEQ ID:99965 detected in mouse EST Accession AW826110.1.

[0960] SEQ ID:99966 detected in mouse EST Accession AW740788.1.

[0961] SEQ ID:99967 detected in mouse EST Accession BI689763.1.

[0962] SEQ ID:99968 detected in mouse EST Accession BI696311.1.

[0963] SEQ ID:99969 detected in mouse EST Accession AA759930.1.

[0964] SEQ ID:99970 detected in mouse EST Accession AW539895.1.

[0965] SEQ ID:99971 detected in mouse EST Accession AW701899.1.

[0966] SEQ ID:99972 detected in mouse EST Accession AA607312.1.

[0967] SEQ ID:99973 detected in mouse EST Accession BF682084.1.

[0968] SEQ ID:99974 detected in mouse EST Accession AW553005.1.

[0969] SEQ ID:99975 detected in mouse EST Accession

BG228840.1.

[0970] SEQ ID:99976 detected in mouse EST Accession BF146940.1.

[0971] SEQ ID:99977 detected in mouse EST Accession BF321728.1.

[0972] SEQ ID:99978 detected in mouse EST Accession AW546398.1.

[0973] SEQ ID:99979 detected in mouse EST Accession BF021319.1.

[0974] SEQ ID:99980 detected in mouse EST Accession BI106289.1.

[0975] SEQ ID:99981 detected in mouse EST Accession BI696116.1.

[0976] SEQ ID:99982 detected in mouse EST Accession BI688477.1.

[0977] SEQ ID:99983 detected in mouse EST Accession BG965895.1.

[0978] SEQ ID:99984 detected in mouse EST Accession BI157176.1.

[0979] SEQ ID:99985 detected in mouse EST Accession BF134327.1.

[0980] SEQ ID:99986 detected in mouse EST Accession BF721465.1.

[0981] SEQ ID:99987 detected in mouse EST Accession BI851153.1.

[0982] SEQ ID:99988 detected in mouse EST Accession AW209084.1.

[0983] SEQ ID:99989 detected in mouse EST Accession BE283285.1.

[0984] SEQ ID:99990 detected in mouse EST Accession BI411767.1.

[0985] SEQ ID:99991 detected in mouse EST Accession BI665369.1.

[0986] SEQ ID:99992 detected in mouse EST Accession BI525644.1.

[0987] SEQ ID:98251 detected in mouse EST Accession BF226484.1.

[0988] SEQ ID:98252 detected in mouse EST Accession BB676512.1.

[0989] SEQ ID:98253 detected in mouse EST Accession BF150596.1.

[0990] SEQ ID:98254 detected in mouse EST Accession BI104796.1.

[0991] SEQ ID:98255 detected in mouse EST Accession BI654440.1.

[0992] SEQ ID:98256 detected in mouse EST Accession

BF148284.1.

[0993] SEQ ID:98257 detected in mouse EST Accession BI105328.1.

[0994] SEQ ID:98258 detected in mouse EST Accession BI149362.1.

[0995] SEQ ID:98259 detected in mouse EST Accession BB737617.1.

[0996] SEQ ID:98260 detected in mouse EST Accession BE554771.1.

[0997] SEQ ID:98261 detected in mouse EST Accession AA474199.1.

[0998] SEQ ID:98262 detected in mouse EST Accession AA591993.1.

[0999] SEQ ID:98263 detected in mouse EST Accession AA967240.1.

[1000] SEQ ID:98264 detected in mouse EST Accession W97241.1.

[1001] SEQ ID:98265 detected in mouse EST Accession AL364621.1.

[1002] SEQ ID:98266 detected in mouse EST Accession BE197506.1.

[1003] SEQ ID:98267 detected in mouse EST Accession BB709368.1.

[1004] SEQ ID:98268 detected in mouse EST Accession BB679787.1.

[1005] SEQ ID:98269 detected in mouse EST Accession AI789853.1.

[1006] SEQ ID:98270 detected in mouse EST Accession AW989030.1.

[1007] SEQ ID:98271 detected in mouse EST Accession BB673745.1.

[1008] SEQ ID:98272 detected in mouse EST Accession BF017567.1.

[1009] SEQ ID:98273 detected in mouse EST Accession AA575633.1.

[1010] SEQ ID:98274 detected in mouse EST Accession AU020487.1.

[1011] SEQ ID:98275 detected in mouse EST Accession BB728791.1.

[1012] SEQ ID:98276 detected in mouse EST Accession AA407163.1.

[1013] SEQ ID:98277 detected in mouse EST Accession BB674898.1.

[1014] SEQ ID:98278 detected in mouse EST Accession BF451434.1.

[1015] SEQ ID:98279 detected in mouse EST Accession

BB676204.1.

[1016] SEQ ID:98280 detected in mouse EST Accession BB687045.1.

[1017] SEQ ID:98281 detected in mouse EST Accession BF318579.1.

[1018] SEQ ID:98282 detected in mouse EST Accession BB676643.1.

[1019] SEQ ID:98283 detected in mouse EST Accession AA616897.1.

[1020] GAM66 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM66 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1021] An enzyme complex designated DICER COMPLEX, dices the GAM66 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM66 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA seg-

ment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM66 RNA is designated SEQ ID:1716, and is provided hereinbelow with reference to the sequence listing part.

[1022] GAM66 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM66 target RNA, herein designated GAM TARGET RNA. GAM66 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1023] GAM66 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM66 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM66 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM66 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM66 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1024] The complementary binding of GAM66 RNA, herein designated GAM RNA, to target binding sites on GAM66 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM66 target RNA, herein designated GAM TARGET RNA, into GAM66 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1025] It is appreciated that GAM66 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM66 target genes. The mRNA of each one of this plu-

rality of GAM66 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM66 RNA, herein designated GAM RNA, and which when bound by GAM66 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM66 target proteins.

[1026] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM66 gene, herein designated GAM GENE, on one or more GAM66 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1027] It is yet further appreciated that specific functions, and accordingly utilities, of GAM66 correlate with, and may be deduced from, the identity of the target genes which GAM66 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1028] Nucleotide sequences of the GAM66 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM66 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM66 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM66 are further described hereinbelow with reference to Table Table1.

[1029] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM66 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1030] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 67 (GAM67) gene, which modulates expression of respective target genes thereof, the function and utility of which

target genes is known in the art.

[1031] GAM67 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM67 was detected is described hereinabove with reference to Figs. 2-8.

[1032] GAM67 gene, herein designated GAM GENE, and GAM67 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1033] GAM67 gene, herein designated GAM GENE, encodes a GAM67 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM67 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM67 precursor RNA is designated SEQ ID:41, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:41 is located at position 1235133 relative to contig NT_008984.13, on chromosome 11.

[1034] GAM67 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse

EST's in which these homologs were detected are:

[1035] SEQ ID:98822 detected in mouse EST Accession BI965972.1.

[1036] SEQ ID:98823 detected in mouse EST Accession AI326210.1.

[1037] SEQ ID:98824 detected in mouse EST Accession BI965652.1.

[1038] GAM67 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM67 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1039] An enzyme complex designated DICER COMPLEX, dices the GAM67 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM67 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is

catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM67 RNA is designated SEQ ID:1717, and is provided hereinbelow with reference to the sequence listing part.

[1040] GAM67 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM67 target RNA, herein designated GAM TARGET RNA. GAM67 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1041] GAM67 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM67 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM67 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM67 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM67 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1042] The complementary binding of GAM67 RNA, herein designated GAM RNA, to target binding sites on GAM67 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM67 target RNA, herein designated GAM TARGET RNA, into GAM67 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1043] It is appreciated that GAM67 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM67 target genes. The mRNA of each one of this plurality of GAM67 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM67 RNA, herein designated GAM RNA, and which when bound by GAM67 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM67 target proteins.

[1044] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM67 gene, herein designated GAM GENE, on one or more GAM67 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1045] It is yet further appreciated that specific functions, and accordingly utilities, of GAM67 correlate with, and may be

deduced from, the identity of the target genes which GAM67 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1046] Nucleotide sequences of the GAM67 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM67 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM67 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM67 are further described hereinbelow with reference to Table Table1.

[1047] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM67 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1048] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 68 (GAM68) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1049] GAM68 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM68 was detected is described hereinabove with reference to Figs. 2-8.

[1050] GAM68 gene, herein designated GAM GENE, and GAM68 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1051] GAM68 gene, herein designated GAM GENE, encodes a GAM68 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM68 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM68 precursor RNA is designated SEQ ID:42, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:42 is located at position 2183835 relative to contig NT_034383.2, on chromosome 1.

[1052] GAM68 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM68 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[1053] An enzyme complex designated DICER COMPLEX, dices the GAM68 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM68 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM68 RNA is designated SEQ ID:1718, and is provided hereinbelow with reference to the sequence listing part.

[1054] GAM68 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM68 target RNA, herein designated GAM TARGET RNA. GAM68 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1055] GAM68 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM68 target RNA, herein desig-

nated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM68 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM68 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM68 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1056] The complementary binding of GAM68 RNA, herein designated GAM RNA, to target binding sites on GAM68 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM68 target RNA, herein designated GAM TARGET RNA, into GAM68 target protein, herein desig-

nated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1057] It is appreciated that GAM68 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM68 target genes. The mRNA of each one of this plurality of GAM68 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM68 RNA, herein designated GAM RNA, and which when bound by GAM68 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM68 target proteins.

[1058] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM68 gene, herein designated GAM GENE, on one or more GAM68 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those

skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1059] It is yet further appreciated that specific functions, and accordingly utilities, of GAM68 correlate with, and may be deduced from, the identity of the target genes which GAM68 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1060] Nucleotide sequences of the GAM68 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM68 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM68 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM68 are further described hereinbelow with reference to Table Table1.

[1061] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM68 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1062] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 69 (GAM69) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1063] GAM69 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM69 was detected is described hereinabove with reference to Figs. 2-8.

[1064] GAM69 gene, herein designated GAM GENE, and GAM69 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1065] GAM69 gene, herein designated GAM GENE, encodes a GAM69 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM69 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM69 precursor RNA is designated SEQ ID:43, and is provided hereinbelow with reference to the sequence listing part.

[1066] GAM69 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM69 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1067] An enzyme complex designated DICER COMPLEX, dices the GAM69 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM69 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM69 RNA is designated SEQ ID:1719, and is provided hereinbelow with reference to the sequence listing part.

[1068] GAM69 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM69 target RNA, herein designated GAM TARGET RNA. GAM69

target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1069] GAM69 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM69 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM69 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM69 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM69 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1070] The complementary binding of GAM69 RNA, herein designated GAM RNA, to target binding sites on GAM69 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM69 target RNA, herein designated GAM TARGET RNA, into GAM69 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1071] It is appreciated that GAM69 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM69 target genes. The mRNA of each one of this plurality of GAM69 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM69 RNA, herein designated GAM RNA, and which when bound by GAM69 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM69 target proteins.

[1072] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM69 gene, herein designated GAM GENE, on one or more GAM69 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1073] It is yet further appreciated that specific functions, and accordingly utilities, of GAM69 correlate with, and may be deduced from, the identity of the target genes which GAM69 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1074] Nucleotide sequences of the GAM69 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM69 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM69 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM69 are further described hereinbelow with reference to Table Table1.

[1075] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM69 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1076] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 70 (GAM70) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1077] GAM70 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM70 was detected is described hereinabove with reference to Figs. 2-8.

[1078] GAM70 gene, herein designated GAM GENE, and GAM70 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1079] GAM70 gene, herein designated GAM GENE, encodes a GAM70 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM70 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM70 precursor RNA is designated SEQ ID:44, and is provided hereinbelow with reference to the sequence listing part.

[1080] GAM70 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM70 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1081] An enzyme complex designated DICER COMPLEX, dices the GAM70 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM70 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is

catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 96%) nucleotide sequence of GAM70 RNA is designated SEQ ID:1720, and is provided hereinbelow with reference to the sequence listing part.

[1082] GAM70 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM70 target RNA, herein designated GAM TARGET RNA. GAM70 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1083] GAM70 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM70 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM70 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM70 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM70 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1084] The complementary binding of GAM70 RNA, herein designated GAM RNA, to target binding sites on GAM70 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM70 target RNA, herein designated GAM TARGET RNA, into GAM70 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1085] It is appreciated that GAM70 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM70 target genes. The mRNA of each one of this plurality of GAM70 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM70 RNA, herein designated GAM RNA, and which when bound by GAM70 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM70 target proteins.

[1086] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM70 gene, herein designated GAM GENE, on one or more GAM70 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1087] It is yet further appreciated that specific functions, and accordingly utilities, of GAM70 correlate with, and may be

deduced from, the identity of the target genes which GAM70 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1088] Nucleotide sequences of the GAM70 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM70 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM70 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM70 are further described hereinbelow with reference to Table Table1.

[1089] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM70 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1090] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 71 (GAM71) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1091] GAM71 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM71 was detected is described hereinabove with reference to Figs. 2-8.

[1092] GAM71 gene, herein designated GAM GENE, and GAM71 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1093] GAM71 gene, herein designated GAM GENE, encodes a GAM71 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM71 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM71 precursor RNA is designated SEQ ID:45, and is provided hereinbelow with reference to the sequence listing part.

[1094] GAM71 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM71 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[1095] An enzyme complex designated DICER COMPLEX, dices the GAM71 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM71 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM71 RNA is designated SEQ ID:1721, and is provided hereinbelow with reference to the sequence listing part.

[1096] GAM71 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM71 target RNA, herein designated GAM TARGET RNA. GAM71 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1097] GAM71 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM71 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM71 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM71 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM71 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1098] The complementary binding of GAM71 RNA, herein designated GAM RNA, to target binding sites on GAM71 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM71 target RNA, herein designated GAM

TARGET RNA, into GAM71 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1099] It is appreciated that GAM71 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM71 target genes. The mRNA of each one of this plurality of GAM71 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM71 RNA, herein designated GAM RNA, and which when bound by GAM71 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM71 target proteins.

[1100] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM71 gene, herein designated GAM GENE, on one or more GAM71 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other re-

cently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1101] It is yet further appreciated that specific functions, and accordingly utilities, of GAM71 correlate with, and may be deduced from, the identity of the target genes which GAM71 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1102] Nucleotide sequences of the GAM71 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM71 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM71 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM71 are further described hereinbelow with reference to Table Table1.

[1103] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM71 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[1104] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 72 (GAM72) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1105] GAM72 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM72 was detected is described hereinabove with reference to Figs. 2-8.

[1106] GAM72 gene, herein designated GAM GENE, and GAM72 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1107] GAM72 gene, herein designated GAM GENE, encodes a GAM72 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM72 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM72 precursor RNA is designated SEQ ID:46, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:46

is located at position 7104477 relative to contig NT_005332.11, on chromosome 2.

[1108] GAM72 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM72 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1109] An enzyme complex designated DICER COMPLEX, dices the GAM72 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM72 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM72 RNA is designated SEQ ID:1722, and is provided hereinbelow with reference to the sequence listing part.

[1110] GAM72 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM72 target RNA, herein designated GAM TARGET RNA. GAM72 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1111] GAM72 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM72 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM72 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM72 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM72 tar-

get RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1112] The complementary binding of GAM72 RNA, herein designated GAM RNA, to target binding sites on GAM72 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM72 target RNA, herein designated GAM TARGET RNA, into GAM72 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1113] It is appreciated that GAM72 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM72 target genes. The mRNA of each one of this plurality of GAM72 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM72 RNA, herein designated GAM RNA, and which when bound by GAM72 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM72 target proteins.

[1114] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM72 gene, herein designated GAM GENE, on one or more GAM72 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1115] It is yet further appreciated that specific functions, and accordingly utilities, of GAM72 correlate with, and may be deduced from, the identity of the target genes which GAM72 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1116] Nucleotide sequences of the GAM72 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM72 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM72 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM72 are further described hereinbelow with reference to Table Table1.

[1117] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM72 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1118] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 73 (GAM73) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1119] GAM73 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM73 was detected is described hereinabove with reference to Figs. 2-8.

[1120] GAM73 gene, herein designated GAM GENE, and GAM73 target gene, herein designated GAM TARGET GENE, are

human genes contained in the human genome.

[1121] GAM73 gene, herein designated GAM GENE, encodes a GAM73 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM73 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM73 precursor RNA is designated SEQ ID:47, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:47 is located at position 1235096 relative to contig NT_009526.11, on chromosome 12.

[1122] GAM73 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[1123] SEQ ID:100323 detected in mouse EST Accession BI965972.1.

[1124] SEQ ID:100324 detected in mouse EST Accession AI326210.1.

[1125] SEQ ID:100325 detected in mouse EST Accession BI965652.1.

[1126] GAM73 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM73 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1127] An enzyme complex designated DICER COMPLEX, dices the GAM73 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM73 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM73 RNA is designated SEQ ID:1723, and is provided hereinbelow with reference to the sequence listing part.

[1128] GAM73 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM73

target RNA, herein designated GAM TARGET RNA. GAM73 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1129] GAM73 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM73 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM73 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM73 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM73 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites

in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1130] The complementary binding of GAM73 RNA, herein designated GAM RNA, to target binding sites on GAM73 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM73 target RNA, herein designated GAM TARGET RNA, into GAM73 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1131] It is appreciated that GAM73 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM73 target genes. The mRNA of each one of this plurality of GAM73 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM73 RNA, herein designated GAM RNA, and which when bound by GAM73 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM73 target proteins.

[1132] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM73 gene, herein designated GAM GENE, on one or more GAM73 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1133] It is yet further appreciated that specific functions, and accordingly utilities, of GAM73 correlate with, and may be deduced from, the identity of the target genes which GAM73 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1134] Nucleotide sequences of the GAM73 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM73 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM73 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM73 are further described hereinbelow with reference to Table Table1.

[1135] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM73 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1136] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 74 (GAM74) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1137] GAM74 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM74 was detected is described hereinabove with reference to Figs. 2-8.

[1138] GAM74 gene, herein designated GAM GENE, and GAM74 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1139] GAM74 gene, herein designated GAM GENE, encodes a

GAM74 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM74 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM74 precursor RNA is designated SEQ ID:48, and is provided hereinbelow with reference to the sequence listing part.

[1140] GAM74 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM74 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1141] An enzyme complex designated DICER COMPLEX, dices the GAM74 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM74 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured

RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM74 RNA is designated SEQ ID:1724, and is provided hereinbelow with reference to the sequence listing part.

[1142] GAM74 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM74 target RNA, herein designated GAM TARGET RNA. GAM74 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1143] GAM74 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM74 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM74 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM74 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM74 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1144] The complementary binding of GAM74 RNA, herein designated GAM RNA, to target binding sites on GAM74 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM74 target RNA, herein designated GAM TARGET RNA, into GAM74 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1145] It is appreciated that GAM74 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM74 target genes. The mRNA of each one of this plurality of GAM74 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM74 RNA, herein designated GAM RNA, and which when bound by GAM74 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM74 target proteins.

[1146] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM74 gene, herein designated GAM GENE, on one or more GAM74 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1147] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM74 correlate with, and may be deduced from, the identity of the target genes which GAM74 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1148] Nucleotide sequences of the GAM74 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM74 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM74 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM74 are further described hereinbelow with reference to Table Table1.

[1149] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM74 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1150] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 76 (GAM76) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1151] GAM76 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM76 was detected is described hereinabove with reference to Figs. 2-8.

[1152] GAM76 gene, herein designated GAM GENE, and GAM76 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1153] GAM76 gene, herein designated GAM GENE, encodes a GAM76 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM76 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM76 precursor RNA is designated SEQ ID:49, and is provided hereinbelow with reference to the sequence listing part.

[1154] GAM76 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM76 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1155] An enzyme complex designated DICER COMPLEX, dices the GAM76 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM76 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM76 RNA is designated SEQ ID:1725, and is provided hereinbelow with reference to the sequence listing part.

[1156] GAM76 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM76 target RNA, herein designated GAM TARGET RNA. GAM76 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1157] GAM76 RNA, herein designated GAM RNA, binds comple-

mentarily to one or more target binding sites located in untranslated regions of GAM76 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM76 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM76 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM76 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1158] The complementary binding of GAM76 RNA, herein designated GAM RNA, to target binding sites on GAM76 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits

translation of GAM76 target RNA, herein designated GAM TARGET RNA, into GAM76 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1159] It is appreciated that GAM76 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM76 target genes. The mRNA of each one of this plurality of GAM76 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM76 RNA, herein designated GAM RNA, and which when bound by GAM76 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM76 target proteins.

[1160] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM76 gene, herein designated GAM GENE, on one or more GAM76 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known

miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1161] It is yet further appreciated that specific functions, and accordingly utilities, of GAM76 correlate with, and may be deduced from, the identity of the target genes which GAM76 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1162] Nucleotide sequences of the GAM76 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM76 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM76 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM76 are further described hereinbelow with reference to Table Table1.

[1163] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM76 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1164] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 77 (GAM77) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1165] GAM77 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM77 was detected is described hereinabove with reference to Figs. 2-8.

[1166] GAM77 gene, herein designated GAM GENE, and GAM77 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1167] GAM77 gene, herein designated GAM GENE, encodes a GAM77 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM77 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM77 precursor RNA is designated SEQ ID:50, and is provided hereinbelow with reference to

the sequence listing part.

[1168] GAM77 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[1169] SEQ ID:100162 detected in mouse EST Accession BF134656.1.

[1170] SEQ ID:100164 detected in mouse EST Accession BI149599.1.

[1171] GAM77 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM77 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1172] An enzyme complex designated DICER COMPLEX, dices the GAM77 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM77 RNA, herein desig-

nated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM77 RNA is designated SEQ ID:1726, and is provided hereinbelow with reference to the sequence listing part.

[1173] GAM77 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM77 target RNA, herein designated GAM TARGET RNA. GAM77 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1174] GAM77 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM77 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM77 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM77 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM77 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1175] The complementary binding of GAM77 RNA, herein designated GAM RNA, to target binding sites on GAM77 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM77 target RNA, herein designated GAM TARGET RNA, into GAM77 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1176] It is appreciated that GAM77 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM77 target genes. The mRNA of each one of this plurality of GAM77 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM77 RNA, herein designated GAM RNA, and which when bound by GAM77 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM77 target proteins.

[1177] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM77 gene, herein designated GAM GENE, on one or more GAM77 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny

RNA world, Science 294,779 (2001)).

[1178] It is yet further appreciated that specific functions, and accordingly utilities, of GAM77 correlate with, and may be deduced from, the identity of the target genes which GAM77 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1179] Nucleotide sequences of the GAM77 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM77 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM77 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM77 are further described hereinbelow with reference to Table Table1.

[1180] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM77 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1181] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 78 (GAM78) gene, which modulates expression of respec-

tive target genes thereof, the function and utility of which target genes is known in the art.

[1182] GAM78 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM78 was detected is described hereinabove with reference to Figs. 2-8.

[1183] GAM78 gene, herein designated GAM GENE, and GAM78 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1184] GAM78 gene, herein designated GAM GENE, encodes a GAM78 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM78 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM78 precursor RNA is designated SEQ ID:51, and is provided hereinbelow with reference to the sequence listing part.

[1185] GAM78 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM78 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1186] An enzyme complex designated DICER COMPLEX, dices the GAM78 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM78 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM78 RNA is designated SEQ ID:1727, and is provided hereinbelow with reference to the sequence listing part.

[1187] GAM78 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM78 target RNA, herein designated GAM TARGET RNA. GAM78 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PRO-

TEIN CODING and 3UTR respectively.

[1188] GAM78 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM78 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM78 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM78 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM78 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1189] The complementary binding of GAM78 RNA, herein designated GAM RNA, to target binding sites on GAM78 target

RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM78 target RNA, herein designated GAM TARGET RNA, into GAM78 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1190] It is appreciated that GAM78 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM78 target genes. The mRNA of each one of this plurality of GAM78 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM78 RNA, herein designated GAM RNA, and which when bound by GAM78 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM78 target proteins.

[1191] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM78 gene, herein designated GAM GENE, on one or more GAM78 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background

section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1192] It is yet further appreciated that specific functions, and accordingly utilities, of GAM78 correlate with, and may be deduced from, the identity of the target genes which GAM78 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1193] Nucleotide sequences of the GAM78 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM78 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM78 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM78 are further described hereinbelow with reference to Table Table1.

[1194] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM78 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1195] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 79 (GAM79) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1196] GAM79 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM79 was detected is described hereinabove with reference to Figs. 2-8.

[1197] GAM79 gene, herein designated GAM GENE, and GAM79 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1198] GAM79 gene, herein designated GAM GENE, encodes a GAM79 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM79 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM79 precursor RNA is designated SEQ ID:52, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:52 is located at position 19308883 relative to contig NT_033899.3, on chromosome 11.

[1199] GAM79 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM79 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1200] An enzyme complex designated DICER COMPLEX, dices the GAM79 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM79 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A

probable (over 89%) nucleotide sequence of GAM79 RNA is designated SEQ ID:1728, and is provided hereinbelow with reference to the sequence listing part.

[1201] GAM79 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM79 target RNA, herein designated GAM TARGET RNA. GAM79 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1202] GAM79 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM79 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM79 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM79 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM79 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1203] The complementary binding of GAM79 RNA, herein designated GAM RNA, to target binding sites on GAM79 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM79 target RNA, herein designated GAM TARGET RNA, into GAM79 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1204] It is appreciated that GAM79 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM79 target genes. The mRNA of each one of this plurality of GAM79 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM79 RNA, herein designated GAM RNA, and which when bound by

GAM79 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM79 target proteins.

[1205] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM79 gene, herein designated GAM GENE, on one or more GAM79 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1206] It is yet further appreciated that specific functions, and accordingly utilities, of GAM79 correlate with, and may be deduced from, the identity of the target genes which GAM79 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[1207] Nucleotide sequences of the GAM79 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM79 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM79 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM79 are further described hereinbelow with reference to Table Table1.

[1208] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM79 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1209] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 80 (GAM80) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1210] GAM80 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM80 was detected is described hereinabove

with reference to Figs. 2-8.

[1211] GAM80 gene, herein designated GAM GENE, and GAM80 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1212] GAM80 gene, herein designated GAM GENE, encodes a GAM80 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM80 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM80 precursor RNA is designated SEQ ID:53, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:53 is located at position 2349689 relative to contig NT_021907.13, on chromosome 1.

[1213] GAM80 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM80 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[1214] An enzyme complex designated DICER COMPLEX, dices the GAM80 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM80 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM80 RNA is designated SEQ ID:1729, and is provided hereinbelow with reference to the sequence listing part.

[1215] GAM80 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM80 target RNA, herein designated GAM TARGET RNA. GAM80 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1216] GAM80 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM80 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM80 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM80 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM80 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1217] The complementary binding of GAM80 RNA, herein designated GAM RNA, to target binding sites on GAM80 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM80 target RNA, herein designated GAM

TARGET RNA, into GAM80 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1218] It is appreciated that GAM80 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM80 target genes. The mRNA of each one of this plurality of GAM80 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM80 RNA, herein designated GAM RNA, and which when bound by GAM80 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM80 target proteins.

[1219] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM80 gene, herein designated GAM GENE, on one or more GAM80 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other re-

cently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1220] It is yet further appreciated that specific functions, and accordingly utilities, of GAM80 correlate with, and may be deduced from, the identity of the target genes which GAM80 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1221] Nucleotide sequences of the GAM80 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM80 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM80 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM80 are further described hereinbelow with reference to Table Table1.

[1222] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM80 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[1223] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 81 (GAM81) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1224] GAM81 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM81 was detected is described hereinabove with reference to Figs. 2-8.

[1225] GAM81 gene, herein designated GAM GENE, and GAM81 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1226] GAM81 gene, herein designated GAM GENE, encodes a GAM81 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM81 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM81 precursor RNA is designated SEQ ID:54, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:54

is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[1227] GAM81 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM81 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1228] An enzyme complex designated DICER COMPLEX, dices the GAM81 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM81 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM81 RNA is designated SEQ ID:1730, and is provided hereinbelow with reference to the sequence listing part.

[1229] GAM81 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM81 target RNA, herein designated GAM TARGET RNA. GAM81 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1230] GAM81 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM81 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM81 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM81 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM81 tar-

get RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1231] The complementary binding of GAM81 RNA, herein designated GAM RNA, to target binding sites on GAM81 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM81 target RNA, herein designated GAM TARGET RNA, into GAM81 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1232] It is appreciated that GAM81 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM81 target genes. The mRNA of each one of this plurality of GAM81 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM81 RNA, herein designated GAM RNA, and which when bound by GAM81 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM81 target proteins.

[1233] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM81 gene, herein designated GAM GENE, on one or more GAM81 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1234] It is yet further appreciated that specific functions, and accordingly utilities, of GAM81 correlate with, and may be deduced from, the identity of the target genes which GAM81 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1235] Nucleotide sequences of the GAM81 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM81 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM81 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM81 are further described hereinbelow with reference to Table Table1.

[1236] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM81 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1237] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 82 (GAM82) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1238] GAM82 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM82 was detected is described hereinabove with reference to Figs. 2-8.

[1239] GAM82 gene, herein designated GAM GENE, and GAM82 target gene, herein designated GAM TARGET GENE, are

human genes contained in the human genome.

[1240] GAM82 gene, herein designated GAM GENE, encodes a GAM82 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM82 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM82 precursor RNA is designated SEQ ID:55, and is provided hereinbelow with reference to the sequence listing part.

[1241] GAM82 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM82 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1242] An enzyme complex designated DICER COMPLEX, dices the GAM82 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM82 RNA, herein desig-

nated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM82 RNA is designated SEQ ID:1731, and is provided hereinbelow with reference to the sequence listing part.

[1243] GAM82 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM82 target RNA, herein designated GAM TARGET RNA. GAM82 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1244] GAM82 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM82 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM82 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM82 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM82 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1245] The complementary binding of GAM82 RNA, herein designated GAM RNA, to target binding sites on GAM82 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM82 target RNA, herein designated GAM TARGET RNA, into GAM82 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1246] It is appreciated that GAM82 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM82 target genes. The mRNA of each one of this plurality of GAM82 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM82 RNA, herein designated GAM RNA, and which when bound by GAM82 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM82 target proteins.

[1247] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM82 gene, herein designated GAM GENE, on one or more GAM82 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny

RNA world, Science 294,779 (2001)).

[1248] It is yet further appreciated that specific functions, and accordingly utilities, of GAM82 correlate with, and may be deduced from, the identity of the target genes which GAM82 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1249] Nucleotide sequences of the GAM82 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM82 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM82 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM82 are further described hereinbelow with reference to Table Table1.

[1250] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM82 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1251] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 83 (GAM83) gene, which modulates expression of respec-

tive target genes thereof, the function and utility of which target genes is known in the art.

[1252] GAM83 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM83 was detected is described hereinabove with reference to Figs. 2-8.

[1253] GAM83 gene, herein designated GAM GENE, and GAM83 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1254] GAM83 gene, herein designated GAM GENE, encodes a GAM83 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM83 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM83 precursor RNA is designated SEQ ID:56, and is provided hereinbelow with reference to the sequence listing part.

[1255] GAM83 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM83 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1256] An enzyme complex designated DICER COMPLEX, dices the GAM83 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM83 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM83 RNA is designated SEQ ID:1732, and is provided hereinbelow with reference to the sequence listing part.

[1257] GAM83 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM83 target RNA, herein designated GAM TARGET RNA. GAM83 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PRO-

TEIN CODING and 3UTR respectively.

[1258] GAM83 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM83 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM83 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM83 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM83 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1259] The complementary binding of GAM83 RNA, herein designated GAM RNA, to target binding sites on GAM83 target

RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM83 target RNA, herein designated GAM TARGET RNA, into GAM83 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1260] It is appreciated that GAM83 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM83 target genes. The mRNA of each one of this plurality of GAM83 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM83 RNA, herein designated GAM RNA, and which when bound by GAM83 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM83 target proteins.

[1261] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM83 gene, herein designated GAM GENE, on one or more GAM83 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background

section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1262] It is yet further appreciated that specific functions, and accordingly utilities, of GAM83 correlate with, and may be deduced from, the identity of the target genes which GAM83 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1263] Nucleotide sequences of the GAM83 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM83 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM83 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM83 are further described hereinbelow with reference to Table Table1.

[1264] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM83 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1265] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 84 (GAM84) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1266] GAM84 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM84 was detected is described hereinabove with reference to Figs. 2-8.

[1267] GAM84 gene, herein designated GAM GENE, and GAM84 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1268] GAM84 gene, herein designated GAM GENE, encodes a GAM84 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM84 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM84 precursor RNA is designated SEQ ID:57, and is provided hereinbelow with reference to the sequence listing part.

[1269] GAM84 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM84 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1270] An enzyme complex designated DICER COMPLEX, dices the GAM84 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM84 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM84 RNA is designated SEQ ID:1733, and is provided hereinbelow with

reference to the sequence listing part.

[1271] GAM84 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM84 target RNA, herein designated GAM TARGET RNA. GAM84 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1272] GAM84 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM84 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM84 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM84 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM84 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1273] The complementary binding of GAM84 RNA, herein designated GAM RNA, to target binding sites on GAM84 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM84 target RNA, herein designated GAM TARGET RNA, into GAM84 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1274] It is appreciated that GAM84 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM84 target genes. The mRNA of each one of this plurality of GAM84 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM84 RNA, herein designated GAM RNA, and which when bound by GAM84 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM84 tar-

get proteins.

[1275] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM84 gene, herein designated GAM GENE, on one or more GAM84 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1276] It is yet further appreciated that specific functions, and accordingly utilities, of GAM84 correlate with, and may be deduced from, the identity of the target genes which GAM84 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1277] Nucleotide sequences of the GAM84 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM84 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM84 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM84 are further described hereinbelow with reference to Table Table1.

[1278] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM84 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1279] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 85 (GAM85) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1280] GAM85 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM85 was detected is described hereinabove with reference to Figs. 2-8.

[1281] GAM85 gene, herein designated GAM GENE, and GAM85

target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1282] GAM85 gene, herein designated GAM GENE, encodes a GAM85 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM85 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM85 precursor RNA is designated SEQ ID:58, and is provided hereinbelow with reference to the sequence listing part.

[1283] GAM85 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM85 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1284] An enzyme complex designated DICER COMPLEX, dices the GAM85 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, into GAM85 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM85 RNA is designated SEQ ID:1734, and is provided hereinbelow with reference to the sequence listing part.

[1285] GAM85 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM85 target RNA, herein designated GAM TARGET RNA. GAM85 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1286] GAM85 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM85 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM85 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM85 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM85 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1287] The complementary binding of GAM85 RNA, herein designated GAM RNA, to target binding sites on GAM85 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM85 target RNA, herein designated GAM TARGET RNA, into GAM85 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1288] It is appreciated that GAM85 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM85 target genes. The mRNA of each one of this plurality of GAM85 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM85 RNA, herein designated GAM RNA, and which when bound by GAM85 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM85 target proteins.

[1289] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM85 gene, herein designated GAM GENE, on one or more GAM85 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not

yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1290] It is yet further appreciated that specific functions, and accordingly utilities, of GAM85 correlate with, and may be deduced from, the identity of the target genes which GAM85 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1291] Nucleotide sequences of the GAM85 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM85 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM85 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM85 are further described hereinbelow with reference to Table Table1.

[1292] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM85 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1293] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

86 (GAM86) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1294] GAM86 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM86 was detected is described hereinabove with reference to Figs. 2-8.

[1295] GAM86 gene, herein designated GAM GENE, and GAM86 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1296] GAM86 gene, herein designated GAM GENE, encodes a GAM86 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM86 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM86 precursor RNA is designated SEQ ID:59, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:59 is located at position 61003 relative to contig NT_005994.13, on chromosome 3.

[1297] GAM86 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM86 folded precur-

sor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1298] An enzyme complex designated DICER COMPLEX, dices the GAM86 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM86 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM86 RNA is designated SEQ ID:1735, and is provided hereinbelow with reference to the sequence listing part.

[1299] GAM86 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM86 target RNA, herein designated GAM TARGET RNA. GAM86 target RNA, herein designated GAM TARGET RNA, com-

prises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1300] GAM86 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM86 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM86 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM86 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM86 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[1301] The complementary binding of GAM86 RNA, herein designated GAM RNA, to target binding sites on GAM86 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM86 target RNA, herein designated GAM TARGET RNA, into GAM86 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1302] It is appreciated that GAM86 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM86 target genes. The mRNA of each one of this plurality of GAM86 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM86 RNA, herein designated GAM RNA, and which when bound by GAM86 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM86 target proteins.

[1303] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM86 gene, herein designated GAM GENE, on one or

more GAM86 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1304] It is yet further appreciated that specific functions, and accordingly utilities, of GAM86 correlate with, and may be deduced from, the identity of the target genes which GAM86 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1305] Nucleotide sequences of the GAM86 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM86 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM86 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM86 are further described

hereinbelow with reference to Table Table1.

[1306] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM86 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1307] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 87 (GAM87) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1308] GAM87 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM87 was detected is described hereinabove with reference to Figs. 2-8.

[1309] GAM87 gene, herein designated GAM GENE, and GAM87 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1310] GAM87 gene, herein designated GAM GENE, encodes a GAM87 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM87 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM87 precursor RNA is designated SEQ ID:60, and is provided hereinbelow with reference to the sequence listing part.

[1311] GAM87 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM87 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1312] An enzyme complex designated DICER COMPLEX, dices the GAM87 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM87 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme

called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM87 RNA is designated SEQ ID:1736, and is provided hereinbelow with reference to the sequence listing part.

[1313] GAM87 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM87 target RNA, herein designated GAM TARGET RNA. GAM87 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1314] GAM87 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM87 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM87 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM87 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM87 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1315] The complementary binding of GAM87 RNA, herein designated GAM RNA, to target binding sites on GAM87 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM87 target RNA, herein designated GAM TARGET RNA, into GAM87 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1316] It is appreciated that GAM87 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM87 target genes. The mRNA of each one of this plurality of GAM87 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM87 RNA,

herein designated GAM RNA, and which when bound by GAM87 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM87 target proteins.

[1317] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM87 gene, herein designated GAM GENE, on one or more GAM87 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1318] It is yet further appreciated that specific functions, and accordingly utilities, of GAM87 correlate with, and may be deduced from, the identity of the target genes which

GAM87 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1319] Nucleotide sequences of the GAM87 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM87 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM87 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM87 are further described hereinbelow with reference to Table Table1.

[1320] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM87 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1321] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 88 (GAM88) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1322] GAM88 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM88 was detected is described hereinabove with reference to Figs. 2-8.

[1323] GAM88 gene, herein designated GAM GENE, and GAM88 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1324] GAM88 gene, herein designated GAM GENE, encodes a GAM88 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM88 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM88 precursor RNA is designated SEQ ID:61, and is provided hereinbelow with reference to the sequence listing part.

[1325] GAM88 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM88 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[1326] An enzyme complex designated DICER COMPLEX, dices the GAM88 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM88 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM88 RNA is designated SEQ ID:1737, and is provided hereinbelow with reference to the sequence listing part.

[1327] GAM88 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM88 target RNA, herein designated GAM TARGET RNA. GAM88 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1328] GAM88 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM88 target RNA, herein desig-

nated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM88 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM88 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM88 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1329] The complementary binding of GAM88 RNA, herein designated GAM RNA, to target binding sites on GAM88 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM88 target RNA, herein designated GAM TARGET RNA, into GAM88 target protein, herein desig-

nated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1330] It is appreciated that GAM88 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM88 target genes. The mRNA of each one of this plurality of GAM88 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM88 RNA, herein designated GAM RNA, and which when bound by GAM88 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM88 target proteins.

[1331] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM88 gene, herein designated GAM GENE, on one or more GAM88 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those

skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1332] It is yet further appreciated that specific functions, and accordingly utilities, of GAM88 correlate with, and may be deduced from, the identity of the target genes which GAM88 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1333] Nucleotide sequences of the GAM88 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM88 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM88 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM88 are further described hereinbelow with reference to Table Table1.

[1334] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM88 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1335] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 89 (GAM89) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1336] GAM89 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM89 was detected is described hereinabove with reference to Figs. 2-8.

[1337] GAM89 gene, herein designated GAM GENE, and GAM89 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1338] GAM89 gene, herein designated GAM GENE, encodes a GAM89 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM89 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM89 precursor RNA is designated SEQ ID:62, and is provided hereinbelow with reference to the sequence listing part.

[1339] GAM89 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM89 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1340] An enzyme complex designated DICER COMPLEX, dices the GAM89 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM89 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM89 RNA is designated SEQ ID:1738, and is provided hereinbelow with reference to the sequence listing part.

[1341] GAM89 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM89 target RNA, herein designated GAM TARGET RNA. GAM89

target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1342] GAM89 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM89 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM89 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM89 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM89 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1343] The complementary binding of GAM89 RNA, herein designated GAM RNA, to target binding sites on GAM89 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM89 target RNA, herein designated GAM TARGET RNA, into GAM89 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1344] It is appreciated that GAM89 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM89 target genes. The mRNA of each one of this plurality of GAM89 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM89 RNA, herein designated GAM RNA, and which when bound by GAM89 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM89 target proteins.

[1345] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM89 gene, herein designated GAM GENE, on one or more GAM89 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1346] It is yet further appreciated that specific functions, and accordingly utilities, of GAM89 correlate with, and may be deduced from, the identity of the target genes which GAM89 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1347] Nucleotide sequences of the GAM89 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM89 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM89 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM89 are further described hereinbelow with reference to Table Table1.

[1348] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM89 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1349] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 90 (GAM90) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1350] GAM90 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM90 was detected is described hereinabove with reference to Figs. 2-8.

[1351] GAM90 gene, herein designated GAM GENE, and GAM90 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1352] GAM90 gene, herein designated GAM GENE, encodes a GAM90 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM90 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM90 precursor RNA is designated SEQ ID:63, and is provided hereinbelow with reference to the sequence listing part.

[1353] GAM90 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM90 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1354] An enzyme complex designated DICER COMPLEX, dices the GAM90 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM90 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is

catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM90 RNA is designated SEQ ID:1739, and is provided hereinbelow with reference to the sequence listing part.

[1355] GAM90 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM90 target RNA, herein designated GAM TARGET RNA. GAM90 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1356] GAM90 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM90 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM90 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM90 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM90 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1357] The complementary binding of GAM90 RNA, herein designated GAM RNA, to target binding sites on GAM90 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM90 target RNA, herein designated GAM TARGET RNA, into GAM90 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1358] It is appreciated that GAM90 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM90 target genes. The mRNA of each one of this plurality of GAM90 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM90 RNA, herein designated GAM RNA, and which when bound by GAM90 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM90 target proteins.

[1359] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM90 gene, herein designated GAM GENE, on one or more GAM90 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1360] It is yet further appreciated that specific functions, and accordingly utilities, of GAM90 correlate with, and may be

deduced from, the identity of the target genes which GAM90 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1361] Nucleotide sequences of the GAM90 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM90 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM90 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM90 are further described hereinbelow with reference to Table Table1.

[1362] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM90 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1363] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 91 (GAM91) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1364] GAM91 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM91 was detected is described hereinabove with reference to Figs. 2-8.

[1365] GAM91 gene, herein designated GAM GENE, and GAM91 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1366] GAM91 gene, herein designated GAM GENE, encodes a GAM91 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM91 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM91 precursor RNA is designated SEQ ID:64, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:64 is located at position 3757784 relative to contig NT_033898.3, on chromosome 10.

[1367] GAM91 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM91 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1368] An enzyme complex designated DICER COMPLEX, dices the GAM91 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM91 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM91 RNA is designated SEQ ID:1740, and is provided hereinbelow with reference to the sequence listing part.

[1369] GAM91 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM91 target RNA, herein designated GAM TARGET RNA. GAM91 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1370] GAM91 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM91 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM91 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM91 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM91 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1371] The complementary binding of GAM91 RNA, herein designated GAM RNA, to target binding sites on GAM91 target RNA, herein designated GAM TARGET RNA, such as BIND-

ING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM91 target RNA, herein designated GAM TARGET RNA, into GAM91 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1372] It is appreciated that GAM91 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM91 target genes. The mRNA of each one of this plurality of GAM91 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM91 RNA, herein designated GAM RNA, and which when bound by GAM91 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM91 target proteins.

[1373] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM91 gene, herein designated GAM GENE, on one or more GAM91 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site

has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1374] It is yet further appreciated that specific functions, and accordingly utilities, of GAM91 correlate with, and may be deduced from, the identity of the target genes which GAM91 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1375] Nucleotide sequences of the GAM91 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM91 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM91 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM91 are further described hereinbelow with reference to Table Table1.

[1376] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM91 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1377] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 92 (GAM92) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1378] GAM92 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM92 was detected is described hereinabove with reference to Figs. 2-8.

[1379] GAM92 gene, herein designated GAM GENE, and GAM92 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1380] GAM92 gene, herein designated GAM GENE, encodes a GAM92 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM92 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM92 precursor RNA is designated

SEQ ID:65, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:65 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[1381] GAM92 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM92 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1382] An enzyme complex designated DICER COMPLEX, dices the GAM92 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM92 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM92 RNA is

designated SEQ ID:1741, and is provided hereinbelow with reference to the sequence listing part.

[1383] GAM92 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM92 target RNA, herein designated GAM TARGET RNA. GAM92 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1384] GAM92 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM92 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM92 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM92 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM92 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1385] The complementary binding of GAM92 RNA, herein designated GAM RNA, to target binding sites on GAM92 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM92 target RNA, herein designated GAM TARGET RNA, into GAM92 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1386] It is appreciated that GAM92 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM92 target genes. The mRNA of each one of this plurality of GAM92 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM92 RNA, herein designated GAM RNA, and which when bound by GAM92 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM92 target proteins.

[1387] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM92 gene, herein designated GAM GENE, on one or more GAM92 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1388] It is yet further appreciated that specific functions, and accordingly utilities, of GAM92 correlate with, and may be deduced from, the identity of the target genes which GAM92 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1389] Nucleotide sequences of the GAM92 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM92 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM92 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM92 are further described hereinbelow with reference to Table Table1.

[1390] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM92 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1391] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 93 (GAM93) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1392] GAM93 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM93 was detected is described hereinabove with reference to Figs. 2-8.

[1393] GAM93 gene, herein designated GAM GENE, and GAM93 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1394] GAM93 gene, herein designated GAM GENE, encodes a GAM93 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM93 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM93 precursor RNA is designated SEQ ID:66, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:66 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[1395] GAM93 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM93 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[1396] An enzyme complex designated DICER COMPLEX, dices the GAM93 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM93 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM93 RNA is designated SEQ ID:1742, and is provided hereinbelow with reference to the sequence listing part.

[1397] GAM93 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM93 target RNA, herein designated GAM TARGET RNA. GAM93 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1398] GAM93 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM93 target RNA, herein desig-

nated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM93 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM93 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM93 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1399] The complementary binding of GAM93 RNA, herein designated GAM RNA, to target binding sites on GAM93 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM93 target RNA, herein designated GAM TARGET RNA, into GAM93 target protein, herein desig-

nated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1400] It is appreciated that GAM93 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM93 target genes. The mRNA of each one of this plurality of GAM93 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM93 RNA, herein designated GAM RNA, and which when bound by GAM93 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM93 target proteins.

[1401] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM93 gene, herein designated GAM GENE, on one or more GAM93 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those

skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1402] It is yet further appreciated that specific functions, and accordingly utilities, of GAM93 correlate with, and may be deduced from, the identity of the target genes which GAM93 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1403] Nucleotide sequences of the GAM93 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM93 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM93 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM93 are further described hereinbelow with reference to Table Table1.

[1404] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM93 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1405] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 94 (GAM94) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1406] GAM94 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM94 was detected is described hereinabove with reference to Figs. 2-8.

[1407] GAM94 gene, herein designated GAM GENE, and GAM94 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1408] GAM94 gene, herein designated GAM GENE, encodes a GAM94 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM94 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM94 precursor RNA is designated SEQ ID:67, and is provided hereinbelow with reference to the sequence listing part.

[1409] GAM94 has 12 highly conserved, expressed mouse ho-

mologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[1410] SEQ ID:99337 detected in mouse EST Accession AI264984.1.

[1411] SEQ ID:99338 detected in mouse EST Accession AI156313.1.

[1412] SEQ ID:99339 detected in mouse EST Accession BG974532.1.

[1413] SEQ ID:99340 detected in mouse EST Accession BG870381.1.

[1414] SEQ ID:99341 detected in mouse EST Accession BG973293.1.

[1415] SEQ ID:99342 detected in mouse EST Accession BF146992.1.

[1416] SEQ ID:99343 detected in mouse EST Accession BG970816.1.

[1417] SEQ ID:99345 detected in mouse EST Accession AA144398.1.

[1418] SEQ ID:99346 detected in mouse EST Accession AW230495.1.

[1419] SEQ ID:99347 detected in mouse EST Accession

BI153175.1.

[1420] SEQ ID:99348 detected in mouse EST Accession BF144364.1.

[1421] SEQ ID:99349 detected in mouse EST Accession BG864461.1.

[1422] GAM94 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM94 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1423] An enzyme complex designated DICER COMPLEX, dices the GAM94 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM94 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A

probable (over 89%) nucleotide sequence of GAM94 RNA is designated SEQ ID:1743, and is provided hereinbelow with reference to the sequence listing part.

[1424] GAM94 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM94 target RNA, herein designated GAM TARGET RNA. GAM94 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1425] GAM94 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM94 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM94 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM94 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM94 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1426] The complementary binding of GAM94 RNA, herein designated GAM RNA, to target binding sites on GAM94 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM94 target RNA, herein designated GAM TARGET RNA, into GAM94 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1427] It is appreciated that GAM94 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM94 target genes. The mRNA of each one of this plurality of GAM94 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM94 RNA, herein designated GAM RNA, and which when bound by

GAM94 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM94 target proteins.

[1428] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM94 gene, herein designated GAM GENE, on one or more GAM94 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1429] It is yet further appreciated that specific functions, and accordingly utilities, of GAM94 correlate with, and may be deduced from, the identity of the target genes which GAM94 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[1430] Nucleotide sequences of the GAM94 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM94 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM94 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM94 are further described hereinbelow with reference to Table Table1.

[1431] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM94 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1432] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 95 (GAM95) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1433] GAM95 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM95 was detected is described hereinabove

with reference to Figs. 2-8.

[1434] GAM95 gene, herein designated GAM GENE, and GAM95 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1435] GAM95 gene, herein designated GAM GENE, encodes a GAM95 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM95 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM95 precursor RNA is designated SEQ ID:68, and is provided hereinbelow with reference to the sequence listing part.

[1436] GAM95 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM95 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1437] An enzyme complex designated DICER COMPLEX, dices the GAM95 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM95 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM95 RNA is designated SEQ ID:1744, and is provided hereinbelow with reference to the sequence listing part.

[1438] GAM95 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM95 target RNA, herein designated GAM TARGET RNA. GAM95 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1439] GAM95 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM95 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM95 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM95 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM95 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1440] The complementary binding of GAM95 RNA, herein designated GAM RNA, to target binding sites on GAM95 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM95 target RNA, herein designated GAM TARGET RNA, into GAM95 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is there-

fore outlined by a broken line.

[1441] It is appreciated that GAM95 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM95 target genes. The mRNA of each one of this plurality of GAM95 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM95 RNA, herein designated GAM RNA, and which when bound by GAM95 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM95 target proteins.

[1442] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM95 gene, herein designated GAM GENE, on one or more GAM95 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes

by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1443] It is yet further appreciated that specific functions, and accordingly utilities, of GAM95 correlate with, and may be deduced from, the identity of the target genes which GAM95 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1444] Nucleotide sequences of the GAM95 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM95 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM95 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM95 are further described hereinbelow with reference to Table Table1.

[1445] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM95 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1446] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 96 (GAM96) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1447] GAM96 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM96 was detected is described hereinabove with reference to Figs. 2-8.

[1448] GAM96 gene, herein designated GAM GENE, and GAM96 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1449] GAM96 gene, herein designated GAM GENE, encodes a GAM96 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM96 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM96 precursor RNA is designated SEQ ID:69, and is provided hereinbelow with reference to the sequence listing part.

[1450] GAM96 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM96 folded precur-

sor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1451] An enzyme complex designated DICER COMPLEX, dices the GAM96 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM96 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM96 RNA is designated SEQ ID:1745, and is provided hereinbelow with reference to the sequence listing part.

[1452] GAM96 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM96 target RNA, herein designated GAM TARGET RNA. GAM96 target RNA, herein designated GAM TARGET RNA, com-

prises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1453] GAM96 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM96 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM96 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM96 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM96 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[1454] The complementary binding of GAM96 RNA, herein designated GAM RNA, to target binding sites on GAM96 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM96 target RNA, herein designated GAM TARGET RNA, into GAM96 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1455] It is appreciated that GAM96 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM96 target genes. The mRNA of each one of this plurality of GAM96 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM96 RNA, herein designated GAM RNA, and which when bound by GAM96 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM96 target proteins.

[1456] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM96 gene, herein designated GAM GENE, on one or

more GAM96 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1457] It is yet further appreciated that specific functions, and accordingly utilities, of GAM96 correlate with, and may be deduced from, the identity of the target genes which GAM96 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1458] Nucleotide sequences of the GAM96 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM96 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM96 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM96 are further described

hereinbelow with reference to Table Table1.

[1459] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM96 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1460] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 97 (GAM97) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1461] GAM97 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM97 was detected is described hereinabove with reference to Figs. 2-8.

[1462] GAM97 gene, herein designated GAM GENE, and GAM97 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1463] GAM97 gene, herein designated GAM GENE, encodes a GAM97 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM97 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM97 precursor RNA is designated SEQ ID:70, and is provided hereinbelow with reference to the sequence listing part.

[1464] GAM97 has 12 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[1465] SEQ ID:99602 detected in mouse EST Accession BF144364.1.

[1466] SEQ ID:99603 detected in mouse EST Accession BG864461.1.

[1467] SEQ ID:99604 detected in mouse EST Accession AA144398.1.

[1468] SEQ ID:99605 detected in mouse EST Accession AI156313.1.

[1469] SEQ ID:99606 detected in mouse EST Accession BG970816.1.

[1470] SEQ ID:99613 detected in mouse EST Accession BF146992.1.

[1471] SEQ ID:99614 detected in mouse EST Accession BG974532.1.

[1472] SEQ ID:99615 detected in mouse EST Accession BG870381.1.

[1473] SEQ ID:99616 detected in mouse EST Accession BG973293.1.

[1474] SEQ ID:99617 detected in mouse EST Accession BI153175.1.

[1475] SEQ ID:99625 detected in mouse EST Accession AI264984.1.

[1476] SEQ ID:99626 detected in mouse EST Accession AW230495.1.

[1477] GAM97 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM97 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1478] An enzyme complex designated DICER COMPLEX, dices

the GAM97 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM97 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM97 RNA is designated SEQ ID:1746, and is provided hereinbelow with reference to the sequence listing part.

[1479] GAM97 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM97 target RNA, herein designated GAM TARGET RNA. GAM97 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1480] GAM97 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM97 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM97

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM97 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM97 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1481] The complementary binding of GAM97 RNA, herein designated GAM RNA, to target binding sites on GAM97 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM97 target RNA, herein designated GAM TARGET RNA, into GAM97 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1482] It is appreciated that GAM97 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM97 target genes. The mRNA of each one of this plurality of GAM97 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM97 RNA, herein designated GAM RNA, and which when bound by GAM97 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM97 target proteins.

[1483] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM97 gene, herein designated GAM GENE, on one or more GAM97 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complemen-

tary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1484] It is yet further appreciated that specific functions, and accordingly utilities, of GAM97 correlate with, and may be deduced from, the identity of the target genes which GAM97 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1485] Nucleotide sequences of the GAM97 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM97 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM97 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM97 are further described hereinbelow with reference to Table Table1.

[1486] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM97 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1487] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 98 (GAM98) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1488] GAM98 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM98 was detected is described hereinabove with reference to Figs. 2-8.

[1489] GAM98 gene, herein designated GAM GENE, and GAM98 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1490] GAM98 gene, herein designated GAM GENE, encodes a GAM98 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM98 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM98 precursor RNA is designated SEQ ID:71, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:71 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[1491] GAM98 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM98 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1492] An enzyme complex designated DICER COMPLEX, dices the GAM98 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM98 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM98 RNA is designated SEQ ID:1747, and is provided hereinbelow with reference to the sequence listing part.

[1493] GAM98 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM98 target RNA, herein designated GAM TARGET RNA. GAM98

target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1494] GAM98 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM98 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM98 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM98 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM98 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1495] The complementary binding of GAM98 RNA, herein designated GAM RNA, to target binding sites on GAM98 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM98 target RNA, herein designated GAM TARGET RNA, into GAM98 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1496] It is appreciated that GAM98 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM98 target genes. The mRNA of each one of this plurality of GAM98 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM98 RNA, herein designated GAM RNA, and which when bound by GAM98 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM98 target proteins.

[1497] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM98 gene, herein designated GAM GENE, on one or more GAM98 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1498] It is yet further appreciated that specific functions, and accordingly utilities, of GAM98 correlate with, and may be deduced from, the identity of the target genes which GAM98 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1499] Nucleotide sequences of the GAM98 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM98 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM98 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM98 are further described hereinbelow with reference to Table Table1.

[1500] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM98 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1501] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 99 (GAM99) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1502] GAM99 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM99 was detected is described hereinabove with reference to Figs. 2-8.

[1503] GAM99 gene, herein designated GAM GENE, and GAM99 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1504] GAM99 gene, herein designated GAM GENE, encodes a GAM99 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM99 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM99 precursor RNA is designated SEQ ID:72, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:72 is located at position 280476 relative to contig NT_007758.8, on chromosome 7.

[1505] GAM99 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM99 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1506] An enzyme complex designated DICER COMPLEX, dices the GAM99 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM99 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA seg-

ment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM99 RNA is designated SEQ ID:1748, and is provided hereinbelow with reference to the sequence listing part.

[1507] GAM99 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM99 target RNA, herein designated GAM TARGET RNA. GAM99 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1508] GAM99 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM99 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM99 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM99 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM99 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1509] The complementary binding of GAM99 RNA, herein designated GAM RNA, to target binding sites on GAM99 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM99 target RNA, herein designated GAM TARGET RNA, into GAM99 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1510] It is appreciated that GAM99 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM99 target genes. The mRNA of each one of this plu-

rality of GAM99 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM99 RNA, herein designated GAM RNA, and which when bound by GAM99 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM99 target proteins.

[1511] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM99 gene, herein designated GAM GENE, on one or more GAM99 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1512] It is yet further appreciated that specific functions, and accordingly utilities, of GAM99 correlate with, and may be deduced from, the identity of the target genes which GAM99 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1513] Nucleotide sequences of the GAM99 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM99 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM99 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM99 are further described hereinbelow with reference to Table Table1.

[1514] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM99 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1515] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 100 (GAM100) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[1516] GAM100 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM100 was detected is described hereinabove with reference to Figs. 2-8.

[1517] GAM100 gene, herein designated GAM GENE, and GAM100 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1518] GAM100 gene, herein designated GAM GENE, encodes a GAM100 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM100 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM100 precursor RNA is designated SEQ ID:73, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:73 is located at position 161375 relative to contig NT_035283.2, on chromosome 12.

[1519] GAM100 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1520] An enzyme complex designated DICER COMPLEX, dices the GAM100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM100 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM100 RNA is designated SEQ ID:1749, and is provided hereinbelow with reference to the sequence listing part.

[1521] GAM100 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM100 target RNA, herein designated GAM TARGET RNA. GAM100 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1522] GAM100 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM100 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM100 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM100 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM100 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1523] The complementary binding of GAM100 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM100 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM100 target RNA, herein designated GAM TARGET RNA, into GAM100 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1524] It is appreciated that GAM100 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM100 target genes. The mRNA of each one of this plurality of GAM100 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM100 RNA, herein designated GAM RNA, and which when bound by GAM100 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM100 target proteins.

[1525] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM100 gene, herein designated GAM GENE, on one or more GAM100 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1526] It is yet further appreciated that specific functions, and accordingly utilities, of GAM100 correlate with, and may be deduced from, the identity of the target genes which GAM100 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1527] Nucleotide sequences of the GAM100 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM100 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM100 are further described hereinbelow with reference to Table Table1.

[1528] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM100 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1529] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 101 (GAM101) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1530] GAM101 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM101 was detected is described hereinabove with reference to Figs. 2-8.

[1531] GAM101 gene, herein designated GAM GENE, and GAM101 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1532] GAM101 gene, herein designated GAM GENE, encodes a GAM101 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM101 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM101 precursor RNA is designated SEQ ID:74, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:74 is located at position 1913378 relative to contig NT_034563.2, on chromosome 3.

[1533] GAM101 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1534] An enzyme complex designated DICER COMPLEX, dices the GAM101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM101 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM101 RNA is designated SEQ ID:1750, and is provided hereinbelow with reference to the sequence listing part.

[1535] GAM101 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM101 target RNA, herein designated GAM TARGET RNA. GAM101 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1536] GAM101 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM101 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM101 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM101 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM101 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1537] The complementary binding of GAM101 RNA, herein designated GAM RNA, to target binding sites on GAM101 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM101 target RNA, herein designated GAM TARGET RNA, into GAM101 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1538] It is appreciated that GAM101 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM101 target genes. The mRNA of each one of this plurality of GAM101 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM101 RNA,

herein designated GAM RNA, and which when bound by GAM101 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM101 target proteins.

[1539] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM101 gene, herein designated GAM GENE, on one or more GAM101 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1540] It is yet further appreciated that specific functions, and accordingly utilities, of GAM101 correlate with, and may be deduced from, the identity of the target genes which

GAM101 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1541] Nucleotide sequences of the GAM101 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM101 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM101 are further described hereinbelow with reference to Table Table1.

[1542] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM101 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1543] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 102 (GAM102) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1544] GAM102 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM102 was detected is described hereinabove with reference to Figs. 2-8.

[1545] GAM102 gene, herein designated GAM GENE, and GAM102 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1546] GAM102 gene, herein designated GAM GENE, encodes a GAM102 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM102 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM102 precursor RNA is designated SEQ ID:75, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:75 is located at position 1012969 relative to contig NT_010823.11, on chromosome 17.

[1547] GAM102 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1548] An enzyme complex designated DICER COMPLEX, dices the GAM102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM102 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM102 RNA is designated SEQ ID:1751, and is provided hereinbelow with reference to the sequence listing part.

[1549] GAM102 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM102 target RNA, herein designated GAM TARGET RNA. GAM102 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1550] GAM102 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM102 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM102 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM102 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM102 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1551] The complementary binding of GAM102 RNA, herein designated GAM RNA, to target binding sites on GAM102 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM102 target RNA, herein designated GAM TARGET RNA, into GAM102 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1552] It is appreciated that GAM102 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM102 target genes. The mRNA of each one of this plurality of GAM102 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM102 RNA, herein designated GAM RNA, and which when bound by GAM102 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM102 target proteins.

[1553] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM102 gene, herein designated GAM GENE, on one or more GAM102 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1554] It is yet further appreciated that specific functions, and accordingly utilities, of GAM102 correlate with, and may be deduced from, the identity of the target genes which GAM102 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1555] Nucleotide sequences of the GAM102 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM102 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM102 are further described hereinbelow with reference to Table Table1.

[1556] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM102 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1557] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 103 (GAM103) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1558] GAM103 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM103 was detected is described hereinabove with reference to Figs. 2-8.

[1559] GAM103 gene, herein designated GAM GENE, and GAM103 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1560] GAM103 gene, herein designated GAM GENE, encodes a GAM103 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM103 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM103 precursor RNA is designated SEQ ID:76, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:76 is located at position 279925 relative to contig NT_009487.13, on chromosome 12.

[1561] GAM103 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM103 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1562] An enzyme complex designated DICER COMPLEX, dices the GAM103 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM103 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM103 RNA is designated SEQ ID:1752, and is provided

hereinbelow with reference to the sequence listing part.

[1563] GAM103 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM103 target RNA, herein designated GAM TARGET RNA.
GAM103 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1564] GAM103 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM103 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM103 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM103 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM103 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1565] The complementary binding of GAM103 RNA, herein designated GAM RNA, to target binding sites on GAM103 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM103 target RNA, herein designated GAM TARGET RNA, into GAM103 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1566] It is appreciated that GAM103 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM103 target genes. The mRNA of each one of this plurality of GAM103 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM103 RNA, herein designated GAM RNA, and which when bound by GAM103 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM103 tar-

get proteins.

[1567] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM103 gene, herein designated GAM GENE, on one or more GAM103 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1568] It is yet further appreciated that specific functions, and accordingly utilities, of GAM103 correlate with, and may be deduced from, the identity of the target genes which GAM103 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1569] Nucleotide sequences of the GAM103 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM103 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM103 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM103 are further described hereinbelow with reference to Table Table1.

[1570] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM103 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1571] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 104 (GAM104) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1572] GAM104 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM104 was detected is described hereinabove with reference to Figs. 2-8.

[1573] GAM104 gene, herein designated GAM GENE, and

GAM104 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1574] GAM104 gene, herein designated GAM GENE, encodes a GAM104 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM104 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM104 precursor RNA is designated SEQ ID:77, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:77 is located at position 14349 relative to contig NT_006081.13, on chromosome 4.

[1575] GAM104 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM104 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1576] An enzyme complex designated DICER COMPLEX, dices the GAM104 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM104 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM104 RNA is designated SEQ ID:1753, and is provided hereinbelow with reference to the sequence listing part.

[1577] GAM104 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM104 target RNA, herein designated GAM TARGET RNA. GAM104 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1578] GAM104 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM104 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM104 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM104 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM104 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1579] The complementary binding of GAM104 RNA, herein designated GAM RNA, to target binding sites on GAM104 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM104 target RNA, herein designated GAM TARGET RNA, into GAM104 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[1580] It is appreciated that GAM104 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM104 target genes. The mRNA of each one of this plurality of GAM104 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM104 RNA, herein designated GAM RNA, and which when bound by GAM104 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM104 target proteins.

[1581] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM104 gene, herein designated GAM GENE, on one or more GAM104 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1582] It is yet further appreciated that specific functions, and accordingly utilities, of GAM104 correlate with, and may be deduced from, the identity of the target genes which GAM104 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1583] Nucleotide sequences of the GAM104 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM104 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM104 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM104 are further described hereinbelow with reference to Table Table1.

[1584] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM104 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1585] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 105 (GAM105) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1586] GAM105 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM105 was detected is described hereinabove with reference to Figs. 2-8.

[1587] GAM105 gene, herein designated GAM GENE, and GAM105 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1588] GAM105 gene, herein designated GAM GENE, encodes a GAM105 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM105 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM105 precursor RNA is designated SEQ ID:78, and is provided hereinbelow with reference to the sequence listing part.

[1589] GAM105 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM105 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1590] An enzyme complex designated DICER COMPLEX, dices the GAM105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM105 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM105 RNA is designated SEQ ID:1754, and is provided hereinbelow with reference to the sequence listing part.

[1591] GAM105 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM105 target RNA, herein designated GAM TARGET RNA. GAM105 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1592] GAM105 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM105 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM105 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM105 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM105 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[1593] The complementary binding of GAM105 RNA, herein designated GAM RNA, to target binding sites on GAM105 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM105 target RNA, herein designated GAM TARGET RNA, into GAM105 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1594] It is appreciated that GAM105 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM105 target genes. The mRNA of each one of this plurality of GAM105 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM105 RNA, herein designated GAM RNA, and which when bound by GAM105 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM105 target proteins.

[1595] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM105 gene, herein designated GAM GENE, on one or

more GAM105 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1596] It is yet further appreciated that specific functions, and accordingly utilities, of GAM105 correlate with, and may be deduced from, the identity of the target genes which GAM105 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1597] Nucleotide sequences of the GAM105 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM105 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM105 are further de-

scribed hereinbelow with reference to Table Table1.

[1598] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM105 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1599] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 106 (GAM106) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1600] GAM106 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM106 was detected is described hereinabove with reference to Figs. 2-8.

[1601] GAM106 gene, herein designated GAM GENE, and GAM106 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1602] GAM106 gene, herein designated GAM GENE, encodes a GAM106 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM106 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM106 precursor RNA is designated SEQ ID:79, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:79 is located at position 33703783 relative to contig NT_007592.11, on chromosome 6.

[1603] GAM106 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1604] An enzyme complex designated DICER COMPLEX, dices the GAM106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM106 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM106 RNA is designated SEQ ID:1755, and is provided hereinbelow with reference to the sequence listing part.

[1605] GAM106 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM106 target RNA, herein designated GAM TARGET RNA. GAM106 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1606] GAM106 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM106 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM106 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM106 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM106 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1607] The complementary binding of GAM106 RNA, herein designated GAM RNA, to target binding sites on GAM106 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM106 target RNA, herein designated GAM TARGET RNA, into GAM106 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1608] It is appreciated that GAM106 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM106 target genes. The mRNA of each one of this plurality of GAM106 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM106 RNA, herein designated GAM RNA, and which when bound by GAM106 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM106 target proteins.

[1609] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM106 gene, herein designated GAM GENE, on one or more GAM106 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1610] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM106 correlate with, and may be deduced from, the identity of the target genes which GAM106 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1611] Nucleotide sequences of the GAM106 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM106 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM106 are further described hereinbelow with reference to Table Table1.

[1612] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM106 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1613] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 107 (GAM107) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1614] GAM107 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM107 was detected is described hereinabove with reference to Figs. 2-8.

[1615] GAM107 gene, herein designated GAM GENE, and GAM107 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1616] GAM107 gene, herein designated GAM GENE, encodes a GAM107 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM107 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM107 precursor RNA is designated SEQ ID:80, and is provided hereinbelow with reference to the sequence listing part.

[1617] GAM107 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM107 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1618] An enzyme complex designated DICER COMPLEX, dices the GAM107 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM107 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM107 RNA is designated SEQ ID:1756, and is provided hereinbelow with reference to the sequence listing part.

[1619] GAM107 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM107 target RNA, herein designated GAM TARGET RNA. GAM107 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1620] GAM107 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM107 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM107 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM107 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM107 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1621] The complementary binding of GAM107 RNA, herein designated GAM RNA, to target binding sites on GAM107 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM107 target RNA, herein designated GAM TARGET RNA, into GAM107 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1622] It is appreciated that GAM107 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM107 target genes. The mRNA of each one of this plurality of GAM107 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM107 RNA, herein designated GAM RNA, and which when bound by GAM107 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM107 target proteins.

[1623] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM107 gene, herein designated GAM GENE, on one or more GAM107 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1624] It is yet further appreciated that specific functions, and accordingly utilities, of GAM107 correlate with, and may be deduced from, the identity of the target genes which GAM107 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1625] Nucleotide sequences of the GAM107 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM107 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM107 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM107 are further described hereinbelow with reference to Table Table1.

[1626] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM107 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1627] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 108 (GAM108) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1628] GAM108 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM108 was detected is described hereinabove with reference to Figs. 2-8.

[1629] GAM108 gene, herein designated GAM GENE, and GAM108 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1630] GAM108 gene, herein designated GAM GENE, encodes a GAM108 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM108 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM108 precursor RNA is designated SEQ ID:81, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:81 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[1631] GAM108 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1632] An enzyme complex designated DICER COMPLEX, dices the GAM108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM108 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM108 RNA is designated SEQ ID:1757, and is provided

hereinbelow with reference to the sequence listing part.

[1633] GAM108 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM108 target RNA, herein designated GAM TARGET RNA. GAM108 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1634] GAM108 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM108 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM108 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM108 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM108 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1635] The complementary binding of GAM108 RNA, herein designated GAM RNA, to target binding sites on GAM108 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM108 target RNA, herein designated GAM TARGET RNA, into GAM108 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1636] It is appreciated that GAM108 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM108 target genes. The mRNA of each one of this plurality of GAM108 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM108 RNA, herein designated GAM RNA, and which when bound by GAM108 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM108 tar-

get proteins.

[1637] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM108 gene, herein designated GAM GENE, on one or more GAM108 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1638] It is yet further appreciated that specific functions, and accordingly utilities, of GAM108 correlate with, and may be deduced from, the identity of the target genes which GAM108 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1639] Nucleotide sequences of the GAM108 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM108 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM108 are further described hereinbelow with reference to Table Table1.

[1640] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM108 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1641] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 109 (GAM109) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1642] GAM109 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM109 was detected is described hereinabove with reference to Figs. 2-8.

[1643] GAM109 gene, herein designated GAM GENE, and

GAM109 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1644] GAM109 gene, herein designated GAM GENE, encodes a GAM109 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM109 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM109 precursor RNA is designated SEQ ID:82, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:82 is located at position 551373 relative to contig NT_010783.11, on chromosome 17.

[1645] GAM109 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1646] An enzyme complex designated DICER COMPLEX, dices the GAM109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM109 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM109 RNA is designated SEQ ID:1758, and is provided hereinbelow with reference to the sequence listing part.

[1647] GAM109 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM109 target RNA, herein designated GAM TARGET RNA. GAM109 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1648] GAM109 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM109 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM109 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM109 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM109 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1649] The complementary binding of GAM109 RNA, herein designated GAM RNA, to target binding sites on GAM109 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM109 target RNA, herein designated GAM TARGET RNA, into GAM109 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[1650] It is appreciated that GAM109 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM109 target genes. The mRNA of each one of this plurality of GAM109 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM109 RNA, herein designated GAM RNA, and which when bound by GAM109 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM109 target proteins.

[1651] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM109 gene, herein designated GAM GENE, on one or more GAM109 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1652] It is yet further appreciated that specific functions, and accordingly utilities, of GAM109 correlate with, and may be deduced from, the identity of the target genes which GAM109 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1653] Nucleotide sequences of the GAM109 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM109 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM109 are further described hereinbelow with reference to Table Table1.

[1654] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM109 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1655] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 110 (GAM110) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1656] GAM110 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM110 was detected is described hereinabove with reference to Figs. 2-8.

[1657] GAM110 gene, herein designated GAM GENE, and GAM110 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1658] GAM110 gene, herein designated GAM GENE, encodes a GAM110 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM110 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM110 precursor RNA is designated SEQ ID:83, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:83 is located at position 2025400 relative to contig NT_005832.12, on chromosome 3.

[1659] GAM110 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1660] An enzyme complex designated DICER COMPLEX, dices the GAM110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM110 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM110 RNA is designated SEQ ID:1759, and is provided hereinbelow with reference to the sequence listing part.

[1661] GAM110 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM110

target RNA, herein designated GAM TARGET RNA.

GAM110 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1662] GAM110 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM110 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM110 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM110 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM110 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1663] The complementary binding of GAM110 RNA, herein designated GAM RNA, to target binding sites on GAM110 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM110 target RNA, herein designated GAM TARGET RNA, into GAM110 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1664] It is appreciated that GAM110 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM110 target genes. The mRNA of each one of this plurality of GAM110 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM110 RNA, herein designated GAM RNA, and which when bound by GAM110 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM110 target proteins.

[1665] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM110 gene, herein designated GAM GENE, on one or more GAM110 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1666] It is yet further appreciated that specific functions, and accordingly utilities, of GAM110 correlate with, and may be deduced from, the identity of the target genes which GAM110 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1667] Nucleotide sequences of the GAM110 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM110 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM110 are further described hereinbelow with reference to Table Table1.

[1668] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM110 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1669] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 111 (GAM111) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1670] GAM111 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM111 was detected is described hereinabove with reference to Figs. 2-8.

[1671] GAM111 gene, herein designated GAM GENE, and GAM111 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1672] GAM111 gene, herein designated GAM GENE, encodes a

GAM111 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM111 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM111 precursor RNA is designated SEQ ID:84, and is provided hereinbelow with reference to the sequence listing part.

[1673] GAM111 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1674] An enzyme complex designated DICER COMPLEX, dices the GAM111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM111 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM111 RNA is designated SEQ ID:1760, and is provided hereinbelow with reference to the sequence listing part.

[1675] GAM111 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM111 target RNA, herein designated GAM TARGET RNA. GAM111 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1676] GAM111 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM111 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM111 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM111 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM111 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1677] The complementary binding of GAM111 RNA, herein designated GAM RNA, to target binding sites on GAM111 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM111 target RNA, herein designated GAM TARGET RNA, into GAM111 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1678] It is appreciated that GAM111 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM111 target genes. The mRNA of each one of this plurality of GAM111 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM111 RNA, herein designated GAM RNA, and which when bound by GAM111 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM111 target proteins.

[1679] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM111 gene, herein designated GAM GENE, on one or more GAM111 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1680] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM111 correlate with, and may be deduced from, the identity of the target genes which GAM111 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1681] Nucleotide sequences of the GAM111 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM111 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM111 are further described hereinbelow with reference to Table Table1.

[1682] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM111 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1683] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 112 (GAM112) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1684] GAM112 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM112 was detected is described hereinabove with reference to Figs. 2-8.

[1685] GAM112 gene, herein designated GAM GENE, and GAM112 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1686] GAM112 gene, herein designated GAM GENE, encodes a GAM112 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM112 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM112 precursor RNA is designated SEQ ID:85, and is provided hereinbelow with reference to the sequence listing part.

[1687] GAM112 has 62 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[1688] SEQ ID:99142 detected in mouse EST Accession AW240449.1.

[1689] SEQ ID:99143 detected in mouse EST Accession BE692663.1.

[1690] SEQ ID:99144 detected in mouse EST Accession AA237479.1.

[1691] SEQ ID:99145 detected in mouse EST Accession BF020203.1.

[1692] SEQ ID:99146 detected in mouse EST Accession AI152470.1.

[1693] SEQ ID:99147 detected in mouse EST Accession AW241043.1.

[1694] SEQ ID:99148 detected in mouse EST Accession AW989706.1.

[1695] SEQ ID:99149 detected in mouse EST Accession BI110254.1.

[1696] SEQ ID:99150 detected in mouse EST Accession BE690578.1.

[1697] SEQ ID:99151 detected in mouse EST Accession BE689588.1.

[1698] SEQ ID:99152 detected in mouse EST Accession BG068359.1.

[1699] SEQ ID:99153 detected in mouse EST Accession BF226299.1.

[1700] SEQ ID:99154 detected in mouse EST Accession

AW909366.1.

[1701] SEQ ID:100078 detected in mouse EST Accession W16182.1.

[1702] SEQ ID:100079 detected in mouse EST Accession BE624221.1.

[1703] SEQ ID:100080 detected in mouse EST Accession BF450285.1.

[1704] SEQ ID:100081 detected in mouse EST Accession AA397121.1.

[1705] SEQ ID:100082 detected in mouse EST Accession BE851242.1.

[1706] SEQ ID:100083 detected in mouse EST Accession BE690148.1.

[1707] SEQ ID:100084 detected in mouse EST Accession AW908422.1.

[1708] SEQ ID:100085 detected in mouse EST Accession AW324490.1.

[1709] SEQ ID:100086 detected in mouse EST Accession AA270973.1.

[1710] SEQ ID:100087 detected in mouse EST Accession AI303167.1.

[1711] SEQ ID:100088 detected in mouse EST Accession BF227510.1.

[1712] SEQ ID:100089 detected in mouse EST Accession AW018407.1.

[1713] SEQ ID:100090 detected in mouse EST Accession BE650065.1.

[1714] SEQ ID:100091 detected in mouse EST Accession AW018398.1.

[1715] SEQ ID:100092 detected in mouse EST Accession AA238246.1.

[1716] SEQ ID:100093 detected in mouse EST Accession AA230354.1.

[1717] SEQ ID:100094 detected in mouse EST Accession AU022691.1.

[1718] SEQ ID:100095 detected in mouse EST Accession BI111409.1.

[1719] SEQ ID:100096 detected in mouse EST Accession AI255679.1.

[1720] SEQ ID:100097 detected in mouse EST Accession AW209037.1.

[1721] SEQ ID:100098 detected in mouse EST Accession AI195467.1.

[1722] SEQ ID:100099 detected in mouse EST Accession AI747413.1.

[1723] SEQ ID:100100 detected in mouse EST Accession

BI246484.1.

[1724] SEQ ID:100101 detected in mouse EST Accession AI194959.1.

[1725] SEQ ID:100102 detected in mouse EST Accession BI250124.1.

[1726] SEQ ID:100103 detected in mouse EST Accession AW113761.1.

[1727] SEQ ID:100104 detected in mouse EST Accession AW110984.1.

[1728] SEQ ID:100105 detected in mouse EST Accession AA237404.1.

[1729] SEQ ID:100106 detected in mouse EST Accession AW113760.1.

[1730] SEQ ID:100107 detected in mouse EST Accession BE689976.1.

[1731] SEQ ID:100108 detected in mouse EST Accession AW322040.1.

[1732] SEQ ID:100109 detected in mouse EST Accession AW987156.1.

[1733] SEQ ID:100110 detected in mouse EST Accession BE335469.1.

[1734] SEQ ID:100111 detected in mouse EST Accession BF116785.1.

[1735] SEQ ID:100112 detected in mouse EST Accession BE199228.1.

[1736] SEQ ID:100113 detected in mouse EST Accession AA239428.1.

[1737] SEQ ID:100114 detected in mouse EST Accession BI248794.1.

[1738] SEQ ID:100115 detected in mouse EST Accession BF179498.1.

[1739] SEQ ID:100116 detected in mouse EST Accession BB009037.2.

[1740] SEQ ID:100117 detected in mouse EST Accession AI323769.1.

[1741] SEQ ID:100118 detected in mouse EST Accession AI114892.1.

[1742] SEQ ID:100119 detected in mouse EST Accession AW110985.1.

[1743] SEQ ID:100120 detected in mouse EST Accession AA764472.1.

[1744] SEQ ID:100121 detected in mouse EST Accession BE199152.1.

[1745] SEQ ID:100122 detected in mouse EST Accession BF227614.1.

[1746] SEQ ID:100123 detected in mouse EST Accession

AI785459.1.

[1747] SEQ ID:100124 detected in mouse EST Accession AW701118.1.

[1748] SEQ ID:100125 detected in mouse EST Accession AI646857.1.

[1749] SEQ ID:100126 detected in mouse EST Accession AW212849.1.

[1750] GAM112 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1751] An enzyme complex designated DICER COMPLEX, dices the GAM112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM112 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM112 RNA is designated SEQ ID:1761, and is provided hereinbelow with reference to the sequence listing part.

[1752] GAM112 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM112 target RNA, herein designated GAM TARGET RNA. GAM112 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1753] GAM112 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM112 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM112 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM112 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM112 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1754] The complementary binding of GAM112 RNA, herein designated GAM RNA, to target binding sites on GAM112 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM112 target RNA, herein designated GAM TARGET RNA, into GAM112 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1755] It is appreciated that GAM112 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM112 target genes. The mRNA of each one of this plurality of GAM112 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM112 RNA, herein designated GAM RNA, and which when bound by GAM112 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM112 target proteins.

[1756] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM112 gene, herein designated GAM GENE, on one or more GAM112 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1757] It is yet further appreciated that specific functions, and accordingly utilities, of GAM112 correlate with, and may

be deduced from, the identity of the target genes which GAM112 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1758] Nucleotide sequences of the GAM112 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM112 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM112 are further described hereinbelow with reference to Table Table1.

[1759] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM112 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1760] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 113 (GAM113) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1761] GAM113 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM113 was detected is described hereinabove with reference to Figs. 2-8.

[1762] GAM113 gene, herein designated GAM GENE, and GAM113 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1763] GAM113 gene, herein designated GAM GENE, encodes a GAM113 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM113 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM113 precursor RNA is designated SEQ ID:86, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:86 is located at position 1135950 relative to contig NT_029289.7, on chromosome 5.

[1764] GAM113 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1765] An enzyme complex designated DICER COMPLEX, dices the GAM113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM113 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM113 RNA is designated SEQ ID:1762, and is provided hereinbelow with reference to the sequence listing part.

[1766] GAM113 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM113 target RNA, herein designated GAM TARGET RNA. GAM113 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1767] GAM113 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM113 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM113 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM113 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM113 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1768] The complementary binding of GAM113 RNA, herein designated GAM RNA, to target binding sites on GAM113 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM113 target RNA, herein designated GAM TARGET RNA, into GAM113 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1769] It is appreciated that GAM113 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM113 target genes. The mRNA of each one of this plurality of GAM113 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM113 RNA, herein designated GAM RNA, and which when bound by GAM113 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM113 target proteins.

[1770] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM113 gene, herein designated GAM GENE, on one or more GAM113 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1771] It is yet further appreciated that specific functions, and accordingly utilities, of GAM113 correlate with, and may be deduced from, the identity of the target genes which GAM113 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1772] Nucleotide sequences of the GAM113 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM113 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM113 are further described hereinbelow with reference to Table Table1.

[1773] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM113 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1774] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 114 (GAM114) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1775] GAM114 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM114 was detected is described hereinabove with reference to Figs. 2-8.

[1776] GAM114 gene, herein designated GAM GENE, and GAM114 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1777] GAM114 gene, herein designated GAM GENE, encodes a GAM114 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM114 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM114 precursor RNA is desig-

nated SEQ ID:87, and is provided hereinbelow with reference to the sequence listing part.

[1778] GAM114 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM114 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1779] An enzyme complex designated DICER COMPLEX, dices the GAM114 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM114 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM114 RNA is designated SEQ ID:1763, and is provided hereinbelow with reference to the sequence listing part.

[1780] GAM114 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM114 target RNA, herein designated GAM TARGET RNA. GAM114 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1781] GAM114 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM114 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM114 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM114 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM114

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1782] The complementary binding of GAM114 RNA, herein designated GAM RNA, to target binding sites on GAM114 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM114 target RNA, herein designated GAM TARGET RNA, into GAM114 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1783] It is appreciated that GAM114 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM114 target genes. The mRNA of each one of this plurality of GAM114 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM114 RNA, herein designated GAM RNA, and which when bound by GAM114 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM114 target proteins.

[1784] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM114 gene, herein designated GAM GENE, on one or more GAM114 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1785] It is yet further appreciated that specific functions, and accordingly utilities, of GAM114 correlate with, and may be deduced from, the identity of the target genes which GAM114 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1786] Nucleotide sequences of the GAM114 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM114 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM114 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM114 are further described hereinbelow with reference to Table Table1.

[1787] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM114 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1788] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 115 (GAM115) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1789] GAM115 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM115 was detected is described hereinabove with reference to Figs. 2-8.

[1790] GAM115 gene, herein designated GAM GENE, and GAM115 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[1791] GAM115 gene, herein designated GAM GENE, encodes a GAM115 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM115 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM115 precursor RNA is designated SEQ ID:88, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:88 is located at position 1366714 relative to contig NT_011520.8, on chromosome 22.

[1792] GAM115 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1793] An enzyme complex designated DICER COMPLEX, dices

the GAM115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM115 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM115 RNA is designated SEQ ID:1764, and is provided hereinbelow with reference to the sequence listing part.

[1794] GAM115 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM115 target RNA, herein designated GAM TARGET RNA. GAM115 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1795] GAM115 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM115 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM115

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM115 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM115 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1796] The complementary binding of GAM115 RNA, herein designated GAM RNA, to target binding sites on GAM115 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM115 target RNA, herein designated GAM TARGET RNA, into GAM115 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1797] It is appreciated that GAM115 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM115 target genes. The mRNA of each one of this plurality of GAM115 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM115 RNA, herein designated GAM RNA, and which when bound by GAM115 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM115 target proteins.

[1798] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM115 gene, herein designated GAM GENE, on one or more GAM115 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1799] It is yet further appreciated that specific functions, and accordingly utilities, of GAM115 correlate with, and may be deduced from, the identity of the target genes which GAM115 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1800] Nucleotide sequences of the GAM115 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM115 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM115 are further described hereinbelow with reference to Table Table1.

[1801] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM115 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1802] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 116 (GAM116) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1803] GAM116 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM116 was detected is described hereinabove with reference to Figs. 2-8.

[1804] GAM116 gene, herein designated GAM GENE, and GAM116 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1805] GAM116 gene, herein designated GAM GENE, encodes a GAM116 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM116 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM116 precursor RNA is designated SEQ ID:89, and is provided hereinbelow with reference to the sequence listing part.

[1806] GAM116 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of

SEQ ID:100145, which mouse homolog is detected in mouse EST accession AA260986.1.

[1807] GAM116 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM116 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1808] An enzyme complex designated DICER COMPLEX, dices the GAM116 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM116 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM116 RNA is designated SEQ ID:1765, and is provided hereinbelow with reference to the sequence listing part.

[1809] GAM116 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM116 target RNA, herein designated GAM TARGET RNA. GAM116 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1810] GAM116 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM116 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM116 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM116 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM116

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1811] The complementary binding of GAM116 RNA, herein designated GAM RNA, to target binding sites on GAM116 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM116 target RNA, herein designated GAM TARGET RNA, into GAM116 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1812] It is appreciated that GAM116 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM116 target genes. The mRNA of each one of this plurality of GAM116 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM116 RNA, herein designated GAM RNA, and which when bound by GAM116 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM116 target proteins.

[1813] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM116 gene, herein designated GAM GENE, on one or more GAM116 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1814] It is yet further appreciated that specific functions, and accordingly utilities, of GAM116 correlate with, and may be deduced from, the identity of the target genes which GAM116 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1815] Nucleotide sequences of the GAM116 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM116 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM116 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM116 are further described hereinbelow with reference to Table Table1.

[1816] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM116 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1817] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 117 (GAM117) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1818] GAM117 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM117 was detected is described hereinabove with reference to Figs. 2-8.

[1819] GAM117 gene, herein designated GAM GENE, and GAM117 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[1820] GAM117 gene, herein designated GAM GENE, encodes a GAM117 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM117 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM117 precursor RNA is designated SEQ ID:90, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:90 is located at position 2554140 relative to contig NT_004852.13, on chromosome 1.

[1821] GAM117 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM117 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1822] An enzyme complex designated DICER COMPLEX, dices

the GAM117 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM117 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM117 RNA is designated SEQ ID:1766, and is provided hereinbelow with reference to the sequence listing part.

[1823] GAM117 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM117 target RNA, herein designated GAM TARGET RNA. GAM117 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1824] GAM117 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM117 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM117

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM117 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM117 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1825] The complementary binding of GAM117 RNA, herein designated GAM RNA, to target binding sites on GAM117 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM117 target RNA, herein designated GAM TARGET RNA, into GAM117 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1826] It is appreciated that GAM117 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM117 target genes. The mRNA of each one of this plurality of GAM117 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM117 RNA, herein designated GAM RNA, and which when bound by GAM117 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM117 target proteins.

[1827] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM117 gene, herein designated GAM GENE, on one or more GAM117 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1828] It is yet further appreciated that specific functions, and accordingly utilities, of GAM117 correlate with, and may be deduced from, the identity of the target genes which GAM117 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1829] Nucleotide sequences of the GAM117 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM117 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM117 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM117 are further described hereinbelow with reference to Table Table1.

[1830] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM117 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1831] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 118 (GAM118) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1832] GAM118 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM118 was detected is described hereinabove with reference to Figs. 2-8.

[1833] GAM118 gene, herein designated GAM GENE, and GAM118 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1834] GAM118 gene, herein designated GAM GENE, encodes a GAM118 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM118 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM118 precursor RNA is designated SEQ ID:91, and is provided hereinbelow with reference to the sequence listing part.

[1835] GAM118 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1836] An enzyme complex designated DICER COMPLEX, dices the GAM118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM118 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM118 RNA is designated SEQ ID:1767, and is provided hereinbelow with reference to the sequence listing part.

[1837] GAM118 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM118 target RNA, herein designated GAM TARGET RNA. GAM118 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1838] GAM118 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM118 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM118 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM118 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM118 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1839] The complementary binding of GAM118 RNA, herein designated GAM RNA, to target binding sites on GAM118 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM118 target RNA, herein designated GAM TARGET RNA, into GAM118 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1840] It is appreciated that GAM118 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM118 target genes. The mRNA of each one of this plurality of GAM118 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM118 RNA, herein designated GAM RNA, and which when bound by GAM118 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM118 target proteins.

[1841] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM118 gene, herein designated GAM GENE, on one or more GAM118 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1842] It is yet further appreciated that specific functions, and accordingly utilities, of GAM118 correlate with, and may be deduced from, the identity of the target genes which GAM118 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1843] Nucleotide sequences of the GAM118 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM118 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM118 are further described hereinbelow with reference to Table Table1.

[1844] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM118 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1845] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 119 (GAM119) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1846] GAM119 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM119 was detected is described hereinabove with reference to Figs. 2-8.

[1847] GAM119 gene, herein designated GAM GENE, and GAM119 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1848] GAM119 gene, herein designated GAM GENE, encodes a GAM119 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM119 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM119 precursor RNA is designated SEQ ID:92, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:92 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[1849] GAM119 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1850] An enzyme complex designated DICER COMPLEX, dices the GAM119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM119 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM119 RNA is designated SEQ ID:1768, and is provided hereinbelow with reference to the sequence listing part.

[1851] GAM119 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM119 target RNA, herein designated GAM TARGET RNA. GAM119 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1852] GAM119 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM119 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM119 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM119 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM119 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1853] The complementary binding of GAM119 RNA, herein designated GAM RNA, to target binding sites on GAM119 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM119 target RNA, herein designated GAM TARGET RNA, into GAM119 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1854] It is appreciated that GAM119 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM119 target genes. The mRNA of each one of this plurality of GAM119 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM119 RNA, herein designated GAM RNA, and which when bound by GAM119 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM119 target proteins.

[1855] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM119 gene, herein designated GAM GENE, on one or more GAM119 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1856] It is yet further appreciated that specific functions, and accordingly utilities, of GAM119 correlate with, and may

be deduced from, the identity of the target genes which GAM119 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1857] Nucleotide sequences of the GAM119 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM119 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM119 are further described hereinbelow with reference to Table Table1.

[1858] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM119 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1859] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 120 (GAM120) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1860] GAM120 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM120 was detected is described hereinabove with reference to Figs. 2-8.

[1861] GAM120 gene, herein designated GAM GENE, and GAM120 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1862] GAM120 gene, herein designated GAM GENE, encodes a GAM120 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM120 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM120 precursor RNA is designated SEQ ID:93, and is provided hereinbelow with reference to the sequence listing part.

[1863] GAM120 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM120 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[1864] An enzyme complex designated DICER COMPLEX, dices the GAM120 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM120 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM120 RNA is designated SEQ ID:1769, and is provided hereinbelow with reference to the sequence listing part.

[1865] GAM120 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM120 target RNA, herein designated GAM TARGET RNA.
GAM120 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1866] GAM120 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM120 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM120 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM120 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM120 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1867] The complementary binding of GAM120 RNA, herein designated GAM RNA, to target binding sites on GAM120 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM120 target RNA, herein desig-

nated GAM TARGET RNA, into GAM120 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1868] It is appreciated that GAM120 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM120 target genes. The mRNA of each one of this plurality of GAM120 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM120 RNA, herein designated GAM RNA, and which when bound by GAM120 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM120 target proteins.

[1869] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM120 gene, herein designated GAM GENE, on one or more GAM120 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1870] It is yet further appreciated that specific functions, and accordingly utilities, of GAM120 correlate with, and may be deduced from, the identity of the target genes which GAM120 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1871] Nucleotide sequences of the GAM120 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM120 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM120 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM120 are further described hereinbelow with reference to Table Table1.

[1872] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM120 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[1873] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 121 (GAM121) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1874] GAM121 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM121 was detected is described hereinabove with reference to Figs. 2-8.

[1875] GAM121 gene, herein designated GAM GENE, and GAM121 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1876] GAM121 gene, herein designated GAM GENE, encodes a GAM121 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM121 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM121 precursor RNA is designated SEQ ID:94, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:94 is located at position 2037087 relative to contig NT_021907.13, on chromosome 1.

[1877] GAM121 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1878] An enzyme complex designated DICER COMPLEX, dices the GAM121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM121 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM121 RNA is designated SEQ ID:1770, and is provided hereinbelow with reference to the sequence listing part.

[1879] GAM121 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM121 target RNA, herein designated GAM TARGET RNA. GAM121 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1880] GAM121 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM121 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM121 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM121 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM121

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1881] The complementary binding of GAM121 RNA, herein designated GAM RNA, to target binding sites on GAM121 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM121 target RNA, herein designated GAM TARGET RNA, into GAM121 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1882] It is appreciated that GAM121 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM121 target genes. The mRNA of each one of this plurality of GAM121 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM121 RNA, herein designated GAM RNA, and which when bound by GAM121 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM121 target proteins.

[1883] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM121 gene, herein designated GAM GENE, on one or more GAM121 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1884] It is yet further appreciated that specific functions, and accordingly utilities, of GAM121 correlate with, and may be deduced from, the identity of the target genes which GAM121 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1885] Nucleotide sequences of the GAM121 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM121 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM121 are further described hereinbelow with reference to Table Table1.

[1886] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM121 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1887] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 122 (GAM122) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1888] GAM122 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM122 was detected is described hereinabove with reference to Figs. 2-8.

[1889] GAM122 gene, herein designated GAM GENE, and GAM122 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[1890] GAM122 gene, herein designated GAM GENE, encodes a GAM122 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM122 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM122 precursor RNA is designated SEQ ID:95, and is provided hereinbelow with reference to the sequence listing part.

[1891] GAM122 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[1892] SEQ ID:98754 detected in mouse EST Accession BG976857.1.

[1893] SEQ ID:98755 detected in mouse EST Accession BF116324.1.

[1894] GAM122 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1895] An enzyme complex designated DICER COMPLEX, dices the GAM122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM122 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM122 RNA is designated SEQ ID:1771, and is provided hereinbelow with reference to the sequence listing part.

[1896] GAM122 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM122 target RNA, herein designated GAM TARGET RNA. GAM122 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1897] GAM122 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM122 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM122 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM122 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM122 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1898] The complementary binding of GAM122 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM122 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM122 target RNA, herein designated GAM TARGET RNA, into GAM122 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1899] It is appreciated that GAM122 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM122 target genes. The mRNA of each one of this plurality of GAM122 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM122 RNA, herein designated GAM RNA, and which when bound by GAM122 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM122 target proteins.

[1900] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM122 gene, herein designated GAM GENE, on one or more GAM122 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1901] It is yet further appreciated that specific functions, and accordingly utilities, of GAM122 correlate with, and may be deduced from, the identity of the target genes which GAM122 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1902] Nucleotide sequences of the GAM122 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM122 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM122 are further described hereinbelow with reference to Table Table1.

[1903] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM122 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1904] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 123 (GAM123) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1905] GAM123 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM123 was detected is described hereinabove with reference to Figs. 2-8.

[1906] GAM123 gene, herein designated GAM GENE, and GAM123 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1907] GAM123 gene, herein designated GAM GENE, encodes a GAM123 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM123 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM123 precursor RNA is designated SEQ ID:96, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:96 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[1908] GAM123 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1909] An enzyme complex designated DICER COMPLEX, dices the GAM123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM123 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM123 RNA is designated SEQ ID:1772, and is provided hereinbelow with reference to the sequence listing part.

[1910] GAM123 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM123 target RNA, herein designated GAM TARGET RNA. GAM123 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1911] GAM123 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM123 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM123 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM123 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM123 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1912] The complementary binding of GAM123 RNA, herein designated GAM RNA, to target binding sites on GAM123 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM123 target RNA, herein designated GAM TARGET RNA, into GAM123 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1913] It is appreciated that GAM123 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM123 target genes. The mRNA of each one of this plurality of GAM123 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM123 RNA,

herein designated GAM RNA, and which when bound by GAM123 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM123 target proteins.

[1914] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM123 gene, herein designated GAM GENE, on one or more GAM123 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1915] It is yet further appreciated that specific functions, and accordingly utilities, of GAM123 correlate with, and may be deduced from, the identity of the target genes which

GAM123 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1916] Nucleotide sequences of the GAM123 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM123 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM123 are further described hereinbelow with reference to Table Table1.

[1917] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM123 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1918] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 124 (GAM124) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1919] GAM124 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM124 was detected is described hereinabove with reference to Figs. 2-8.

[1920] GAM124 gene, herein designated GAM GENE, and GAM124 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1921] GAM124 gene, herein designated GAM GENE, encodes a GAM124 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM124 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM124 precursor RNA is designated SEQ ID:97, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:97 is located at position 2865607 relative to contig NT_011512.7, on chromosome 21.

[1922] GAM124 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1923] An enzyme complex designated DICER COMPLEX, dices the GAM124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM124 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM124 RNA is designated SEQ ID:1773, and is provided hereinbelow with reference to the sequence listing part.

[1924] GAM124 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM124 target RNA, herein designated GAM TARGET RNA. GAM124 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1925] GAM124 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM124 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM124 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM124 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM124 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1926] The complementary binding of GAM124 RNA, herein designated GAM RNA, to target binding sites on GAM124 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM124 target RNA, herein designated GAM TARGET RNA, into GAM124 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1927] It is appreciated that GAM124 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM124 target genes. The mRNA of each one of this plurality of GAM124 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM124 RNA, herein designated GAM RNA, and which when bound by GAM124 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM124 target proteins.

[1928] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM124 gene, herein designated GAM GENE, on one or more GAM124 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1929] It is yet further appreciated that specific functions, and accordingly utilities, of GAM124 correlate with, and may be deduced from, the identity of the target genes which GAM124 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1930] Nucleotide sequences of the GAM124 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM124 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM124 are further described hereinbelow with reference to Table Table1.

[1931] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM124 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1932] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 125 (GAM125) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1933] GAM125 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM125 was detected is described hereinabove with reference to Figs. 2-8.

[1934] GAM125 gene, herein designated GAM GENE, and GAM125 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1935] GAM125 gene, herein designated GAM GENE, encodes a GAM125 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM125 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM125 precursor RNA is designated SEQ ID:98, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:98 is located at position 1820906 relative to contig NT_005612.11, on chromosome 3.

[1936] GAM125 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[1937] SEQ ID:99362 detected in mouse EST Accession AA065653.1.

[1938] SEQ ID:99363 detected in mouse EST Accession AI153186.1.

[1939] SEQ ID:99364 detected in mouse EST Accession BG261697.1.

[1940] SEQ ID:99563 detected in mouse EST Accession BF152625.1.

[1941] SEQ ID:99564 detected in mouse EST Accession AW744693.1.

[1942] SEQ ID:99565 detected in mouse EST Accession BF101508.1.

[1943] SEQ ID:99566 detected in mouse EST Accession AI614809.1.

[1944] GAM125 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1945] An enzyme complex designated DICER COMPLEX, dices the GAM125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM125 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM125 RNA is designated SEQ ID:1774, and is provided hereinbelow with reference to the sequence listing part.

[1946] GAM125 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM125 target RNA, herein designated GAM TARGET RNA.

GAM125 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1947] GAM125 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM125 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM125 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM125 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM125 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1948] The complementary binding of GAM125 RNA, herein designated GAM RNA, to target binding sites on GAM125 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM125 target RNA, herein designated GAM TARGET RNA, into GAM125 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1949] It is appreciated that GAM125 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM125 target genes. The mRNA of each one of this plurality of GAM125 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM125 RNA, herein designated GAM RNA, and which when bound by GAM125 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM125 target proteins.

[1950] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM125 gene, herein designated GAM GENE, on one or more GAM125 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1951] It is yet further appreciated that specific functions, and accordingly utilities, of GAM125 correlate with, and may be deduced from, the identity of the target genes which GAM125 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1952] Nucleotide sequences of the GAM125 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM125 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM125 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM125 are further described hereinbelow with reference to Table Table1.

[1953] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM125 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1954] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 126 (GAM126) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1955] GAM126 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM126 was detected is described hereinabove with reference to Figs. 2-8.

[1956] GAM126 gene, herein designated GAM GENE, and GAM126 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1957] GAM126 gene, herein designated GAM GENE, encodes a GAM126 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM126 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM126 precursor RNA is designated SEQ ID:99, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:99 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[1958] GAM126 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1959] An enzyme complex designated DICER COMPLEX, dices the GAM126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM126 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM126 RNA is designated SEQ ID:1775, and is provided hereinbelow with reference to the sequence listing part.

[1960] GAM126 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM126 target RNA, herein designated GAM TARGET RNA. GAM126 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1961] GAM126 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM126 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM126 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM126 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM126 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1962] The complementary binding of GAM126 RNA, herein designated GAM RNA, to target binding sites on GAM126 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM126 target RNA, herein designated GAM TARGET RNA, into GAM126 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1963] It is appreciated that GAM126 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM126 target genes. The mRNA of each one of this plu-

rality of GAM126 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM126 RNA, herein designated GAM RNA, and which when bound by GAM126 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM126 target proteins.

[1964] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM126 gene, herein designated GAM GENE, on one or more GAM126 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1965] It is yet further appreciated that specific functions, and accordingly utilities, of GAM126 correlate with, and may be deduced from, the identity of the target genes which GAM126 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1966] Nucleotide sequences of the GAM126 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM126 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM126 are further described hereinbelow with reference to Table Table1.

[1967] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM126 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1968] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 127 (GAM127) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[1969] GAM127 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM127 was detected is described hereinabove with reference to Figs. 2-8.

[1970] GAM127 gene, herein designated GAM GENE, and GAM127 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1971] GAM127 gene, herein designated GAM GENE, encodes a GAM127 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM127 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM127 precursor RNA is designated SEQ ID:100, and is provided hereinbelow with reference to the sequence listing part.

[1972] GAM127 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[1973] SEQ ID:99548 detected in mouse EST Accession

BI965972.1.

[1974] SEQ ID:99549 detected in mouse EST Accession AI326210.1.

[1975] SEQ ID:99550 detected in mouse EST Accession BI965652.1.

[1976] SEQ ID:99551 detected in mouse EST Accession AI553186.1.

[1977] GAM127 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[1978] An enzyme complex designated DICER COMPLEX, dices the GAM127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM127 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM127 RNA is designated SEQ ID:1776, and is provided hereinbelow with reference to the sequence listing part.

[1979] GAM127 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM127 target RNA, herein designated GAM TARGET RNA. GAM127 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1980] GAM127 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM127 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM127 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM127 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM127 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1981] The complementary binding of GAM127 RNA, herein designated GAM RNA, to target binding sites on GAM127 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM127 target RNA, herein designated GAM TARGET RNA, into GAM127 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1982] It is appreciated that GAM127 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM127 target genes. The mRNA of each one of this plurality of GAM127 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM127 RNA, herein designated GAM RNA, and which when bound by GAM127 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM127 target proteins.

[1983] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM127 gene, herein designated GAM GENE, on one or more GAM127 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1984] It is yet further appreciated that specific functions, and accordingly utilities, of GAM127 correlate with, and may

be deduced from, the identity of the target genes which GAM127 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1985] Nucleotide sequences of the GAM127 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM127 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM127 are further described hereinbelow with reference to Table Table1.

[1986] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM127 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[1987] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 128 (GAM128) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[1988] GAM128 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM128 was detected is described hereinabove with reference to Figs. 2-8.

[1989] GAM128 gene, herein designated GAM GENE, and GAM128 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[1990] GAM128 gene, herein designated GAM GENE, encodes a GAM128 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM128 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM128 precursor RNA is designated SEQ ID:101, and is provided hereinbelow with reference to the sequence listing part.

[1991] GAM128 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[1992] An enzyme complex designated DICER COMPLEX, dices the GAM128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM128 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM128 RNA is designated SEQ ID:1777, and is provided hereinbelow with reference to the sequence listing part.

[1993] GAM128 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM128 target RNA, herein designated GAM TARGET RNA.
GAM128 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[1994] GAM128 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM128 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM128 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM128 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM128 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[1995] The complementary binding of GAM128 RNA, herein designated GAM RNA, to target binding sites on GAM128 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM128 target RNA, herein desig-

nated GAM TARGET RNA, into GAM128 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[1996] It is appreciated that GAM128 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM128 target genes. The mRNA of each one of this plurality of GAM128 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM128 RNA, herein designated GAM RNA, and which when bound by GAM128 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM128 target proteins.

[1997] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM128 gene, herein designated GAM GENE, on one or more GAM128 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[1998] It is yet further appreciated that specific functions, and accordingly utilities, of GAM128 correlate with, and may be deduced from, the identity of the target genes which GAM128 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[1999] Nucleotide sequences of the GAM128 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM128 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM128 are further described hereinbelow with reference to Table Table1.

[2000] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM128 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[2001] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 129 (GAM129) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2002] GAM129 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM129 was detected is described hereinabove with reference to Figs. 2-8.

[2003] GAM129 gene, herein designated GAM GENE, and GAM129 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2004] GAM129 gene, herein designated GAM GENE, encodes a GAM129 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM129 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM129 precursor RNA is designated SEQ ID:102, and is provided hereinbelow with reference to the sequence listing part.

[2005] GAM129 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2006] An enzyme complex designated DICER COMPLEX, dices the GAM129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM129 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM129 RNA is designated SEQ ID:1778, and is provided hereinbelow with reference to the sequence listing part.

[2007] GAM129 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM129

target RNA, herein designated GAM TARGET RNA.

GAM129 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2008] GAM129 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM129 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM129 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM129 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM129 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2009] The complementary binding of GAM129 RNA, herein designated GAM RNA, to target binding sites on GAM129 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM129 target RNA, herein designated GAM TARGET RNA, into GAM129 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2010] It is appreciated that GAM129 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM129 target genes. The mRNA of each one of this plurality of GAM129 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM129 RNA, herein designated GAM RNA, and which when bound by GAM129 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM129 target proteins.

[2011] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM129 gene, herein designated GAM GENE, on one or more GAM129 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2012] It is yet further appreciated that specific functions, and accordingly utilities, of GAM129 correlate with, and may be deduced from, the identity of the target genes which GAM129 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2013] Nucleotide sequences of the GAM129 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM129 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM129 are further described hereinbelow with reference to Table Table1.

[2014] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM129 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2015] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 130 (GAM130) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2016] GAM130 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM130 was detected is described hereinabove with reference to Figs. 2-8.

[2017] GAM130 gene, herein designated GAM GENE, and GAM130 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2018] GAM130 gene, herein designated GAM GENE, encodes a

GAM130 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM130 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM130 precursor RNA is designated SEQ ID:103, and is provided hereinbelow with reference to the sequence listing part.

[2019] GAM130 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2020] An enzyme complex designated DICER COMPLEX, dices the GAM130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM130 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM130 RNA is designated SEQ ID:1779, and is provided hereinbelow with reference to the sequence listing part.

[2021] GAM130 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM130 target RNA, herein designated GAM TARGET RNA. GAM130 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2022] GAM130 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM130 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM130 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM130 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM130 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2023] The complementary binding of GAM130 RNA, herein designated GAM RNA, to target binding sites on GAM130 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM130 target RNA, herein designated GAM TARGET RNA, into GAM130 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2024] It is appreciated that GAM130 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM130 target genes. The mRNA of each one of this plurality of GAM130 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM130 RNA, herein designated GAM RNA, and which when bound by GAM130 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM130 target proteins.

[2025] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM130 gene, herein designated GAM GENE, on one or more GAM130 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2026] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM130 correlate with, and may be deduced from, the identity of the target genes which GAM130 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2027] Nucleotide sequences of the GAM130 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM130 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM130 are further described hereinbelow with reference to Table Table1.

[2028] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM130 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2029] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 131 (GAM131) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2030] GAM131 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM131 was detected is described hereinabove with reference to Figs. 2-8.

[2031] GAM131 gene, herein designated GAM GENE, and GAM131 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2032] GAM131 gene, herein designated GAM GENE, encodes a GAM131 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM131 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM131 precursor RNA is designated SEQ ID:104, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:104 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[2033] GAM131 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2034] An enzyme complex designated DICER COMPLEX, dices the GAM131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM131 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM131 RNA is designated SEQ ID:1780, and is provided hereinbelow with reference to the sequence listing part.

[2035] GAM131 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM131 target RNA, herein designated GAM TARGET RNA.
GAM131 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[2036] GAM131 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM131 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM131 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM131 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM131 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2037] The complementary binding of GAM131 RNA, herein designated GAM RNA, to target binding sites on GAM131 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM131 target RNA, herein designated GAM TARGET RNA, into GAM131 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2038] It is appreciated that GAM131 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM131 target genes. The mRNA of each one of this plurality of GAM131 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM131 RNA, herein designated GAM RNA, and which when bound by GAM131 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM131 target proteins.

[2039] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM131 gene, herein designated GAM GENE, on one or more GAM131 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2040] It is yet further appreciated that specific functions, and accordingly utilities, of GAM131 correlate with, and may be deduced from, the identity of the target genes which GAM131 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2041] Nucleotide sequences of the GAM131 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM131 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM131 are further described hereinbelow with reference to Table Table1.

[2042] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM131 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2043] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 132 (GAM132) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2044] GAM132 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM132 was detected is described hereinabove with reference to Figs. 2-8.

[2045] GAM132 gene, herein designated GAM GENE, and GAM132 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2046] GAM132 gene, herein designated GAM GENE, encodes a GAM132 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM132 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM132 precursor RNA is designated SEQ ID:105, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:105 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[2047] GAM132 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2048] An enzyme complex designated DICER COMPLEX, dices the GAM132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM132 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM132 RNA is designated SEQ ID:1781, and is provided hereinbelow with reference to the sequence listing part.

[2049] GAM132 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM132 target RNA, herein designated GAM TARGET RNA. GAM132 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2050] GAM132 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM132 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM132 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM132 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM132 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2051] The complementary binding of GAM132 RNA, herein designated GAM RNA, to target binding sites on GAM132 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM132 target RNA, herein designated GAM TARGET RNA, into GAM132 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2052] It is appreciated that GAM132 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM132 target genes. The mRNA of each one of this plurality of GAM132 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM132 RNA, herein designated GAM RNA, and which when bound by

GAM132 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM132 target proteins.

[2053] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM132 gene, herein designated GAM GENE, on one or more GAM132 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2054] It is yet further appreciated that specific functions, and accordingly utilities, of GAM132 correlate with, and may be deduced from, the identity of the target genes which GAM132 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[2055] Nucleotide sequences of the GAM132 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM132 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM132 are further described hereinbelow with reference to Table Table1.

[2056] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM132 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2057] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 133 (GAM133) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2058] GAM133 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM133 was detected is described hereinabove

with reference to Figs. 2-8.

[2059] GAM133 gene, herein designated GAM GENE, and GAM133 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2060] GAM133 gene, herein designated GAM GENE, encodes a GAM133 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM133 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM133 precursor RNA is designated SEQ ID:106, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:106 is located at position 19308883 relative to contig NT_033899.3, on chromosome 11.

[2061] GAM133 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[2062] An enzyme complex designated DICER COMPLEX, dices the GAM133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM133 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM133 RNA is designated SEQ ID:1782, and is provided hereinbelow with reference to the sequence listing part.

[2063] GAM133 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM133 target RNA, herein designated GAM TARGET RNA.
GAM133 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2064] GAM133 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM133 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM133 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM133 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM133 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2065] The complementary binding of GAM133 RNA, herein designated GAM RNA, to target binding sites on GAM133 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM133 target RNA, herein designated GAM TARGET RNA, into GAM133 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2066] It is appreciated that GAM133 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM133 target genes. The mRNA of each one of this plurality of GAM133 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM133 RNA, herein designated GAM RNA, and which when bound by GAM133 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM133 target proteins.

[2067] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM133 gene, herein designated GAM GENE, on one or more GAM133 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2068] It is yet further appreciated that specific functions, and accordingly utilities, of GAM133 correlate with, and may be deduced from, the identity of the target genes which GAM133 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2069] Nucleotide sequences of the GAM133 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM133 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM133 are further described hereinbelow with reference to Table Table1.

[2070] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM133 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2071] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 134 (GAM134) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2072] GAM134 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM134 was detected is described hereinabove with reference to Figs. 2-8.

[2073] GAM134 gene, herein designated GAM GENE, and GAM134 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2074] GAM134 gene, herein designated GAM GENE, encodes a GAM134 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM134 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM134 precursor RNA is designated SEQ ID:107, and is provided hereinbelow with reference to the sequence listing part.

[2075] GAM134 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2076] An enzyme complex designated DICER COMPLEX, dices the GAM134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM134 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM134 RNA is designated SEQ ID:1783, and is provided hereinbelow with reference to the sequence listing part.

[2077] GAM134 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM134 target RNA, herein designated GAM TARGET RNA. GAM134 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2078] GAM134 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM134 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM134 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM134 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM134 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2079] The complementary binding of GAM134 RNA, herein designated GAM RNA, to target binding sites on GAM134 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM134 target RNA, herein designated GAM TARGET RNA, into GAM134 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2080] It is appreciated that GAM134 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM134 target genes. The mRNA of each one of this plurality of GAM134 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM134 RNA, herein designated GAM RNA, and which when bound by

GAM134 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM134 target proteins.

[2081] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM134 gene, herein designated GAM GENE, on one or more GAM134 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2082] It is yet further appreciated that specific functions, and accordingly utilities, of GAM134 correlate with, and may be deduced from, the identity of the target genes which GAM134 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[2083] Nucleotide sequences of the GAM134 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM134 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM134 are further described hereinbelow with reference to Table Table1.

[2084] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM134 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2085] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 135 (GAM135) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2086] GAM135 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM135 was detected is described hereinabove

with reference to Figs. 2-8.

[2087] GAM135 gene, herein designated GAM GENE, and GAM135 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2088] GAM135 gene, herein designated GAM GENE, encodes a GAM135 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM135 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM135 precursor RNA is designated SEQ ID:108, and is provided hereinbelow with reference to the sequence listing part.

[2089] GAM135 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2090] An enzyme complex designated DICER COMPLEX, dices the GAM135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM135 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM135 RNA is designated SEQ ID:1784, and is provided hereinbelow with reference to the sequence listing part.

[2091] GAM135 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM135 target RNA, herein designated GAM TARGET RNA. GAM135 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2092] GAM135 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM135 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM135 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM135 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM135 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2093] The complementary binding of GAM135 RNA, herein designated GAM RNA, to target binding sites on GAM135 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM135 target RNA, herein designated GAM TARGET RNA, into GAM135 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[2094] It is appreciated that GAM135 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM135 target genes. The mRNA of each one of this plurality of GAM135 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM135 RNA, herein designated GAM RNA, and which when bound by GAM135 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM135 target proteins.

[2095] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM135 gene, herein designated GAM GENE, on one or more GAM135 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2096] It is yet further appreciated that specific functions, and accordingly utilities, of GAM135 correlate with, and may be deduced from, the identity of the target genes which GAM135 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2097] Nucleotide sequences of the GAM135 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM135 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM135 are further described hereinbelow with reference to Table Table1.

[2098] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM135 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2099] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 136 (GAM136) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2100] GAM136 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM136 was detected is described hereinabove with reference to Figs. 2-8.

[2101] GAM136 gene, herein designated GAM GENE, and GAM136 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2102] GAM136 gene, herein designated GAM GENE, encodes a GAM136 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM136 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM136 precursor RNA is designated SEQ ID:109, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:109 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[2103] GAM136 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[2104] SEQ ID:98666 detected in mouse EST Accession BB609859.1.

[2105] SEQ ID:98667 detected in mouse EST Accession AA671455.1.

[2106] SEQ ID:98668 detected in mouse EST Accession AW824753.1.

[2107] SEQ ID:98669 detected in mouse EST Accession BE943987.1.

[2108] SEQ ID:98670 detected in mouse EST Accession BE691447.1.

[2109] SEQ ID:98671 detected in mouse EST Accession BG808025.1.

[2110] SEQ ID:98672 detected in mouse EST Accession BG808010.1.

[2111] SEQ ID:98673 detected in mouse EST Accession BG807850.1.

[2112] SEQ ID:98674 detected in mouse EST Accession BG805970.1.

[2113] SEQ ID:98675 detected in mouse EST Accession BG145596.1.

[2114] SEQ ID:98676 detected in mouse EST Accession BE692802.1.

[2115] SEQ ID:98677 detected in mouse EST Accession BB610842.1.

[2116] SEQ ID:98679 detected in mouse EST Accession AA144533.1.

[2117] SEQ ID:98680 detected in mouse EST Accession BE691413.1.

[2118] SEQ ID:98681 detected in mouse EST Accession AW208601.1.

[2119] GAM136 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2120] An enzyme complex designated DICER COMPLEX, dices

the GAM136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM136 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM136 RNA is designated SEQ ID:1785, and is provided hereinbelow with reference to the sequence listing part.

[2121] GAM136 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM136 target RNA, herein designated GAM TARGET RNA. GAM136 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2122] GAM136 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM136 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM136

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM136 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM136 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2123] The complementary binding of GAM136 RNA, herein designated GAM RNA, to target binding sites on GAM136 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM136 target RNA, herein designated GAM TARGET RNA, into GAM136 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2124] It is appreciated that GAM136 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM136 target genes. The mRNA of each one of this plurality of GAM136 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM136 RNA, herein designated GAM RNA, and which when bound by GAM136 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM136 target proteins.

[2125] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM136 gene, herein designated GAM GENE, on one or more GAM136 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2126] It is yet further appreciated that specific functions, and accordingly utilities, of GAM136 correlate with, and may be deduced from, the identity of the target genes which GAM136 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2127] Nucleotide sequences of the GAM136 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM136 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM136 are further described hereinbelow with reference to Table Table1.

[2128] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM136 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2129] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 137 (GAM137) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2130] GAM137 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM137 was detected is described hereinabove with reference to Figs. 2-8.

[2131] GAM137 gene, herein designated GAM GENE, and GAM137 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2132] GAM137 gene, herein designated GAM GENE, encodes a GAM137 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM137 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM137 precursor RNA is designated SEQ ID:110, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:110 is located at position 4492011 relative to contig NT_033896.3, on chromosome 10.

[2133] GAM137 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2134] An enzyme complex designated DICER COMPLEX, dices the GAM137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM137 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM137 RNA is designated SEQ ID:1786, and is provided hereinbelow with reference to the sequence listing part.

[2135] GAM137 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM137 target RNA, herein designated GAM TARGET RNA.

GAM137 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2136] GAM137 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM137 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM137 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM137 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM137 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2137] The complementary binding of GAM137 RNA, herein designated GAM RNA, to target binding sites on GAM137 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM137 target RNA, herein designated GAM TARGET RNA, into GAM137 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2138] It is appreciated that GAM137 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM137 target genes. The mRNA of each one of this plurality of GAM137 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM137 RNA, herein designated GAM RNA, and which when bound by GAM137 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM137 target proteins.

[2139] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM137 gene, herein designated GAM GENE, on one or more GAM137 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2140] It is yet further appreciated that specific functions, and accordingly utilities, of GAM137 correlate with, and may be deduced from, the identity of the target genes which GAM137 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2141] Nucleotide sequences of the GAM137 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM137 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM137 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM137 are further described hereinbelow with reference to Table Table1.

[2142] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM137 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2143] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 138 (GAM138) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2144] GAM138 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM138 was detected is described hereinabove with reference to Figs. 2-8.

[2145] GAM138 gene, herein designated GAM GENE, and GAM138 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2146] GAM138 gene, herein designated GAM GENE, encodes a GAM138 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM138 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM138 precursor RNA is designated SEQ ID:111, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:111 is located at position 119354 relative to contig NT_011568.10, on chromosome X.

[2147] GAM138 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2148] An enzyme complex designated DICER COMPLEX, dices the GAM138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM138 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM138 RNA is designated SEQ ID:1787, and is provided hereinbelow with reference to the sequence listing part.

[2149] GAM138 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM138 target RNA, herein designated GAM TARGET RNA. GAM138 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2150] GAM138 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM138 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM138 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM138 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM138 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2151] The complementary binding of GAM138 RNA, herein designated GAM RNA, to target binding sites on GAM138 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM138 target RNA, herein designated GAM TARGET RNA, into GAM138 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2152] It is appreciated that GAM138 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM138 target genes. The mRNA of each one of this plu-

rality of GAM138 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM138 RNA, herein designated GAM RNA, and which when bound by GAM138 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM138 target proteins.

[2153] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM138 gene, herein designated GAM GENE, on one or more GAM138 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2154] It is yet further appreciated that specific functions, and accordingly utilities, of GAM138 correlate with, and may be deduced from, the identity of the target genes which GAM138 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2155] Nucleotide sequences of the GAM138 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM138 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM138 are further described hereinbelow with reference to Table Table1.

[2156] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM138 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2157] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 139 (GAM139) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[2158] GAM139 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM139 was detected is described hereinabove with reference to Figs. 2-8.

[2159] GAM139 gene, herein designated GAM GENE, and GAM139 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2160] GAM139 gene, herein designated GAM GENE, encodes a GAM139 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM139 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM139 precursor RNA is designated SEQ ID:112, and is provided hereinbelow with reference to the sequence listing part.

[2161] GAM139 has 12 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[2162] SEQ ID:98045 detected in mouse EST Accession

BF146992.1.

[2163] SEQ ID:98046 detected in mouse EST Accession AA144398.1.

[2164] SEQ ID:98047 detected in mouse EST Accession AW230495.1.

[2165] SEQ ID:98048 detected in mouse EST Accession BG970816.1.

[2166] SEQ ID:98049 detected in mouse EST Accession BG974532.1.

[2167] SEQ ID:98050 detected in mouse EST Accession BG870381.1.

[2168] SEQ ID:98051 detected in mouse EST Accession BG973293.1.

[2169] SEQ ID:98052 detected in mouse EST Accession BI153175.1.

[2170] SEQ ID:98053 detected in mouse EST Accession BF144364.1.

[2171] SEQ ID:98054 detected in mouse EST Accession AI264984.1.

[2172] SEQ ID:98055 detected in mouse EST Accession AI156313.1.

[2173] SEQ ID:98056 detected in mouse EST Accession BG864461.1.

[2174] GAM139 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2175] An enzyme complex designated DICER COMPLEX, dices the GAM139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM139 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM139 RNA is designated SEQ ID:1788, and is provided hereinbelow with reference to the sequence listing part.

[2176] GAM139 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM139

target RNA, herein designated GAM TARGET RNA.

GAM139 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2177] GAM139 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM139 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM139 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM139 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM139 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2178] The complementary binding of GAM139 RNA, herein designated GAM RNA, to target binding sites on GAM139 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM139 target RNA, herein designated GAM TARGET RNA, into GAM139 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2179] It is appreciated that GAM139 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM139 target genes. The mRNA of each one of this plurality of GAM139 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM139 RNA, herein designated GAM RNA, and which when bound by GAM139 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM139 target proteins.

[2180] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM139 gene, herein designated GAM GENE, on one or more GAM139 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2181] It is yet further appreciated that specific functions, and accordingly utilities, of GAM139 correlate with, and may be deduced from, the identity of the target genes which GAM139 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2182] Nucleotide sequences of the GAM139 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM139 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM139 are further described hereinbelow with reference to Table Table1.

[2183] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM139 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2184] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 140 (GAM140) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2185] GAM140 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM140 was detected is described hereinabove with reference to Figs. 2-8.

[2186] GAM140 gene, herein designated GAM GENE, and GAM140 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2187] GAM140 gene, herein designated GAM GENE, encodes a

GAM140 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM140 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM140 precursor RNA is designated SEQ ID:113, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:113 is located at position 1698742 relative to contig NT_028309.8, on chromosome 11.

[2188] GAM140 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2189] An enzyme complex designated DICER COMPLEX, dices the GAM140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM140 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM140 RNA is designated SEQ ID:1789, and is provided hereinbelow with reference to the sequence listing part.

[2190] GAM140 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM140 target RNA, herein designated GAM TARGET RNA. GAM140 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2191] GAM140 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM140 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM140 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM140 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM140 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2192] The complementary binding of GAM140 RNA, herein designated GAM RNA, to target binding sites on GAM140 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM140 target RNA, herein designated GAM TARGET RNA, into GAM140 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2193] It is appreciated that GAM140 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM140 target genes. The mRNA of each one of this plurality of GAM140 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM140 RNA, herein designated GAM RNA, and which when bound by GAM140 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM140 target proteins.

[2194] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM140 gene, herein designated GAM GENE, on one or more GAM140 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[2195] It is yet further appreciated that specific functions, and accordingly utilities, of GAM140 correlate with, and may be deduced from, the identity of the target genes which GAM140 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2196] Nucleotide sequences of the GAM140 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM140 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM140 are further described hereinbelow with reference to Table Table1.

[2197] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM140 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2198] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 141 (GAM141) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[2199] GAM141 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM141 was detected is described hereinabove with reference to Figs. 2-8.

[2200] GAM141 gene, herein designated GAM GENE, and GAM141 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2201] GAM141 gene, herein designated GAM GENE, encodes a GAM141 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM141 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM141 precursor RNA is designated SEQ ID:114, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:114 is located at position 405177 relative to contig NT_035431.2, on chromosome 17.

[2202] GAM141 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2203] An enzyme complex designated DICER COMPLEX, dices the GAM141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM141 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM141 RNA is designated SEQ ID:1790, and is provided hereinbelow with reference to the sequence listing part.

[2204] GAM141 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM141 target RNA, herein designated GAM TARGET RNA. GAM141 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2205] GAM141 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM141 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM141 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM141 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM141 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2206] The complementary binding of GAM141 RNA, herein designated GAM RNA, to target binding sites on GAM141 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM141 target RNA, herein designated GAM TARGET RNA, into GAM141 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2207] It is appreciated that GAM141 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM141 target genes. The mRNA of each one of this plurality of GAM141 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM141 RNA, herein designated GAM RNA, and which when bound by GAM141 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM141 target proteins.

[2208] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM141 gene, herein designated GAM GENE, on one or more GAM141 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2209] It is yet further appreciated that specific functions, and accordingly utilities, of GAM141 correlate with, and may be deduced from, the identity of the target genes which GAM141 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2210] Nucleotide sequences of the GAM141 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM141 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM141 are further described hereinbelow with reference to Table Table1.

[2211] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM141 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2212] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 142 (GAM142) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2213] GAM142 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM142 was detected is described hereinabove with reference to Figs. 2-8.

[2214] GAM142 gene, herein designated GAM GENE, and GAM142 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2215] GAM142 gene, herein designated GAM GENE, encodes a GAM142 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM142 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM142 precursor RNA is designated SEQ ID:115, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:115 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[2216] GAM142 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2217] An enzyme complex designated DICER COMPLEX, dices the GAM142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM142 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM142 RNA is designated SEQ ID:1791, and is provided hereinbelow with reference to the sequence listing part.

[2218] GAM142 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM142 target RNA, herein designated GAM TARGET RNA. GAM142 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2219] GAM142 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM142 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM142 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM142 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM142 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2220] The complementary binding of GAM142 RNA, herein designated GAM RNA, to target binding sites on GAM142 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM142 target RNA, herein designated GAM TARGET RNA, into GAM142 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2221] It is appreciated that GAM142 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM142 target genes. The mRNA of each one of this plurality of GAM142 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM142 RNA, herein designated GAM RNA, and which when bound by GAM142 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM142 target proteins.

[2222] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM142 gene, herein designated GAM GENE, on one or more GAM142 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2223] It is yet further appreciated that specific functions, and accordingly utilities, of GAM142 correlate with, and may

be deduced from, the identity of the target genes which GAM142 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2224] Nucleotide sequences of the GAM142 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM142 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM142 are further described hereinbelow with reference to Table Table1.

[2225] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM142 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2226] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 143 (GAM143) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2227] GAM143 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM143 was detected is described hereinabove with reference to Figs. 2-8.

[2228] GAM143 gene, herein designated GAM GENE, and GAM143 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2229] GAM143 gene, herein designated GAM GENE, encodes a GAM143 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM143 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM143 precursor RNA is designated SEQ ID:116, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:116 is located at position 36924270 relative to contig NT_007592.11, on chromosome 6.

[2230] GAM143 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2231] An enzyme complex designated DICER COMPLEX, dices the GAM143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM143 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM143 RNA is designated SEQ ID:1792, and is provided hereinbelow with reference to the sequence listing part.

[2232] GAM143 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM143 target RNA, herein designated GAM TARGET RNA.
GAM143 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2233] GAM143 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM143 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM143 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM143 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM143 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2234] The complementary binding of GAM143 RNA, herein designated GAM RNA, to target binding sites on GAM143 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM143 target RNA, herein designated GAM TARGET RNA, into GAM143 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2235] It is appreciated that GAM143 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM143 target genes. The mRNA of each one of this plurality of GAM143 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM143 RNA, herein designated GAM RNA, and which when bound by GAM143 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM143 target proteins.

[2236] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM143 gene, herein designated GAM GENE, on one or more GAM143 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2237] It is yet further appreciated that specific functions, and accordingly utilities, of GAM143 correlate with, and may be deduced from, the identity of the target genes which GAM143 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2238] Nucleotide sequences of the GAM143 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM143 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM143 are further described hereinbelow with reference to Table Table1.

[2239] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM143 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2240] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 144 (GAM144) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2241] GAM144 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM144 was detected is described hereinabove with reference to Figs. 2-8.

[2242] GAM144 gene, herein designated GAM GENE, and GAM144 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2243] GAM144 gene, herein designated GAM GENE, encodes a GAM144 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM144 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM144 precursor RNA is desig-

nated SEQ ID:117, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:117 is located at position 3415385 relative to contig NT_008046.11, on chromosome 8.

[2244] GAM144 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2245] An enzyme complex designated DICER COMPLEX, dices the GAM144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM144 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM144 RNA is designated SEQ ID:1793, and is provided hereinbelow with reference to the sequence listing part.

[2246] GAM144 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM144 target RNA, herein designated GAM TARGET RNA. GAM144 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2247] GAM144 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM144 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM144 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM144 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM144 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2248] The complementary binding of GAM144 RNA, herein designated GAM RNA, to target binding sites on GAM144 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM144 target RNA, herein designated GAM TARGET RNA, into GAM144 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2249] It is appreciated that GAM144 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM144 target genes. The mRNA of each one of this plurality of GAM144 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM144 RNA, herein designated GAM RNA, and which when bound by GAM144 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM144 target proteins.

[2250] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM144 gene, herein designated GAM GENE, on one or more GAM144 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2251] It is yet further appreciated that specific functions, and accordingly utilities, of GAM144 correlate with, and may be deduced from, the identity of the target genes which GAM144 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2252] Nucleotide sequences of the GAM144 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM144 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM144 are further described hereinbelow with reference to Table Table1.

[2253] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM144 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2254] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 145 (GAM145) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2255] GAM145 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM145 was detected is described hereinabove with reference to Figs. 2-8.

[2256] GAM145 gene, herein designated GAM GENE, and GAM145 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2257] GAM145 gene, herein designated GAM GENE, encodes a GAM145 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM145 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM145 precursor RNA is designated SEQ ID:118, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:118 is located at position 10716412 relative to contig NT_033899.3, on chromosome 11.

[2258] GAM145 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[2259] An enzyme complex designated DICER COMPLEX, dices the GAM145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM145 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM145 RNA is designated SEQ ID:1794, and is provided hereinbelow with reference to the sequence listing part.

[2260] GAM145 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM145 target RNA, herein designated GAM TARGET RNA.

GAM145 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2261] GAM145 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM145 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM145 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM145 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM145 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2262] The complementary binding of GAM145 RNA, herein designated GAM RNA, to target binding sites on GAM145 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM145 target RNA, herein designated GAM TARGET RNA, into GAM145 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2263] It is appreciated that GAM145 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM145 target genes. The mRNA of each one of this plurality of GAM145 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM145 RNA, herein designated GAM RNA, and which when bound by GAM145 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM145 target proteins.

[2264] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM145 gene, herein designated GAM GENE, on one or more GAM145 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2265] It is yet further appreciated that specific functions, and accordingly utilities, of GAM145 correlate with, and may be deduced from, the identity of the target genes which GAM145 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2266] Nucleotide sequences of the GAM145 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM145 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM145 are further described hereinbelow with reference to Table Table1.

[2267] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM145 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2268] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 146 (GAM146) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2269] GAM146 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM146 was detected is described hereinabove with reference to Figs. 2-8.

[2270] GAM146 gene, herein designated GAM GENE, and GAM146 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2271] GAM146 gene, herein designated GAM GENE, encodes a GAM146 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM146 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM146 precursor RNA is designated SEQ ID:119, and is provided hereinbelow with reference to the sequence listing part.

[2272] GAM146 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2273] An enzyme complex designated DICER COMPLEX, dices the GAM146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM146 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM146 RNA is designated SEQ ID:1795, and is provided hereinbelow with reference to the sequence listing part.

[2274] GAM146 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM146 target RNA, herein designated GAM TARGET RNA.

GAM146 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2275] GAM146 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM146 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM146 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM146 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM146 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2276] The complementary binding of GAM146 RNA, herein designated GAM RNA, to target binding sites on GAM146 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM146 target RNA, herein designated GAM TARGET RNA, into GAM146 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2277] It is appreciated that GAM146 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM146 target genes. The mRNA of each one of this plurality of GAM146 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM146 RNA, herein designated GAM RNA, and which when bound by GAM146 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM146 target proteins.

[2278] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM146 gene, herein designated GAM GENE, on one or more GAM146 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2279] It is yet further appreciated that specific functions, and accordingly utilities, of GAM146 correlate with, and may be deduced from, the identity of the target genes which GAM146 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2280] Nucleotide sequences of the GAM146 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM146 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM146 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM146 are further described hereinbelow with reference to Table Table1.

[2281] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM146 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2282] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 147 (GAM147) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2283] GAM147 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM147 was detected is described hereinabove with reference to Figs. 2-8.

[2284] GAM147 gene, herein designated GAM GENE, and GAM147 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2285] GAM147 gene, herein designated GAM GENE, encodes a GAM147 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM147 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM147 precursor RNA is designated SEQ ID:120, and is provided hereinbelow with reference to the sequence listing part.

[2286] GAM147 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2287] An enzyme complex designated DICER COMPLEX, dices the GAM147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM147 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM147 RNA is designated SEQ ID:1796, and is provided hereinbelow with reference to the sequence listing part.

[2288] GAM147 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM147 target RNA, herein designated GAM TARGET RNA. GAM147 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2289] GAM147 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM147 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM147 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM147 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM147 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2290] The complementary binding of GAM147 RNA, herein designated GAM RNA, to target binding sites on GAM147 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM147 target RNA, herein designated GAM TARGET RNA, into GAM147 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2291] It is appreciated that GAM147 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM147 target genes. The mRNA of each one of this plurality of GAM147 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM147 RNA, herein designated GAM RNA, and which when bound by GAM147 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM147 target proteins.

[2292] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM147 gene, herein designated GAM GENE, on one or more GAM147 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2293] It is yet further appreciated that specific functions, and accordingly utilities, of GAM147 correlate with, and may

be deduced from, the identity of the target genes which GAM147 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2294] Nucleotide sequences of the GAM147 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM147 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM147 are further described hereinbelow with reference to Table Table1.

[2295] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM147 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2296] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 148 (GAM148) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2297] GAM148 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM148 was detected is described hereinabove with reference to Figs. 2-8.

[2298] GAM148 gene, herein designated GAM GENE, and GAM148 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2299] GAM148 gene, herein designated GAM GENE, encodes a GAM148 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM148 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM148 precursor RNA is designated SEQ ID:121, and is provided hereinbelow with reference to the sequence listing part.

[2300] GAM148 has 51 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[2301] SEQ ID:100163 detected in mouse EST Accession BE287378.1.

[2302] SEQ ID:100165 detected in mouse EST Accession

AL364038.1.

[2303] SEQ ID:100166 detected in mouse EST Accession AI303965.1.

[2304] SEQ ID:100167 detected in mouse EST Accession AI528379.1.

[2305] SEQ ID:100168 detected in mouse EST Accession BF785982.1.

[2306] SEQ ID:100169 detected in mouse EST Accession BE944495.1.

[2307] SEQ ID:100170 detected in mouse EST Accession AI892596.1.

[2308] SEQ ID:100171 detected in mouse EST Accession BE286095.1.

[2309] SEQ ID:100172 detected in mouse EST Accession AA674322.1.

[2310] SEQ ID:100173 detected in mouse EST Accession AA118832.1.

[2311] SEQ ID:100174 detected in mouse EST Accession AI020701.1.

[2312] SEQ ID:100175 detected in mouse EST Accession AI930460.1.

[2313] SEQ ID:100176 detected in mouse EST Accession W97106.1.

[2314] SEQ ID:100177 detected in mouse EST Accession AA244463.1.

[2315] SEQ ID:98284 detected in mouse EST Accession BE689919.1.

[2316] SEQ ID:98285 detected in mouse EST Accession BE623891.1.

[2317] SEQ ID:98286 detected in mouse EST Accession AA153061.1.

[2318] SEQ ID:98287 detected in mouse EST Accession AW742226.1.

[2319] SEQ ID:98288 detected in mouse EST Accession BG061469.1.

[2320] SEQ ID:98289 detected in mouse EST Accession AA137720.1.

[2321] SEQ ID:98290 detected in mouse EST Accession BE287861.1.

[2322] SEQ ID:98291 detected in mouse EST Accession BG088490.1.

[2323] SEQ ID:98292 detected in mouse EST Accession BI456602.1.

[2324] SEQ ID:98293 detected in mouse EST Accession BE368312.1.

[2325] SEQ ID:98294 detected in mouse EST Accession

BI110585.1.

[2326] SEQ ID:98295 detected in mouse EST Accession BI657877.1.

[2327] SEQ ID:98296 detected in mouse EST Accession BI109950.1.

[2328] SEQ ID:98297 detected in mouse EST Accession BI409746.1.

[2329] SEQ ID:98298 detected in mouse EST Accession BI659922.1.

[2330] SEQ ID:98299 detected in mouse EST Accession BG919976.1.

[2331] SEQ ID:98300 detected in mouse EST Accession BI905262.1.

[2332] SEQ ID:98301 detected in mouse EST Accession BG246570.1.

[2333] SEQ ID:98302 detected in mouse EST Accession BI107635.1.

[2334] SEQ ID:98303 detected in mouse EST Accession BF233222.1.

[2335] SEQ ID:98304 detected in mouse EST Accession BE571953.1.

[2336] SEQ ID:98305 detected in mouse EST Accession BI656535.1.

[2337] SEQ ID:98306 detected in mouse EST Accession BF233226.1.

[2338] SEQ ID:98307 detected in mouse EST Accession BG175457.1.

[2339] SEQ ID:98308 detected in mouse EST Accession BI416118.1.

[2340] SEQ ID:98309 detected in mouse EST Accession BG245640.1.

[2341] SEQ ID:98310 detected in mouse EST Accession BG865442.1.

[2342] SEQ ID:98311 detected in mouse EST Accession AA717623.1.

[2343] SEQ ID:98312 detected in mouse EST Accession AU079751.1.

[2344] SEQ ID:98313 detected in mouse EST Accession BI106831.1.

[2345] SEQ ID:98314 detected in mouse EST Accession BF162828.1.

[2346] SEQ ID:98315 detected in mouse EST Accession BG519331.1.

[2347] SEQ ID:98316 detected in mouse EST Accession W48327.1.

[2348] SEQ ID:98317 detected in mouse EST Accession

BG174174.1.

[2349] SEQ ID:98318 detected in mouse EST Accession BI685041.1.

[2350] SEQ ID:98319 detected in mouse EST Accession BI409951.1.

[2351] SEQ ID:98320 detected in mouse EST Accession BG245107.1.

[2352] GAM148 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2353] An enzyme complex designated DICER COMPLEX, dices the GAM148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM148 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM148 RNA is designated SEQ ID:1797, and is provided hereinbelow with reference to the sequence listing part.

[2354] GAM148 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM148 target RNA, herein designated GAM TARGET RNA. GAM148 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2355] GAM148 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM148 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM148 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM148 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM148 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2356] The complementary binding of GAM148 RNA, herein designated GAM RNA, to target binding sites on GAM148 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM148 target RNA, herein designated GAM TARGET RNA, into GAM148 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2357] It is appreciated that GAM148 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM148 target genes. The mRNA of each one of this plurality of GAM148 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM148 RNA, herein designated GAM RNA, and which when bound by GAM148 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM148 target proteins.

[2358] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM148 gene, herein designated GAM GENE, on one or more GAM148 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2359] It is yet further appreciated that specific functions, and accordingly utilities, of GAM148 correlate with, and may

be deduced from, the identity of the target genes which GAM148 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2360] Nucleotide sequences of the GAM148 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM148 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM148 are further described hereinbelow with reference to Table Table1.

[2361] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM148 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2362] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 149 (GAM149) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2363] GAM149 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM149 was detected is described hereinabove with reference to Figs. 2-8.

[2364] GAM149 gene, herein designated GAM GENE, and GAM149 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2365] GAM149 gene, herein designated GAM GENE, encodes a GAM149 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM149 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM149 precursor RNA is designated SEQ ID:122, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:122 is located at position 24602429 relative to contig NT_009952.11, on chromosome 13.

[2366] GAM149 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2367] An enzyme complex designated DICER COMPLEX, dices the GAM149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM149 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM149 RNA is designated SEQ ID:1798, and is provided hereinbelow with reference to the sequence listing part.

[2368] GAM149 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM149 target RNA, herein designated GAM TARGET RNA. GAM149 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2369] GAM149 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM149 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM149 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM149 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM149 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2370] The complementary binding of GAM149 RNA, herein designated GAM RNA, to target binding sites on GAM149 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM149 target RNA, herein designated GAM TARGET RNA, into GAM149 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2371] It is appreciated that GAM149 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM149 target genes. The mRNA of each one of this plurality of GAM149 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM149 RNA, herein designated GAM RNA, and which when bound by GAM149 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM149 target proteins.

[2372] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM149 gene, herein designated GAM GENE, on one or more GAM149 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2373] It is yet further appreciated that specific functions, and accordingly utilities, of GAM149 correlate with, and may be deduced from, the identity of the target genes which GAM149 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2374] Nucleotide sequences of the GAM149 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM149 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM149 are further described hereinbelow with reference to Table Table1.

[2375] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM149 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2376] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 150 (GAM150) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2377] GAM150 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM150 was detected is described hereinabove with reference to Figs. 2-8.

[2378] GAM150 gene, herein designated GAM GENE, and GAM150 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2379] GAM150 gene, herein designated GAM GENE, encodes a GAM150 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM150 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM150 precursor RNA is desig-

nated SEQ ID:123, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:123 is located at position 1065102 relative to contig NT_029973.6, on chromosome 5.

[2380] GAM150 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2381] An enzyme complex designated DICER COMPLEX, dices the GAM150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM150 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of

GAM150 RNA is designated SEQ ID:1799, and is provided hereinbelow with reference to the sequence listing part.

[2382] GAM150 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM150 target RNA, herein designated GAM TARGET RNA. GAM150 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2383] GAM150 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM150 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM150 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM150 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM150 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2384] The complementary binding of GAM150 RNA, herein designated GAM RNA, to target binding sites on GAM150 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM150 target RNA, herein designated GAM TARGET RNA, into GAM150 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2385] It is appreciated that GAM150 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM150 target genes. The mRNA of each one of this plurality of GAM150 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM150 RNA, herein designated GAM RNA, and which when bound by GAM150 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM150 target proteins.

[2386] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM150 gene, herein designated GAM GENE, on one or more GAM150 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2387] It is yet further appreciated that specific functions, and accordingly utilities, of GAM150 correlate with, and may be deduced from, the identity of the target genes which GAM150 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2388] Nucleotide sequences of the GAM150 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM150 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM150 are further described hereinbelow with reference to Table Table1.

[2389] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM150 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2390] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 151 (GAM151) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2391] GAM151 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM151 was detected is described hereinabove with reference to Figs. 2-8.

[2392] GAM151 gene, herein designated GAM GENE, and GAM151 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2393] GAM151 gene, herein designated GAM GENE, encodes a GAM151 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM151 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM151 precursor RNA is designated SEQ ID:124, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:124 is located at position 1235063 relative to contig NT_009526.11, on chromosome 12.

[2394] GAM151 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[2395] SEQ ID:99286 detected in mouse EST Accession BI965972.1.

[2396] SEQ ID:99287 detected in mouse EST Accession BI965652.1.

[2397] SEQ ID:99288 detected in mouse EST Accession AI326210.1.

[2398] GAM151 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2399] An enzyme complex designated DICER COMPLEX, dices the GAM151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM151 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM151 RNA is designated SEQ ID:1800, and is provided hereinbelow with reference to the sequence listing part.

[2400] GAM151 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM151 target RNA, herein designated GAM TARGET RNA. GAM151 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2401] GAM151 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM151 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM151 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM151 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM151

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2402] The complementary binding of GAM151 RNA, herein designated GAM RNA, to target binding sites on GAM151 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM151 target RNA, herein designated GAM TARGET RNA, into GAM151 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2403] It is appreciated that GAM151 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM151 target genes. The mRNA of each one of this plurality of GAM151 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM151 RNA, herein designated GAM RNA, and which when bound by GAM151 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM151 target proteins.

[2404] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM151 gene, herein designated GAM GENE, on one or more GAM151 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2405] It is yet further appreciated that specific functions, and accordingly utilities, of GAM151 correlate with, and may be deduced from, the identity of the target genes which GAM151 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2406] Nucleotide sequences of the GAM151 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM151 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM151 are further described hereinbelow with reference to Table Table1.

[2407] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM151 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2408] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 152 (GAM152) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2409] GAM152 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM152 was detected is described hereinabove with reference to Figs. 2-8.

[2410] GAM152 gene, herein designated GAM GENE, and GAM152 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[2411] GAM152 gene, herein designated GAM GENE, encodes a GAM152 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM152 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM152 precursor RNA is designated SEQ ID:125, and is provided hereinbelow with reference to the sequence listing part.

[2412] GAM152 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2413] An enzyme complex designated DICER COMPLEX, dices the GAM152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM152 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM152 RNA is designated SEQ ID:1801, and is provided hereinbelow with reference to the sequence listing part.

[2414] GAM152 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM152 target RNA, herein designated GAM TARGET RNA. GAM152 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2415] GAM152 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM152 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM152 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM152 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM152 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2416] The complementary binding of GAM152 RNA, herein designated GAM RNA, to target binding sites on GAM152 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM152 target RNA, herein designated GAM TARGET RNA, into GAM152 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2417] It is appreciated that GAM152 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM152 target genes. The mRNA of each one of this plurality of GAM152 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM152 RNA, herein designated GAM RNA, and which when bound by GAM152 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM152 target proteins.

[2418] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM152 gene, herein designated GAM GENE, on one or more GAM152 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[2419] It is yet further appreciated that specific functions, and accordingly utilities, of GAM152 correlate with, and may be deduced from, the identity of the target genes which GAM152 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2420] Nucleotide sequences of the GAM152 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM152 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM152 are further described hereinbelow with reference to Table Table1.

[2421] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM152 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2422] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 153 (GAM153) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[2423] GAM153 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM153 was detected is described hereinabove with reference to Figs. 2-8.

[2424] GAM153 gene, herein designated GAM GENE, and GAM153 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2425] GAM153 gene, herein designated GAM GENE, encodes a GAM153 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM153 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM153 precursor RNA is designated SEQ ID:126, and is provided hereinbelow with reference to the sequence listing part.

[2426] GAM153 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2427] An enzyme complex designated DICER COMPLEX, dices the GAM153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM153 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM153 RNA is designated SEQ ID:1802, and is provided hereinbelow with reference to the sequence listing part.

[2428] GAM153 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM153 target RNA, herein designated GAM TARGET RNA.
GAM153 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[2429] GAM153 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM153 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM153 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM153 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM153 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2430] The complementary binding of GAM153 RNA, herein designated GAM RNA, to target binding sites on GAM153 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM153 target RNA, herein designated GAM TARGET RNA, into GAM153 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2431] It is appreciated that GAM153 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM153 target genes. The mRNA of each one of this plurality of GAM153 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM153 RNA, herein designated GAM RNA, and which when bound by GAM153 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM153 target proteins.

[2432] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM153 gene, herein designated GAM GENE, on one or more GAM153 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2433] It is yet further appreciated that specific functions, and accordingly utilities, of GAM153 correlate with, and may be deduced from, the identity of the target genes which GAM153 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2434] Nucleotide sequences of the GAM153 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM153 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM153 are further described hereinbelow with reference to Table Table1.

[2435] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM153 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2436] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 154 (GAM154) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2437] GAM154 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM154 was detected is described hereinabove with reference to Figs. 2-8.

[2438] GAM154 gene, herein designated GAM GENE, and GAM154 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2439] GAM154 gene, herein designated GAM GENE, encodes a GAM154 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM154 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM154 precursor RNA is designated SEQ ID:127, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:127 is located at position 6185718 relative to contig NT_005332.11, on chromosome 2.

[2440] GAM154 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2441] An enzyme complex designated DICER COMPLEX, dices the GAM154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM154 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM154 RNA is designated SEQ ID:1803, and is provided hereinbelow with reference to the sequence listing part.

[2442] GAM154 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM154 target RNA, herein designated GAM TARGET RNA. GAM154 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2443] GAM154 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM154 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM154 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM154 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM154 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2444] The complementary binding of GAM154 RNA, herein designated GAM RNA, to target binding sites on GAM154 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM154 target RNA, herein designated GAM TARGET RNA, into GAM154 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2445] It is appreciated that GAM154 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM154 target genes. The mRNA of each one of this plurality of GAM154 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM154 RNA, herein designated GAM RNA, and which when bound by

GAM154 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM154 target proteins.

[2446] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM154 gene, herein designated GAM GENE, on one or more GAM154 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2447] It is yet further appreciated that specific functions, and accordingly utilities, of GAM154 correlate with, and may be deduced from, the identity of the target genes which GAM154 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[2448] Nucleotide sequences of the GAM154 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM154 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM154 are further described hereinbelow with reference to Table Table1.

[2449] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM154 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2450] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 155 (GAM155) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2451] GAM155 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM155 was detected is described hereinabove

with reference to Figs. 2-8.

[2452] GAM155 gene, herein designated GAM GENE, and GAM155 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2453] GAM155 gene, herein designated GAM GENE, encodes a GAM155 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM155 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM155 precursor RNA is designated SEQ ID:128, and is provided hereinbelow with reference to the sequence listing part.

[2454] GAM155 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2455] An enzyme complex designated DICER COMPLEX, dices the GAM155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM155 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM155 RNA is designated SEQ ID:1804, and is provided hereinbelow with reference to the sequence listing part.

[2456] GAM155 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM155 target RNA, herein designated GAM TARGET RNA. GAM155 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2457] GAM155 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM155 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM155 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM155 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM155 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2458] The complementary binding of GAM155 RNA, herein designated GAM RNA, to target binding sites on GAM155 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM155 target RNA, herein designated GAM TARGET RNA, into GAM155 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[2459] It is appreciated that GAM155 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM155 target genes. The mRNA of each one of this plurality of GAM155 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM155 RNA, herein designated GAM RNA, and which when bound by GAM155 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM155 target proteins.

[2460] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM155 gene, herein designated GAM GENE, on one or more GAM155 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2461] It is yet further appreciated that specific functions, and accordingly utilities, of GAM155 correlate with, and may be deduced from, the identity of the target genes which GAM155 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2462] Nucleotide sequences of the GAM155 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM155 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM155 are further described hereinbelow with reference to Table Table1.

[2463] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM155 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2464] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 156 (GAM156) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2465] GAM156 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM156 was detected is described hereinabove with reference to Figs. 2-8.

[2466] GAM156 gene, herein designated GAM GENE, and GAM156 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2467] GAM156 gene, herein designated GAM GENE, encodes a GAM156 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM156 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM156 precursor RNA is designated SEQ ID:129, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:129 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[2468] GAM156 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2469] An enzyme complex designated DICER COMPLEX, dices the GAM156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM156 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM156 RNA is designated SEQ ID:1805, and is provided hereinbelow with reference to the sequence listing part.

[2470] GAM156 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM156

target RNA, herein designated GAM TARGET RNA.

GAM156 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2471] GAM156 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM156 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM156 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM156 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM156 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2472] The complementary binding of GAM156 RNA, herein designated GAM RNA, to target binding sites on GAM156 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM156 target RNA, herein designated GAM TARGET RNA, into GAM156 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2473] It is appreciated that GAM156 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM156 target genes. The mRNA of each one of this plurality of GAM156 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM156 RNA, herein designated GAM RNA, and which when bound by GAM156 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM156 target proteins.

[2474] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM156 gene, herein designated GAM GENE, on one or more GAM156 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2475] It is yet further appreciated that specific functions, and accordingly utilities, of GAM156 correlate with, and may be deduced from, the identity of the target genes which GAM156 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2476] Nucleotide sequences of the GAM156 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM156 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM156 are further described hereinbelow with reference to Table Table1.

[2477] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM156 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2478] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 157 (GAM157) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2479] GAM157 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM157 was detected is described hereinabove with reference to Figs. 2-8.

[2480] GAM157 gene, herein designated GAM GENE, and GAM157 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2481] GAM157 gene, herein designated GAM GENE, encodes a

GAM157 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM157 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM157 precursor RNA is designated SEQ ID:130, and is provided hereinbelow with reference to the sequence listing part.

[2482] GAM157 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2483] An enzyme complex designated DICER COMPLEX, dices the GAM157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM157 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM157 RNA is designated SEQ ID:1806, and is provided hereinbelow with reference to the sequence listing part.

[2484] GAM157 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM157 target RNA, herein designated GAM TARGET RNA. GAM157 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2485] GAM157 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM157 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM157 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM157 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM157 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2486] The complementary binding of GAM157 RNA, herein designated GAM RNA, to target binding sites on GAM157 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM157 target RNA, herein designated GAM TARGET RNA, into GAM157 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2487] It is appreciated that GAM157 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM157 target genes. The mRNA of each one of this plurality of GAM157 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM157 RNA, herein designated GAM RNA, and which when bound by GAM157 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM157 target proteins.

[2488] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM157 gene, herein designated GAM GENE, on one or more GAM157 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2489] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM157 correlate with, and may be deduced from, the identity of the target genes which GAM157 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2490] Nucleotide sequences of the GAM157 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM157 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM157 are further described hereinbelow with reference to Table Table1.

[2491] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM157 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2492] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 158 (GAM158) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2493] GAM158 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM158 was detected is described hereinabove with reference to Figs. 2-8.

[2494] GAM158 gene, herein designated GAM GENE, and GAM158 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2495] GAM158 gene, herein designated GAM GENE, encodes a GAM158 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM158 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM158 precursor RNA is designated SEQ ID:131, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:131 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[2496] GAM158 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[2497] SEQ ID:99736 detected in mouse EST Accession AA144533.1.

[2498] SEQ ID:99737 detected in mouse EST Accession BE943987.1.

[2499] SEQ ID:99738 detected in mouse EST Accession BE691447.1.

[2500] SEQ ID:99739 detected in mouse EST Accession BG808025.1.

[2501] SEQ ID:99740 detected in mouse EST Accession BG808010.1.

[2502] SEQ ID:99741 detected in mouse EST Accession BG807850.1.

[2503] SEQ ID:99742 detected in mouse EST Accession BG805970.1.

[2504] SEQ ID:99743 detected in mouse EST Accession BG145596.1.

[2505] SEQ ID:99744 detected in mouse EST Accession BE692802.1.

[2506] SEQ ID:99745 detected in mouse EST Accession AW208601.1.

[2507] SEQ ID:99746 detected in mouse EST Accession BB610842.1.

[2508] SEQ ID:99747 detected in mouse EST Accession

BB609859.1.

[2509] SEQ ID:99748 detected in mouse EST Accession AA671455.1.

[2510] SEQ ID:98820 detected in mouse EST Accession AW824753.1.

[2511] SEQ ID:98821 detected in mouse EST Accession BE691413.1.

[2512] GAM158 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2513] An enzyme complex designated DICER COMPLEX, dices the GAM158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM158 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM158 RNA is designated SEQ ID:1807, and is provided hereinbelow with reference to the sequence listing part.

[2514] GAM158 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM158 target RNA, herein designated GAM TARGET RNA. GAM158 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2515] GAM158 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM158 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM158 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM158 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM158 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2516] The complementary binding of GAM158 RNA, herein designated GAM RNA, to target binding sites on GAM158 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM158 target RNA, herein designated GAM TARGET RNA, into GAM158 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2517] It is appreciated that GAM158 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM158 target genes. The mRNA of each one of this plurality of GAM158 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM158 RNA, herein designated GAM RNA, and which when bound by GAM158 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM158 target proteins.

[2518] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM158 gene, herein designated GAM GENE, on one or more GAM158 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2519] It is yet further appreciated that specific functions, and accordingly utilities, of GAM158 correlate with, and may

be deduced from, the identity of the target genes which GAM158 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2520] Nucleotide sequences of the GAM158 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM158 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM158 are further described hereinbelow with reference to Table Table1.

[2521] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM158 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2522] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 159 (GAM159) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2523] GAM159 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM159 was detected is described hereinabove with reference to Figs. 2-8.

[2524] GAM159 gene, herein designated GAM GENE, and GAM159 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2525] GAM159 gene, herein designated GAM GENE, encodes a GAM159 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM159 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM159 precursor RNA is designated SEQ ID:132, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:132 is located at position 1469616 relative to contig NT_008251.11, on chromosome 8.

[2526] GAM159 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2527] An enzyme complex designated DICER COMPLEX, dices the GAM159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM159 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM159 RNA is designated SEQ ID:1808, and is provided hereinbelow with reference to the sequence listing part.

[2528] GAM159 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM159 target RNA, herein designated GAM TARGET RNA. GAM159 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2529] GAM159 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM159 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM159 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM159 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM159 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2530] The complementary binding of GAM159 RNA, herein designated GAM RNA, to target binding sites on GAM159 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM159 target RNA, herein designated GAM TARGET RNA, into GAM159 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2531] It is appreciated that GAM159 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM159 target genes. The mRNA of each one of this plurality of GAM159 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM159 RNA, herein designated GAM RNA, and which when bound by GAM159 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM159 target proteins.

[2532] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM159 gene, herein designated GAM GENE, on one or more GAM159 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2533] It is yet further appreciated that specific functions, and accordingly utilities, of GAM159 correlate with, and may be deduced from, the identity of the target genes which GAM159 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2534] Nucleotide sequences of the GAM159 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM159 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM159 are further described hereinbelow with reference to Table Table1.

[2535] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM159 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2536] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 160 (GAM160) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2537] GAM160 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM160 was detected is described hereinabove with reference to Figs. 2-8.

[2538] GAM160 gene, herein designated GAM GENE, and GAM160 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2539] GAM160 gene, herein designated GAM GENE, encodes a GAM160 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM160 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM160 precursor RNA is desig-

nated SEQ ID:133, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:133 is located at position 2349675 relative to contig NT_021907.13, on chromosome 1.

[2540] GAM160 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2541] An enzyme complex designated DICER COMPLEX, dices the GAM160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM160 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM160 RNA is designated SEQ ID:1809, and is provided hereinbelow with reference to the sequence listing part.

[2542] GAM160 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM160 target RNA, herein designated GAM TARGET RNA. GAM160 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2543] GAM160 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM160 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM160 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM160 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM160 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2544] The complementary binding of GAM160 RNA, herein designated GAM RNA, to target binding sites on GAM160 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM160 target RNA, herein designated GAM TARGET RNA, into GAM160 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2545] It is appreciated that GAM160 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM160 target genes. The mRNA of each one of this plurality of GAM160 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM160 RNA, herein designated GAM RNA, and which when bound by GAM160 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM160 target proteins.

[2546] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM160 gene, herein designated GAM GENE, on one or more GAM160 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2547] It is yet further appreciated that specific functions, and accordingly utilities, of GAM160 correlate with, and may be deduced from, the identity of the target genes which GAM160 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2548] Nucleotide sequences of the GAM160 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM160 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM160 are further described hereinbelow with reference to Table Table1.

[2549] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM160 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2550] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 161 (GAM161) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2551] GAM161 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM161 was detected is described hereinabove with reference to Figs. 2-8.

[2552] GAM161 gene, herein designated GAM GENE, and GAM161 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2553] GAM161 gene, herein designated GAM GENE, encodes a GAM161 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM161 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM161 precursor RNA is designated SEQ ID:134, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:134 is located at position 464461 relative to contig NT_010692.9, on chromosome 17.

[2554] GAM161 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[2555] SEQ ID:99177 detected in mouse EST Accession AA068787.1.

[2556] SEQ ID:99178 detected in mouse EST Accession BG296866.1.

[2557] SEQ ID:99179 detected in mouse EST Accession AA823029.1.

[2558] SEQ ID:99180 detected in mouse EST Accession BI792530.1.

[2559] SEQ ID:99181 detected in mouse EST Accession BE309708.1.

[2560] SEQ ID:99182 detected in mouse EST Accession BI100916.1.

[2561] SEQ ID:98694 detected in mouse EST Accession BE625629.1.

[2562] SEQ ID:98695 detected in mouse EST Accession BE380224.1.

[2563] GAM161 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2564] An enzyme complex designated DICER COMPLEX, dices

the GAM161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM161 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 97%) nucleotide sequence of GAM161 RNA is designated SEQ ID:1810, and is provided hereinbelow with reference to the sequence listing part.

[2565] GAM161 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM161 target RNA, herein designated GAM TARGET RNA. GAM161 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2566] GAM161 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM161 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM161

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM161 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM161 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2567] The complementary binding of GAM161 RNA, herein designated GAM RNA, to target binding sites on GAM161 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM161 target RNA, herein designated GAM TARGET RNA, into GAM161 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2568] It is appreciated that GAM161 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM161 target genes. The mRNA of each one of this plurality of GAM161 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM161 RNA, herein designated GAM RNA, and which when bound by GAM161 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM161 target proteins.

[2569] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM161 gene, herein designated GAM GENE, on one or more GAM161 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2570] It is yet further appreciated that specific functions, and accordingly utilities, of GAM161 correlate with, and may be deduced from, the identity of the target genes which GAM161 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2571] Nucleotide sequences of the GAM161 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM161 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM161 are further described hereinbelow with reference to Table Table1.

[2572] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM161 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2573] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 162 (GAM162) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2574] GAM162 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM162 was detected is described hereinabove with reference to Figs. 2-8.

[2575] GAM162 gene, herein designated GAM GENE, and GAM162 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2576] GAM162 gene, herein designated GAM GENE, encodes a GAM162 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM162 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM162 precursor RNA is designated SEQ ID:135, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:135 is located at position 1265865 relative to contig NT_022567.9, on chromosome 3.

[2577] GAM162 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2578] An enzyme complex designated DICER COMPLEX, dices the GAM162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM162 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM162 RNA is designated SEQ ID:1811, and is provided hereinbelow with reference to the sequence listing part.

[2579] GAM162 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM162 target RNA, herein designated GAM TARGET RNA.

GAM162 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2580] GAM162 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM162 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM162 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM162 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM162 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2581] The complementary binding of GAM162 RNA, herein designated GAM RNA, to target binding sites on GAM162 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM162 target RNA, herein designated GAM TARGET RNA, into GAM162 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2582] It is appreciated that GAM162 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM162 target genes. The mRNA of each one of this plurality of GAM162 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM162 RNA, herein designated GAM RNA, and which when bound by GAM162 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM162 target proteins.

[2583] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM162 gene, herein designated GAM GENE, on one or more GAM162 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2584] It is yet further appreciated that specific functions, and accordingly utilities, of GAM162 correlate with, and may be deduced from, the identity of the target genes which GAM162 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2585] Nucleotide sequences of the GAM162 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM162 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM162 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM162 are further described hereinbelow with reference to Table Table1.

[2586] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM162 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2587] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 163 (GAM163) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2588] GAM163 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM163 was detected is described hereinabove with reference to Figs. 2-8.

[2589] GAM163 gene, herein designated GAM GENE, and GAM163 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2590] GAM163 gene, herein designated GAM GENE, encodes a GAM163 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM163 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM163 precursor RNA is designated SEQ ID:136, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:136 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[2591] GAM163 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2592] An enzyme complex designated DICER COMPLEX, dices the GAM163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM163 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM163 RNA is designated SEQ ID:1812, and is provided hereinbelow with reference to the sequence listing part.

[2593] GAM163 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM163 target RNA, herein designated GAM TARGET RNA. GAM163 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2594] GAM163 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM163 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM163 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM163 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM163 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2595] The complementary binding of GAM163 RNA, herein designated GAM RNA, to target binding sites on GAM163 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM163 target RNA, herein designated GAM TARGET RNA, into GAM163 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2596] It is appreciated that GAM163 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM163 target genes. The mRNA of each one of this plu-

rality of GAM163 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM163 RNA, herein designated GAM RNA, and which when bound by GAM163 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM163 target proteins.

[2597] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM163 gene, herein designated GAM GENE, on one or more GAM163 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2598] It is yet further appreciated that specific functions, and accordingly utilities, of GAM163 correlate with, and may be deduced from, the identity of the target genes which GAM163 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2599] Nucleotide sequences of the GAM163 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM163 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM163 are further described hereinbelow with reference to Table Table1.

[2600] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM163 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2601] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 164 (GAM164) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[2602] GAM164 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM164 was detected is described hereinabove with reference to Figs. 2-8.

[2603] GAM164 gene, herein designated GAM GENE, and GAM164 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2604] GAM164 gene, herein designated GAM GENE, encodes a GAM164 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM164 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM164 precursor RNA is designated SEQ ID:137, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:137 is located at position 6961161 relative to contig NT_011196.11, on chromosome 19.

[2605] GAM164 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2606] An enzyme complex designated DICER COMPLEX, dices the GAM164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM164 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM164 RNA is designated SEQ ID:1813, and is provided hereinbelow with reference to the sequence listing part.

[2607] GAM164 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM164 target RNA, herein designated GAM TARGET RNA. GAM164 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2608] GAM164 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM164 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM164 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM164 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM164 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2609] The complementary binding of GAM164 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM164 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM164 target RNA, herein designated GAM TARGET RNA, into GAM164 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2610] It is appreciated that GAM164 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM164 target genes. The mRNA of each one of this plurality of GAM164 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM164 RNA, herein designated GAM RNA, and which when bound by GAM164 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM164 target proteins.

[2611] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM164 gene, herein designated GAM GENE, on one or more GAM164 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2612] It is yet further appreciated that specific functions, and accordingly utilities, of GAM164 correlate with, and may be deduced from, the identity of the target genes which GAM164 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2613] Nucleotide sequences of the GAM164 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM164 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM164 are further described hereinbelow with reference to Table Table1.

[2614] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM164 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2615] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 165 (GAM165) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2616] GAM165 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM165 was detected is described hereinabove with reference to Figs. 2-8.

[2617] GAM165 gene, herein designated GAM GENE, and GAM165 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2618] GAM165 gene, herein designated GAM GENE, encodes a GAM165 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM165 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM165 precursor RNA is designated SEQ ID:138, and is provided hereinbelow with reference to the sequence listing part.

[2619] GAM165 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2620] An enzyme complex designated DICER COMPLEX, dices the GAM165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM165 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM165 RNA is designated SEQ ID:1814, and is provided hereinbelow with reference to the sequence listing part.

[2621] GAM165 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM165 target RNA, herein designated GAM TARGET RNA. GAM165 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2622] GAM165 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM165 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM165 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM165 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM165 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2623] The complementary binding of GAM165 RNA, herein designated GAM RNA, to target binding sites on GAM165 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM165 target RNA, herein designated GAM TARGET RNA, into GAM165 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2624] It is appreciated that GAM165 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM165 target genes. The mRNA of each one of this plurality of GAM165 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM165 RNA, herein designated GAM RNA, and which when bound by GAM165 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM165 target proteins.

[2625] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM165 gene, herein designated GAM GENE, on one or more GAM165 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2626] It is yet further appreciated that specific functions, and accordingly utilities, of GAM165 correlate with, and may be deduced from, the identity of the target genes which GAM165 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2627] Nucleotide sequences of the GAM165 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM165 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM165 are further described hereinbelow with reference to Table Table1.

[2628] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM165 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2629] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 166 (GAM166) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2630] GAM166 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM166 was detected is described hereinabove with reference to Figs. 2-8.

[2631] GAM166 gene, herein designated GAM GENE, and GAM166 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2632] GAM166 gene, herein designated GAM GENE, encodes a GAM166 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM166 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM166 precursor RNA is designated SEQ ID:139, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:139 is located at position 1487922 relative to contig NT_019273.13, on chromosome 1.

[2633] GAM166 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[2634] An enzyme complex designated DICER COMPLEX, dices the GAM166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM166 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM166 RNA is designated SEQ ID:1815, and is provided hereinbelow with reference to the sequence listing part.

[2635] GAM166 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM166 target RNA, herein designated GAM TARGET RNA. GAM166 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2636] GAM166 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM166 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM166 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM166 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM166 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2637] The complementary binding of GAM166 RNA, herein designated GAM RNA, to target binding sites on GAM166 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM166 target RNA, herein designated GAM TARGET RNA, into GAM166 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2638] It is appreciated that GAM166 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM166 target genes. The mRNA of each one of this plurality of GAM166 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM166 RNA, herein designated GAM RNA, and which when bound by GAM166 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM166 target proteins.

[2639] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM166 gene, herein designated GAM GENE, on one or more GAM166 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2640] It is yet further appreciated that specific functions, and accordingly utilities, of GAM166 correlate with, and may be deduced from, the identity of the target genes which GAM166 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2641] Nucleotide sequences of the GAM166 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM166 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM166 are further described hereinbelow with reference to Table Table1.

[2642] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM166 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2643] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 167 (GAM167) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2644] GAM167 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM167 was detected is described hereinabove with reference to Figs. 2-8.

[2645] GAM167 gene, herein designated GAM GENE, and GAM167 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2646] GAM167 gene, herein designated GAM GENE, encodes a GAM167 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM167 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM167 precursor RNA is designated SEQ ID:140, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:140 is located at position 10716414 relative to

contig NT_033899.3, on chromosome 11.

[2647] GAM167 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2648] An enzyme complex designated DICER COMPLEX, dices the GAM167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM167 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM167 RNA is designated SEQ ID:1816, and is provided hereinbelow with reference to the sequence listing part.

[2649] GAM167 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM167 target RNA, herein designated GAM TARGET RNA.

GAM167 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2650] GAM167 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM167 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM167 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM167 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM167 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2651] The complementary binding of GAM167 RNA, herein designated GAM RNA, to target binding sites on GAM167 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM167 target RNA, herein designated GAM TARGET RNA, into GAM167 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2652] It is appreciated that GAM167 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM167 target genes. The mRNA of each one of this plurality of GAM167 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM167 RNA, herein designated GAM RNA, and which when bound by GAM167 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM167 target proteins.

[2653] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM167 gene, herein designated GAM GENE, on one or more GAM167 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2654] It is yet further appreciated that specific functions, and accordingly utilities, of GAM167 correlate with, and may be deduced from, the identity of the target genes which GAM167 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2655] Nucleotide sequences of the GAM167 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM167 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM167 are further described hereinbelow with reference to Table Table1.

[2656] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM167 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2657] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 168 (GAM168) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2658] GAM168 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM168 was detected is described hereinabove with reference to Figs. 2-8.

[2659] GAM168 gene, herein designated GAM GENE, and GAM168 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2660] GAM168 gene, herein designated GAM GENE, encodes a GAM168 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM168 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM168 precursor RNA is designated SEQ ID:141, and is provided hereinbelow with reference to the sequence listing part.

[2661] GAM168 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2662] An enzyme complex designated DICER COMPLEX, dices the GAM168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM168 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM168 RNA is designated SEQ ID:1817, and is provided hereinbelow with reference to the sequence listing part.

[2663] GAM168 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM168 target RNA, herein designated GAM TARGET RNA. GAM168 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2664] GAM168 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM168 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM168 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM168 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM168 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2665] The complementary binding of GAM168 RNA, herein designated GAM RNA, to target binding sites on GAM168 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM168 target RNA, herein designated GAM TARGET RNA, into GAM168 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2666] It is appreciated that GAM168 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM168 target genes. The mRNA of each one of this plu-

rality of GAM168 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM168 RNA, herein designated GAM RNA, and which when bound by GAM168 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM168 target proteins.

[2667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM168 gene, herein designated GAM GENE, on one or more GAM168 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2668] It is yet further appreciated that specific functions, and accordingly utilities, of GAM168 correlate with, and may be deduced from, the identity of the target genes which GAM168 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2669] Nucleotide sequences of the GAM168 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM168 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM168 are further described hereinbelow with reference to Table Table1.

[2670] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM168 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2671] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 169 (GAM169) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[2672] GAM169 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM169 was detected is described hereinabove with reference to Figs. 2-8.

[2673] GAM169 gene, herein designated GAM GENE, and GAM169 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2674] GAM169 gene, herein designated GAM GENE, encodes a GAM169 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM169 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM169 precursor RNA is designated SEQ ID:142, and is provided hereinbelow with reference to the sequence listing part.

[2675] GAM169 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2676] An enzyme complex designated DICER COMPLEX, dices the GAM169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM169 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM169 RNA is designated SEQ ID:1818, and is provided hereinbelow with reference to the sequence listing part.

[2677] GAM169 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM169 target RNA, herein designated GAM TARGET RNA.
GAM169 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2678] GAM169 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM169 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM169 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM169 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM169 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2679] The complementary binding of GAM169 RNA, herein designated GAM RNA, to target binding sites on GAM169 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM169 target RNA, herein designated GAM TARGET RNA, into GAM169 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2680] It is appreciated that GAM169 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM169 target genes. The mRNA of each one of this plurality of GAM169 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM169 RNA, herein designated GAM RNA, and which when bound by GAM169 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM169 target proteins.

[2681] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM169 gene, herein designated GAM GENE, on one or more GAM169 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2682] It is yet further appreciated that specific functions, and accordingly utilities, of GAM169 correlate with, and may be deduced from, the identity of the target genes which GAM169 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2683] Nucleotide sequences of the GAM169 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM169 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM169 are further described hereinbelow with reference to Table Table1.

[2684] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM169 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2685] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 170 (GAM170) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2686] GAM170 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM170 was detected is described hereinabove with reference to Figs. 2-8.

[2687] GAM170 gene, herein designated GAM GENE, and GAM170 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2688] GAM170 gene, herein designated GAM GENE, encodes a GAM170 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM170 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM170 precursor RNA is desig-

nated SEQ ID:143, and is provided hereinbelow with reference to the sequence listing part.

[2689] GAM170 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2690] An enzyme complex designated DICER COMPLEX, dices the GAM170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM170 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM170 RNA is designated SEQ ID:1819, and is provided hereinbelow with reference to the sequence listing part.

[2691] GAM170 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM170 target RNA, herein designated GAM TARGET RNA. GAM170 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2692] GAM170 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM170 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM170 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM170 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM170

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2693] The complementary binding of GAM170 RNA, herein designated GAM RNA, to target binding sites on GAM170 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM170 target RNA, herein designated GAM TARGET RNA, into GAM170 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2694] It is appreciated that GAM170 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM170 target genes. The mRNA of each one of this plurality of GAM170 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM170 RNA, herein designated GAM RNA, and which when bound by GAM170 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM170 target proteins.

[2695] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM170 gene, herein designated GAM GENE, on one or more GAM170 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2696] It is yet further appreciated that specific functions, and accordingly utilities, of GAM170 correlate with, and may be deduced from, the identity of the target genes which GAM170 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2697] Nucleotide sequences of the GAM170 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM170 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM170 are further described hereinbelow with reference to Table Table1.

[2698] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM170 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2699] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 171 (GAM171) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2700] GAM171 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM171 was detected is described hereinabove with reference to Figs. 2-8.

[2701] GAM171 gene, herein designated GAM GENE, and GAM171 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[2702] GAM171 gene, herein designated GAM GENE, encodes a GAM171 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM171 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM171 precursor RNA is designated SEQ ID:144, and is provided hereinbelow with reference to the sequence listing part.

[2703] GAM171 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2704] An enzyme complex designated DICER COMPLEX, dices the GAM171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM171 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM171 RNA is designated SEQ ID:1820, and is provided hereinbelow with reference to the sequence listing part.

[2705] GAM171 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM171 target RNA, herein designated GAM TARGET RNA. GAM171 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2706] GAM171 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM171 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM171 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM171 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM171 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2707] The complementary binding of GAM171 RNA, herein designated GAM RNA, to target binding sites on GAM171 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM171 target RNA, herein designated GAM TARGET RNA, into GAM171 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2708] It is appreciated that GAM171 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM171 target genes. The mRNA of each one of this plurality of GAM171 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM171 RNA, herein designated GAM RNA, and which when bound by GAM171 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM171 target proteins.

[2709] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM171 gene, herein designated GAM GENE, on one or more GAM171 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[2710] It is yet further appreciated that specific functions, and accordingly utilities, of GAM171 correlate with, and may be deduced from, the identity of the target genes which GAM171 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2711] Nucleotide sequences of the GAM171 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM171 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM171 are further described hereinbelow with reference to Table Table1.

[2712] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM171 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2713] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 172 (GAM172) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[2714] GAM172 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM172 was detected is described hereinabove with reference to Figs. 2-8.

[2715] GAM172 gene, herein designated GAM GENE, and GAM172 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2716] GAM172 gene, herein designated GAM GENE, encodes a GAM172 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM172 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM172 precursor RNA is designated SEQ ID:145, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:145 is located at position 14900478 relative to contig NT_033899.3, on chromosome 11.

[2717] GAM172 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2718] An enzyme complex designated DICER COMPLEX, dices the GAM172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM172 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM172 RNA is designated SEQ ID:1821, and is provided hereinbelow with reference to the sequence listing part.

[2719] GAM172 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM172 target RNA, herein designated GAM TARGET RNA. GAM172 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2720] GAM172 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM172 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM172 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM172 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM172 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2721] The complementary binding of GAM172 RNA, herein designated GAM RNA, to target binding sites on GAM172 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM172 target RNA, herein designated GAM TARGET RNA, into GAM172 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2722] It is appreciated that GAM172 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM172 target genes. The mRNA of each one of this plurality of GAM172 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM172 RNA, herein designated GAM RNA, and which when bound by GAM172 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM172 target proteins.

[2723] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM172 gene, herein designated GAM GENE, on one or more GAM172 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2724] It is yet further appreciated that specific functions, and accordingly utilities, of GAM172 correlate with, and may be deduced from, the identity of the target genes which GAM172 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2725] Nucleotide sequences of the GAM172 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM172 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM172 are further described hereinbelow with reference to Table Table1.

[2726] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM172 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2727] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 173 (GAM173) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2728] GAM173 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM173 was detected is described hereinabove with reference to Figs. 2-8.

[2729] GAM173 gene, herein designated GAM GENE, and GAM173 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2730] GAM173 gene, herein designated GAM GENE, encodes a GAM173 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM173 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM173 precursor RNA is designated SEQ ID:146, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:146 is located at position 1065102 relative to contig NT_029973.6, on chromosome 5.

[2731] GAM173 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2732] An enzyme complex designated DICER COMPLEX, dices the GAM173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM173 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM173 RNA is designated SEQ ID:1822, and is provided hereinbelow with reference to the sequence listing part.

[2733] GAM173 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM173 target RNA, herein designated GAM TARGET RNA. GAM173 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2734] GAM173 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM173 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM173 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM173 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM173 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2735] The complementary binding of GAM173 RNA, herein designated GAM RNA, to target binding sites on GAM173 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM173 target RNA, herein designated GAM TARGET RNA, into GAM173 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2736] It is appreciated that GAM173 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM173 target genes. The mRNA of each one of this plurality of GAM173 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM173 RNA, herein designated GAM RNA, and which when bound by GAM173 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM173 target proteins.

[2737] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM173 gene, herein designated GAM GENE, on one or more GAM173 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2738] It is yet further appreciated that specific functions, and accordingly utilities, of GAM173 correlate with, and may

be deduced from, the identity of the target genes which GAM173 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2739] Nucleotide sequences of the GAM173 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM173 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM173 are further described hereinbelow with reference to Table Table1.

[2740] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM173 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2741] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 174 (GAM174) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2742] GAM174 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM174 was detected is described hereinabove with reference to Figs. 2-8.

[2743] GAM174 gene, herein designated GAM GENE, and GAM174 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2744] GAM174 gene, herein designated GAM GENE, encodes a GAM174 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM174 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM174 precursor RNA is designated SEQ ID:147, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:147 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[2745] GAM174 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2746] An enzyme complex designated DICER COMPLEX, dices the GAM174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM174 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM174 RNA is designated SEQ ID:1823, and is provided hereinbelow with reference to the sequence listing part.

[2747] GAM174 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM174 target RNA, herein designated GAM TARGET RNA. GAM174 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2748] GAM174 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM174 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM174 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM174 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM174 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2749] The complementary binding of GAM174 RNA, herein designated GAM RNA, to target binding sites on GAM174 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM174 target RNA, herein designated GAM TARGET RNA, into GAM174 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2750] It is appreciated that GAM174 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM174 target genes. The mRNA of each one of this plurality of GAM174 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM174 RNA, herein designated GAM RNA, and which when bound by GAM174 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM174 target proteins.

[2751] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM174 gene, herein designated GAM GENE, on one or more GAM174 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2752] It is yet further appreciated that specific functions, and accordingly utilities, of GAM174 correlate with, and may be deduced from, the identity of the target genes which GAM174 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2753] Nucleotide sequences of the GAM174 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM174 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM174 are further described hereinbelow with reference to Table Table1.

[2754] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM174 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2755] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 175 (GAM175) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2756] GAM175 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM175 was detected is described hereinabove with reference to Figs. 2-8.

[2757] GAM175 gene, herein designated GAM GENE, and GAM175 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2758] GAM175 gene, herein designated GAM GENE, encodes a GAM175 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM175 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM175 precursor RNA is desig-

nated SEQ ID:148, and is provided hereinbelow with reference to the sequence listing part.

[2759] GAM175 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[2760] SEQ ID:100071 detected in mouse EST Accession AA106737.1.

[2761] SEQ ID:100072 detected in mouse EST Accession AA500296.1.

[2762] SEQ ID:100073 detected in mouse EST Accession BE554084.1.

[2763] SEQ ID:100074 detected in mouse EST Accession BG922170.1.

[2764] GAM175 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[2765] An enzyme complex designated DICER COMPLEX, dices the GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM175 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM175 RNA is designated SEQ ID:1824, and is provided hereinbelow with reference to the sequence listing part.

[2766] GAM175 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM175 target RNA, herein designated GAM TARGET RNA.
GAM175 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2767] GAM175 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM175 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM175 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM175 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM175 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2768] The complementary binding of GAM175 RNA, herein designated GAM RNA, to target binding sites on GAM175 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM175 target RNA, herein desig-

nated GAM TARGET RNA, into GAM175 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2769] It is appreciated that GAM175 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM175 target genes. The mRNA of each one of this plurality of GAM175 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM175 RNA, herein designated GAM RNA, and which when bound by GAM175 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM175 target proteins.

[2770] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM175 gene, herein designated GAM GENE, on one or more GAM175 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2771] It is yet further appreciated that specific functions, and accordingly utilities, of GAM175 correlate with, and may be deduced from, the identity of the target genes which GAM175 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2772] Nucleotide sequences of the GAM175 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM175 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM175 are further described hereinbelow with reference to Table Table1.

[2773] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM175 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[2774] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 176 (GAM176) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2775] GAM176 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM176 was detected is described hereinabove with reference to Figs. 2-8.

[2776] GAM176 gene, herein designated GAM GENE, and GAM176 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2777] GAM176 gene, herein designated GAM GENE, encodes a GAM176 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM176 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM176 precursor RNA is designated SEQ ID:149, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:149 is located at position 3102327 relative to contig NT_011109.13, on chromosome 19.

[2778] GAM176 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2779] An enzyme complex designated DICER COMPLEX, dices the GAM176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM176 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM176 RNA is designated SEQ ID:1825, and is provided hereinbelow with reference to the sequence listing part.

[2780] GAM176 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM176 target RNA, herein designated GAM TARGET RNA. GAM176 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2781] GAM176 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM176 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM176 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM176 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM176

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2782] The complementary binding of GAM176 RNA, herein designated GAM RNA, to target binding sites on GAM176 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM176 target RNA, herein designated GAM TARGET RNA, into GAM176 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2783] It is appreciated that GAM176 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM176 target genes. The mRNA of each one of this plurality of GAM176 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM176 RNA, herein designated GAM RNA, and which when bound by GAM176 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM176 target proteins.

[2784] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM176 gene, herein designated GAM GENE, on one or more GAM176 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2785] It is yet further appreciated that specific functions, and accordingly utilities, of GAM176 correlate with, and may be deduced from, the identity of the target genes which GAM176 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2786] Nucleotide sequences of the GAM176 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM176 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM176 are further described hereinbelow with reference to Table Table1.

[2787] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM176 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2788] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 177 (GAM177) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2789] GAM177 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM177 was detected is described hereinabove with reference to Figs. 2-8.

[2790] GAM177 gene, herein designated GAM GENE, and GAM177 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[2791] GAM177 gene, herein designated GAM GENE, encodes a GAM177 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM177 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM177 precursor RNA is designated SEQ ID:150, and is provided hereinbelow with reference to the sequence listing part.

[2792] GAM177 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2793] An enzyme complex designated DICER COMPLEX, dices the GAM177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM177 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM177 RNA is designated SEQ ID:1826, and is provided hereinbelow with reference to the sequence listing part.

[2794] GAM177 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM177 target RNA, herein designated GAM TARGET RNA. GAM177 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2795] GAM177 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM177 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM177 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM177 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM177 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2796] The complementary binding of GAM177 RNA, herein designated GAM RNA, to target binding sites on GAM177 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM177 target RNA, herein designated GAM TARGET RNA, into GAM177 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2797] It is appreciated that GAM177 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM177 target genes. The mRNA of each one of this plurality of GAM177 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM177 RNA, herein designated GAM RNA, and which when bound by GAM177 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM177 target proteins.

[2798] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM177 gene, herein designated GAM GENE, on one or more GAM177 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[2799] It is yet further appreciated that specific functions, and accordingly utilities, of GAM177 correlate with, and may be deduced from, the identity of the target genes which GAM177 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2800] Nucleotide sequences of the GAM177 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM177 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM177 are further described hereinbelow with reference to Table Table1.

[2801] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM177 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2802] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 178 (GAM178) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[2803] GAM178 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM178 was detected is described hereinabove with reference to Figs. 2-8.

[2804] GAM178 gene, herein designated GAM GENE, and GAM178 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2805] GAM178 gene, herein designated GAM GENE, encodes a GAM178 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM178 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM178 precursor RNA is designated SEQ ID:151, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:151 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[2806] GAM178 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2807] An enzyme complex designated DICER COMPLEX, dices the GAM178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM178 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM178 RNA is designated SEQ ID:1827, and is provided hereinbelow with reference to the sequence listing part.

[2808] GAM178 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM178 target RNA, herein designated GAM TARGET RNA. GAM178 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2809] GAM178 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM178 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM178 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM178 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM178 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2810] The complementary binding of GAM178 RNA, herein designated GAM RNA, to target binding sites on GAM178 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM178 target RNA, herein designated GAM TARGET RNA, into GAM178 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2811] It is appreciated that GAM178 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM178 target genes. The mRNA of each one of this plurality of GAM178 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM178 RNA, herein designated GAM RNA, and which when bound by GAM178 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM178 target proteins.

[2812] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM178 gene, herein designated GAM GENE, on one or more GAM178 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2813] It is yet further appreciated that specific functions, and accordingly utilities, of GAM178 correlate with, and may be deduced from, the identity of the target genes which GAM178 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2814] Nucleotide sequences of the GAM178 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM178 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM178 are further described hereinbelow with reference to Table Table1.

[2815] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM178 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2816] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 179 (GAM179) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2817] GAM179 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM179 was detected is described hereinabove with reference to Figs. 2-8.

[2818] GAM179 gene, herein designated GAM GENE, and GAM179 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2819] GAM179 gene, herein designated GAM GENE, encodes a GAM179 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM179 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM179 precursor RNA is designated SEQ ID:152, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:152 is located at position 469334 relative to contig NT_005823.12, on chromosome 3.

[2820] GAM179 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2821] An enzyme complex designated DICER COMPLEX, dices the GAM179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM179 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM179 RNA is designated SEQ ID:1828, and is provided hereinbelow with reference to the sequence listing part.

[2822] GAM179 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM179 target RNA, herein designated GAM TARGET RNA. GAM179 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2823] GAM179 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM179 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM179 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM179 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM179 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2824] The complementary binding of GAM179 RNA, herein designated GAM RNA, to target binding sites on GAM179 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM179 target RNA, herein designated GAM TARGET RNA, into GAM179 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2825] It is appreciated that GAM179 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM179 target genes. The mRNA of each one of this plurality of GAM179 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM179 RNA, herein designated GAM RNA, and which when bound by GAM179 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM179 target proteins.

[2826] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM179 gene, herein designated GAM GENE, on one or more GAM179 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2827] It is yet further appreciated that specific functions, and accordingly utilities, of GAM179 correlate with, and may

be deduced from, the identity of the target genes which GAM179 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2828] Nucleotide sequences of the GAM179 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM179 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM179 are further described hereinbelow with reference to Table Table1.

[2829] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM179 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2830] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 180 (GAM180) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2831] GAM180 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM180 was detected is described hereinabove with reference to Figs. 2-8.

[2832] GAM180 gene, herein designated GAM GENE, and GAM180 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2833] GAM180 gene, herein designated GAM GENE, encodes a GAM180 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM180 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM180 precursor RNA is designated SEQ ID:153, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:153 is located at position 6961165 relative to contig NT_011196.11, on chromosome 19.

[2834] GAM180 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2835] An enzyme complex designated DICER COMPLEX, dices the GAM180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM180 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM180 RNA is designated SEQ ID:1829, and is provided hereinbelow with reference to the sequence listing part.

[2836] GAM180 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM180 target RNA, herein designated GAM TARGET RNA.
GAM180 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2837] GAM180 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM180 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM180 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM180 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM180 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2838] The complementary binding of GAM180 RNA, herein designated GAM RNA, to target binding sites on GAM180 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM180 target RNA, herein designated GAM TARGET RNA, into GAM180 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2839] It is appreciated that GAM180 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM180 target genes. The mRNA of each one of this plurality of GAM180 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM180 RNA, herein designated GAM RNA, and which when bound by GAM180 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM180 target proteins.

[2840] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM180 gene, herein designated GAM GENE, on one or more GAM180 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2841] It is yet further appreciated that specific functions, and accordingly utilities, of GAM180 correlate with, and may be deduced from, the identity of the target genes which GAM180 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2842] Nucleotide sequences of the GAM180 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM180 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM180 are further described hereinbelow with reference to Table Table1.

[2843] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM180 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2844] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 181 (GAM181) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2845] GAM181 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM181 was detected is described hereinabove with reference to Figs. 2-8.

[2846] GAM181 gene, herein designated GAM GENE, and GAM181 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2847] GAM181 gene, herein designated GAM GENE, encodes a GAM181 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM181 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM181 precursor RNA is desig-

nated SEQ ID:154, and is provided hereinbelow with reference to the sequence listing part.

[2848] GAM181 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2849] An enzyme complex designated DICER COMPLEX, dices the GAM181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM181 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM181 RNA is designated SEQ ID:1830, and is provided hereinbelow with reference to the sequence listing part.

[2850] GAM181 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM181 target RNA, herein designated GAM TARGET RNA. GAM181 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2851] GAM181 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM181 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM181 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM181 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM181

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2852] The complementary binding of GAM181 RNA, herein designated GAM RNA, to target binding sites on GAM181 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM181 target RNA, herein designated GAM TARGET RNA, into GAM181 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2853] It is appreciated that GAM181 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM181 target genes. The mRNA of each one of this plurality of GAM181 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM181 RNA, herein designated GAM RNA, and which when bound by GAM181 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM181 target proteins.

[2854] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM181 gene, herein designated GAM GENE, on one or more GAM181 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2855] It is yet further appreciated that specific functions, and accordingly utilities, of GAM181 correlate with, and may be deduced from, the identity of the target genes which GAM181 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2856] Nucleotide sequences of the GAM181 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM181 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM181 are further described hereinbelow with reference to Table Table1.

[2857] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM181 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2858] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 182 (GAM182) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2859] GAM182 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM182 was detected is described hereinabove with reference to Figs. 2-8.

[2860] GAM182 gene, herein designated GAM GENE, and GAM182 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[2861] GAM182 gene, herein designated GAM GENE, encodes a GAM182 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM182 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM182 precursor RNA is designated SEQ ID:155, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:155 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[2862] GAM182 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2863] An enzyme complex designated DICER COMPLEX, dices

the GAM182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM182 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM182 RNA is designated SEQ ID:1831, and is provided hereinbelow with reference to the sequence listing part.

[2864] GAM182 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM182 target RNA, herein designated GAM TARGET RNA. GAM182 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2865] GAM182 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM182 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM182

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM182 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM182 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2866] The complementary binding of GAM182 RNA, herein designated GAM RNA, to target binding sites on GAM182 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM182 target RNA, herein designated GAM TARGET RNA, into GAM182 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2867] It is appreciated that GAM182 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM182 target genes. The mRNA of each one of this plurality of GAM182 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM182 RNA, herein designated GAM RNA, and which when bound by GAM182 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM182 target proteins.

[2868] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM182 gene, herein designated GAM GENE, on one or more GAM182 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2869] It is yet further appreciated that specific functions, and accordingly utilities, of GAM182 correlate with, and may be deduced from, the identity of the target genes which GAM182 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2870] Nucleotide sequences of the GAM182 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM182 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM182 are further described hereinbelow with reference to Table Table1.

[2871] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM182 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2872] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 183 (GAM183) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2873] GAM183 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM183 was detected is described hereinabove with reference to Figs. 2-8.

[2874] GAM183 gene, herein designated GAM GENE, and GAM183 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2875] GAM183 gene, herein designated GAM GENE, encodes a GAM183 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM183 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM183 precursor RNA is designated SEQ ID:156, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:156 is located at position 7218840 relative to contig NT_011812.10, on chromosome X.

[2876] GAM183 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2877] An enzyme complex designated DICER COMPLEX, dices the GAM183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM183 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM183 RNA is designated SEQ ID:1832, and is provided hereinbelow with reference to the sequence listing part.

[2878] GAM183 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM183 target RNA, herein designated GAM TARGET RNA.

GAM183 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2879] GAM183 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM183 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM183 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM183 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM183 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2880] The complementary binding of GAM183 RNA, herein designated GAM RNA, to target binding sites on GAM183 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM183 target RNA, herein designated GAM TARGET RNA, into GAM183 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2881] It is appreciated that GAM183 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM183 target genes. The mRNA of each one of this plurality of GAM183 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM183 RNA, herein designated GAM RNA, and which when bound by GAM183 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM183 target proteins.

[2882] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM183 gene, herein designated GAM GENE, on one or more GAM183 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2883] It is yet further appreciated that specific functions, and accordingly utilities, of GAM183 correlate with, and may be deduced from, the identity of the target genes which GAM183 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2884] Nucleotide sequences of the GAM183 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM183 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM183 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM183 are further described hereinbelow with reference to Table Table1.

[2885] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM183 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2886] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 184 (GAM184) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2887] GAM184 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM184 was detected is described hereinabove with reference to Figs. 2-8.

[2888] GAM184 gene, herein designated GAM GENE, and GAM184 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2889] GAM184 gene, herein designated GAM GENE, encodes a GAM184 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM184 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM184 precursor RNA is designated SEQ ID:157, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:157 is located at position 28177 relative to contig NT_026397.11, on chromosome 12.

[2890] GAM184 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[2891] SEQ ID:99112 detected in mouse EST Accession AI326210.1.

[2892] SEQ ID:99113 detected in mouse EST Accession BI965652.1.

[2893] SEQ ID:100322 detected in mouse EST Accession BI965972.1.

[2894] GAM184 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2895] An enzyme complex designated DICER COMPLEX, dices the GAM184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM184 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM184 RNA is designated SEQ ID:1833, and is provided hereinbelow with reference to the sequence listing part.

[2896] GAM184 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM184 target RNA, herein designated GAM TARGET RNA. GAM184 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2897] GAM184 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM184 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM184 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM184 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM184 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2898] The complementary binding of GAM184 RNA, herein designated GAM RNA, to target binding sites on GAM184 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM184 target RNA, herein designated GAM TARGET RNA, into GAM184 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2899] It is appreciated that GAM184 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM184 target genes. The mRNA of each one of this plurality of GAM184 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM184 RNA, herein designated GAM RNA, and which when bound by GAM184 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM184 target proteins.

[2900] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM184 gene, herein designated GAM GENE, on one or more GAM184 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2901] It is yet further appreciated that specific functions, and accordingly utilities, of GAM184 correlate with, and may be deduced from, the identity of the target genes which GAM184 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2902] Nucleotide sequences of the GAM184 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM184 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM184 are further described hereinbelow with reference to Table Table1.

[2903] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM184 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2904] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 185 (GAM185) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2905] GAM185 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM185 was detected is described hereinabove with reference to Figs. 2-8.

[2906] GAM185 gene, herein designated GAM GENE, and GAM185 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2907] GAM185 gene, herein designated GAM GENE, encodes a GAM185 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM185 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM185 precursor RNA is designated SEQ ID:158, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:158 is located at position 1265865 relative to contig NT_022567.9, on chromosome 3.

[2908] GAM185 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2909] An enzyme complex designated DICER COMPLEX, dices the GAM185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM185 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM185 RNA is designated SEQ ID:1834, and is provided hereinbelow with reference to the sequence listing part.

[2910] GAM185 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM185 target RNA, herein designated GAM TARGET RNA. GAM185 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2911] GAM185 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM185 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM185 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM185 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM185 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2912] The complementary binding of GAM185 RNA, herein designated GAM RNA, to target binding sites on GAM185 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM185 target RNA, herein designated GAM TARGET RNA, into GAM185 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2913] It is appreciated that GAM185 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM185 target genes. The mRNA of each one of this plurality of GAM185 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM185 RNA, herein designated GAM RNA, and which when bound by GAM185 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM185 target proteins.

[2914] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM185 gene, herein designated GAM GENE, on one or more GAM185 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2915] It is yet further appreciated that specific functions, and accordingly utilities, of GAM185 correlate with, and may

be deduced from, the identity of the target genes which GAM185 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2916] Nucleotide sequences of the GAM185 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM185 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM185 are further described hereinbelow with reference to Table Table1.

[2917] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM185 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2918] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 186 (GAM186) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2919] GAM186 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM186 was detected is described hereinabove with reference to Figs. 2-8.

[2920] GAM186 gene, herein designated GAM GENE, and GAM186 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2921] GAM186 gene, herein designated GAM GENE, encodes a GAM186 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM186 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM186 precursor RNA is designated SEQ ID:159, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:159 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[2922] GAM186 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2923] An enzyme complex designated DICER COMPLEX, dices the GAM186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM186 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM186 RNA is designated SEQ ID:1835, and is provided hereinbelow with reference to the sequence listing part.

[2924] GAM186 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM186 target RNA, herein designated GAM TARGET RNA. GAM186 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2925] GAM186 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM186 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM186 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM186 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM186 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2926] The complementary binding of GAM186 RNA, herein designated GAM RNA, to target binding sites on GAM186 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM186 target RNA, herein designated GAM TARGET RNA, into GAM186 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2927] It is appreciated that GAM186 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM186 target genes. The mRNA of each one of this plurality of GAM186 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM186 RNA, herein designated GAM RNA, and which when bound by GAM186 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM186 target proteins.

[2928] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM186 gene, herein designated GAM GENE, on one or more GAM186 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2929] It is yet further appreciated that specific functions, and accordingly utilities, of GAM186 correlate with, and may be deduced from, the identity of the target genes which GAM186 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2930] Nucleotide sequences of the GAM186 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM186 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM186 are further described hereinbelow with reference to Table Table1.

[2931] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM186 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2932] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 187 (GAM187) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2933] GAM187 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM187 was detected is described hereinabove with reference to Figs. 2-8.

[2934] GAM187 gene, herein designated GAM GENE, and GAM187 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2935] GAM187 gene, herein designated GAM GENE, encodes a GAM187 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM187 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM187 precursor RNA is desig-

nated SEQ ID:160, and is provided hereinbelow with reference to the sequence listing part.

[2936] GAM187 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2937] An enzyme complex designated DICER COMPLEX, dices the GAM187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM187 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM187 RNA is designated SEQ ID:1836, and is provided hereinbelow with reference to the sequence listing part.

[2938] GAM187 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM187 target RNA, herein designated GAM TARGET RNA. GAM187 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2939] GAM187 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM187 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM187 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM187 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM187

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2940] The complementary binding of GAM187 RNA, herein designated GAM RNA, to target binding sites on GAM187 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM187 target RNA, herein designated GAM TARGET RNA, into GAM187 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2941] It is appreciated that GAM187 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM187 target genes. The mRNA of each one of this plurality of GAM187 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM187 RNA, herein designated GAM RNA, and which when bound by GAM187 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM187 target proteins.

[2942] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM187 gene, herein designated GAM GENE, on one or more GAM187 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2943] It is yet further appreciated that specific functions, and accordingly utilities, of GAM187 correlate with, and may be deduced from, the identity of the target genes which GAM187 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2944] Nucleotide sequences of the GAM187 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM187 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM187 are further described hereinbelow with reference to Table Table1.

[2945] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM187 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2946] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 188 (GAM188) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2947] GAM188 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM188 was detected is described hereinabove with reference to Figs. 2-8.

[2948] GAM188 gene, herein designated GAM GENE, and GAM188 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[2949] GAM188 gene, herein designated GAM GENE, encodes a GAM188 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM188 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM188 precursor RNA is designated SEQ ID:161, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:161 is located at position 13476908 relative to contig NT_017568.11, on chromosome 9.

[2950] GAM188 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2951] An enzyme complex designated DICER COMPLEX, dices

the GAM188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM188 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM188 RNA is designated SEQ ID:1837, and is provided hereinbelow with reference to the sequence listing part.

[2952] GAM188 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM188 target RNA, herein designated GAM TARGET RNA. GAM188 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2953] GAM188 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM188 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM188

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM188 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM188 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2954] The complementary binding of GAM188 RNA, herein designated GAM RNA, to target binding sites on GAM188 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM188 target RNA, herein designated GAM TARGET RNA, into GAM188 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2955] It is appreciated that GAM188 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM188 target genes. The mRNA of each one of this plurality of GAM188 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM188 RNA, herein designated GAM RNA, and which when bound by GAM188 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM188 target proteins.

[2956] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM188 gene, herein designated GAM GENE, on one or more GAM188 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2957] It is yet further appreciated that specific functions, and accordingly utilities, of GAM188 correlate with, and may be deduced from, the identity of the target genes which GAM188 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2958] Nucleotide sequences of the GAM188 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM188 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM188 are further described hereinbelow with reference to Table Table1.

[2959] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM188 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2960] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 189 (GAM189) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2961] GAM189 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM189 was detected is described hereinabove with reference to Figs. 2-8.

[2962] GAM189 gene, herein designated GAM GENE, and GAM189 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2963] GAM189 gene, herein designated GAM GENE, encodes a GAM189 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM189 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM189 precursor RNA is designated SEQ ID:162, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:162 is located at position 5750768 relative to contig NT_010966.11, on chromosome 18.

[2964] GAM189 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2965] An enzyme complex designated DICER COMPLEX, dices the GAM189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM189 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM189 RNA is designated SEQ ID:1838, and is provided hereinbelow with reference to the sequence listing part.

[2966] GAM189 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM189 target RNA, herein designated GAM TARGET RNA.

GAM189 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2967] GAM189 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM189 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM189 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM189 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM189 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2968] The complementary binding of GAM189 RNA, herein designated GAM RNA, to target binding sites on GAM189 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM189 target RNA, herein designated GAM TARGET RNA, into GAM189 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2969] It is appreciated that GAM189 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM189 target genes. The mRNA of each one of this plurality of GAM189 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM189 RNA, herein designated GAM RNA, and which when bound by GAM189 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM189 target proteins.

[2970] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM189 gene, herein designated GAM GENE, on one or more GAM189 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2971] It is yet further appreciated that specific functions, and accordingly utilities, of GAM189 correlate with, and may be deduced from, the identity of the target genes which GAM189 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2972] Nucleotide sequences of the GAM189 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM189 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM189 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM189 are further described hereinbelow with reference to Table Table1.

[2973] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM189 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2974] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 190 (GAM190) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[2975] GAM190 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM190 was detected is described hereinabove with reference to Figs. 2-8.

[2976] GAM190 gene, herein designated GAM GENE, and GAM190 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2977] GAM190 gene, herein designated GAM GENE, encodes a GAM190 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM190 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM190 precursor RNA is designated SEQ ID:163, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:163 is located at position 5037657 relative to contig NT_011109.13, on chromosome 19.

[2978] GAM190 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2979] An enzyme complex designated DICER COMPLEX, dices the GAM190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM190 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM190 RNA is designated SEQ ID:1839, and is provided hereinbelow with reference to the sequence listing part.

[2980] GAM190 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM190 target RNA, herein designated GAM TARGET RNA. GAM190 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2981] GAM190 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM190 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM190 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM190 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM190 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2982] The complementary binding of GAM190 RNA, herein designated GAM RNA, to target binding sites on GAM190 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM190 target RNA, herein designated GAM TARGET RNA, into GAM190 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2983] It is appreciated that GAM190 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM190 target genes. The mRNA of each one of this plu-

rality of GAM190 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM190 RNA, herein designated GAM RNA, and which when bound by GAM190 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM190 target proteins.

[2984] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM190 gene, herein designated GAM GENE, on one or more GAM190 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2985] It is yet further appreciated that specific functions, and accordingly utilities, of GAM190 correlate with, and may be deduced from, the identity of the target genes which GAM190 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[2986] Nucleotide sequences of the GAM190 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM190 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM190 are further described hereinbelow with reference to Table Table1.

[2987] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM190 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[2988] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 191 (GAM191) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[2989] GAM191 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM191 was detected is described hereinabove with reference to Figs. 2-8.

[2990] GAM191 gene, herein designated GAM GENE, and GAM191 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[2991] GAM191 gene, herein designated GAM GENE, encodes a GAM191 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM191 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM191 precursor RNA is designated SEQ ID:164, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:164 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[2992] GAM191 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[2993] An enzyme complex designated DICER COMPLEX, dices the GAM191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM191 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM191 RNA is designated SEQ ID:1840, and is provided hereinbelow with reference to the sequence listing part.

[2994] GAM191 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM191 target RNA, herein designated GAM TARGET RNA. GAM191 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[2995] GAM191 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM191 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM191 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM191 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM191 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[2996] The complementary binding of GAM191 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM191 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM191 target RNA, herein designated GAM TARGET RNA, into GAM191 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[2997] It is appreciated that GAM191 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM191 target genes. The mRNA of each one of this plurality of GAM191 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM191 RNA, herein designated GAM RNA, and which when bound by GAM191 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM191 target proteins.

[2998] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM191 gene, herein designated GAM GENE, on one or more GAM191 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[2999] It is yet further appreciated that specific functions, and accordingly utilities, of GAM191 correlate with, and may be deduced from, the identity of the target genes which GAM191 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3000] Nucleotide sequences of the GAM191 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM191 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM191 are further described hereinbelow with reference to Table Table1.

[3001] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM191 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3002] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 192 (GAM192) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3003] GAM192 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM192 was detected is described hereinabove with reference to Figs. 2-8.

[3004] GAM192 gene, herein designated GAM GENE, and GAM192 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3005] GAM192 gene, herein designated GAM GENE, encodes a GAM192 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM192 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM192 precursor RNA is designated SEQ ID:165, and is provided hereinbelow with reference to the sequence listing part.

[3006] GAM192 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3007] An enzyme complex designated DICER COMPLEX, dices the GAM192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM192 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM192 RNA is designated SEQ ID:1841, and is provided hereinbelow with reference to the sequence listing part.

[3008] GAM192 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM192 target RNA, herein designated GAM TARGET RNA. GAM192 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3009] GAM192 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM192 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM192 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM192 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM192 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3010] The complementary binding of GAM192 RNA, herein designated GAM RNA, to target binding sites on GAM192 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM192 target RNA, herein designated GAM TARGET RNA, into GAM192 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3011] It is appreciated that GAM192 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM192 target genes. The mRNA of each one of this plurality of GAM192 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM192 RNA, herein designated GAM RNA, and which when bound by GAM192 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM192 target proteins.

[3012] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM192 gene, herein designated GAM GENE, on one or more GAM192 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3013] It is yet further appreciated that specific functions, and accordingly utilities, of GAM192 correlate with, and may be deduced from, the identity of the target genes which GAM192 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3014] Nucleotide sequences of the GAM192 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM192 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM192 are further described hereinbelow with reference to Table Table1.

[3015] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM192 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3016] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 193 (GAM193) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3017] GAM193 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM193 was detected is described hereinabove with reference to Figs. 2-8.

[3018] GAM193 gene, herein designated GAM GENE, and GAM193 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3019] GAM193 gene, herein designated GAM GENE, encodes a GAM193 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM193 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM193 precursor RNA is designated SEQ ID:166, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:166 is located at position 10716414 relative to contig NT_033899.3, on chromosome 11.

[3020] GAM193 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[3021] An enzyme complex designated DICER COMPLEX, dices the GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM193 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM193 RNA is designated SEQ ID:1842, and is provided hereinbelow with reference to the sequence listing part.

[3022] GAM193 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM193 target RNA, herein designated GAM TARGET RNA. GAM193 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3023] GAM193 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM193 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM193 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM193 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM193 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3024] The complementary binding of GAM193 RNA, herein designated GAM RNA, to target binding sites on GAM193 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM193 target RNA, herein designated GAM TARGET RNA, into GAM193 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3025] It is appreciated that GAM193 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM193 target genes. The mRNA of each one of this plurality of GAM193 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM193 RNA, herein designated GAM RNA, and which when bound by GAM193 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM193 target proteins.

[3026] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM193 gene, herein designated GAM GENE, on one or more GAM193 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3027] It is yet further appreciated that specific functions, and accordingly utilities, of GAM193 correlate with, and may be deduced from, the identity of the target genes which GAM193 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3028] Nucleotide sequences of the GAM193 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM193 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM193 are further described hereinbelow with reference to Table Table1.

[3029] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM193 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3030] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 194 (GAM194) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3031] GAM194 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM194 was detected is described hereinabove with reference to Figs. 2-8.

[3032] GAM194 gene, herein designated GAM GENE, and GAM194 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3033] GAM194 gene, herein designated GAM GENE, encodes a GAM194 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM194 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM194 precursor RNA is designated SEQ ID:167, and is provided hereinbelow with reference to the sequence listing part.

[3034] GAM194 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3035] An enzyme complex designated DICER COMPLEX, dices the GAM194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM194 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM194 RNA is designated SEQ ID:1843, and is provided hereinbelow with reference to the sequence listing part.

[3036] GAM194 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM194 target RNA, herein designated GAM TARGET RNA.

GAM194 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3037] GAM194 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM194 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM194 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM194 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM194 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3038] The complementary binding of GAM194 RNA, herein designated GAM RNA, to target binding sites on GAM194 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM194 target RNA, herein designated GAM TARGET RNA, into GAM194 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3039] It is appreciated that GAM194 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM194 target genes. The mRNA of each one of this plurality of GAM194 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM194 RNA, herein designated GAM RNA, and which when bound by GAM194 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM194 target proteins.

[3040] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM194 gene, herein designated GAM GENE, on one or more GAM194 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3041] It is yet further appreciated that specific functions, and accordingly utilities, of GAM194 correlate with, and may be deduced from, the identity of the target genes which GAM194 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3042] Nucleotide sequences of the GAM194 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM194 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM194 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM194 are further described hereinbelow with reference to Table Table1.

[3043] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM194 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3044] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 195 (GAM195) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3045] GAM195 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM195 was detected is described hereinabove with reference to Figs. 2-8.

[3046] GAM195 gene, herein designated GAM GENE, and GAM195 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3047] GAM195 gene, herein designated GAM GENE, encodes a GAM195 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM195 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM195 precursor RNA is designated SEQ ID:168, and is provided hereinbelow with reference to the sequence listing part.

[3048] GAM195 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3049] An enzyme complex designated DICER COMPLEX, dices the GAM195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM195 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM195 RNA is designated SEQ ID:1844, and is provided hereinbelow with reference to the sequence listing part.

[3050] GAM195 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM195 target RNA, herein designated GAM TARGET RNA. GAM195 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3051] GAM195 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM195 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM195 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM195 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM195 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3052] The complementary binding of GAM195 RNA, herein designated GAM RNA, to target binding sites on GAM195 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM195 target RNA, herein designated GAM TARGET RNA, into GAM195 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3053] It is appreciated that GAM195 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM195 target genes. The mRNA of each one of this plurality of GAM195 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM195 RNA, herein designated GAM RNA, and which when bound by GAM195 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM195 target proteins.

[3054] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM195 gene, herein designated GAM GENE, on one or more GAM195 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3055] It is yet further appreciated that specific functions, and accordingly utilities, of GAM195 correlate with, and may

be deduced from, the identity of the target genes which GAM195 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3056] Nucleotide sequences of the GAM195 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM195 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM195 are further described hereinbelow with reference to Table Table1.

[3057] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM195 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3058] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 196 (GAM196) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3059] GAM196 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM196 was detected is described hereinabove with reference to Figs. 2-8.

[3060] GAM196 gene, herein designated GAM GENE, and GAM196 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3061] GAM196 gene, herein designated GAM GENE, encodes a GAM196 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM196 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM196 precursor RNA is designated SEQ ID:169, and is provided hereinbelow with reference to the sequence listing part.

[3062] GAM196 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[3063] SEQ ID:99350 detected in mouse EST Accession BE554084.1.

[3064] SEQ ID:99351 detected in mouse EST Accession

BG922170.1.

[3065] SEQ ID:99354 detected in mouse EST Accession AA106737.1.

[3066] SEQ ID:99355 detected in mouse EST Accession AA500296.1.

[3067] GAM196 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3068] An enzyme complex designated DICER COMPLEX, dices the GAM196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM196 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM196 RNA is designated SEQ ID:1845, and is provided hereinbelow with reference to the sequence listing part.

[3069] GAM196 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM196 target RNA, herein designated GAM TARGET RNA. GAM196 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3070] GAM196 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM196 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM196 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM196 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM196 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3071] The complementary binding of GAM196 RNA, herein designated GAM RNA, to target binding sites on GAM196 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM196 target RNA, herein designated GAM TARGET RNA, into GAM196 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3072] It is appreciated that GAM196 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM196 target genes. The mRNA of each one of this plurality of GAM196 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM196 RNA, herein designated GAM RNA, and which when bound by

GAM196 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM196 target proteins.

[3073] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM196 gene, herein designated GAM GENE, on one or more GAM196 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3074] It is yet further appreciated that specific functions, and accordingly utilities, of GAM196 correlate with, and may be deduced from, the identity of the target genes which GAM196 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[3075] Nucleotide sequences of the GAM196 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM196 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM196 are further described hereinbelow with reference to Table Table1.

[3076] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM196 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3077] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 197 (GAM197) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3078] GAM197 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM197 was detected is described hereinabove

with reference to Figs. 2-8.

[3079] GAM197 gene, herein designated GAM GENE, and GAM197 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3080] GAM197 gene, herein designated GAM GENE, encodes a GAM197 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM197 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM197 precursor RNA is designated SEQ ID:170, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:170 is located at position 1235058 relative to contig NT_009526.11, on chromosome 12.

[3081] GAM197 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[3082] SEQ ID:98496 detected in mouse EST Accession BI965972.1.

[3083] SEQ ID:98497 detected in mouse EST Accession

AI326210.1.

[3084] SEQ ID:98498 detected in mouse EST Accession BI965652.1.

[3085] GAM197 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3086] An enzyme complex designated DICER COMPLEX, dices the GAM197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM197 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM197 RNA is designated SEQ ID:1846, and is provided hereinbelow with reference to the sequence listing part.

[3087] GAM197 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM197 target RNA, herein designated GAM TARGET RNA. GAM197 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3088] GAM197 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM197 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM197 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM197 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM197

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3089] The complementary binding of GAM197 RNA, herein designated GAM RNA, to target binding sites on GAM197 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM197 target RNA, herein designated GAM TARGET RNA, into GAM197 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3090] It is appreciated that GAM197 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM197 target genes. The mRNA of each one of this plurality of GAM197 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM197 RNA, herein designated GAM RNA, and which when bound by GAM197 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM197 target proteins.

[3091] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM197 gene, herein designated GAM GENE, on one or more GAM197 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3092] It is yet further appreciated that specific functions, and accordingly utilities, of GAM197 correlate with, and may be deduced from, the identity of the target genes which GAM197 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3093] Nucleotide sequences of the GAM197 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM197 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM197 are further described hereinbelow with reference to Table Table1.

[3094] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM197 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3095] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 198 (GAM198) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3096] GAM198 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM198 was detected is described hereinabove with reference to Figs. 2-8.

[3097] GAM198 gene, herein designated GAM GENE, and GAM198 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[3098] GAM198 gene, herein designated GAM GENE, encodes a GAM198 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM198 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM198 precursor RNA is designated SEQ ID:171, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:171 is located at position 2820500 relative to contig NT_011812.10, on chromosome X.

[3099] GAM198 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3100] An enzyme complex designated DICER COMPLEX, dices

the GAM198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM198 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM198 RNA is designated SEQ ID:1847, and is provided hereinbelow with reference to the sequence listing part.

[3101] GAM198 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM198 target RNA, herein designated GAM TARGET RNA. GAM198 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3102] GAM198 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM198 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM198

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM198 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM198 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3103] The complementary binding of GAM198 RNA, herein designated GAM RNA, to target binding sites on GAM198 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM198 target RNA, herein designated GAM TARGET RNA, into GAM198 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3104] It is appreciated that GAM198 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM198 target genes. The mRNA of each one of this plurality of GAM198 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM198 RNA, herein designated GAM RNA, and which when bound by GAM198 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM198 target proteins.

[3105] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM198 gene, herein designated GAM GENE, on one or more GAM198 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3106] It is yet further appreciated that specific functions, and accordingly utilities, of GAM198 correlate with, and may be deduced from, the identity of the target genes which GAM198 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3107] Nucleotide sequences of the GAM198 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM198 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM198 are further described hereinbelow with reference to Table Table1.

[3108] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM198 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3109] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 199 (GAM199) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3110] GAM199 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM199 was detected is described hereinabove with reference to Figs. 2-8.

[3111] GAM199 gene, herein designated GAM GENE, and GAM199 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3112] GAM199 gene, herein designated GAM GENE, encodes a GAM199 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM199 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM199 precursor RNA is designated SEQ ID:172, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:172 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[3113] GAM199 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3114] An enzyme complex designated DICER COMPLEX, dices the GAM199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM199 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM199 RNA is designated SEQ ID:1848, and is provided hereinbelow with reference to the sequence listing part.

[3115] GAM199 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM199 target RNA, herein designated GAM TARGET RNA.

GAM199 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3116] GAM199 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM199 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM199 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM199 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM199 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3117] The complementary binding of GAM199 RNA, herein designated GAM RNA, to target binding sites on GAM199 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM199 target RNA, herein designated GAM TARGET RNA, into GAM199 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3118] It is appreciated that GAM199 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM199 target genes. The mRNA of each one of this plurality of GAM199 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM199 RNA, herein designated GAM RNA, and which when bound by GAM199 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM199 target proteins.

[3119] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM199 gene, herein designated GAM GENE, on one or more GAM199 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3120] It is yet further appreciated that specific functions, and accordingly utilities, of GAM199 correlate with, and may be deduced from, the identity of the target genes which GAM199 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3121] Nucleotide sequences of the GAM199 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM199 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM199 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM199 are further described hereinbelow with reference to Table Table1.

[3122] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM199 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3123] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 200 (GAM200) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3124] GAM200 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM200 was detected is described hereinabove with reference to Figs. 2-8.

[3125] GAM200 gene, herein designated GAM GENE, and GAM200 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3126] GAM200 gene, herein designated GAM GENE, encodes a GAM200 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM200 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM200 precursor RNA is designated SEQ ID:173, and is provided hereinbelow with reference to the sequence listing part.

[3127] GAM200 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3128] An enzyme complex designated DICER COMPLEX, dices the GAM200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM200 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM200 RNA is designated SEQ ID:1849, and is provided hereinbelow with reference to the sequence listing part.

[3129] GAM200 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM200 target RNA, herein designated GAM TARGET RNA. GAM200 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3130] GAM200 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM200 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM200 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM200 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM200 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3131] The complementary binding of GAM200 RNA, herein designated GAM RNA, to target binding sites on GAM200 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM200 target RNA, herein designated GAM TARGET RNA, into GAM200 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3132] It is appreciated that GAM200 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM200 target genes. The mRNA of each one of this plurality of GAM200 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM200 RNA, herein designated GAM RNA, and which when bound by GAM200 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM200 target proteins.

[3133] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM200 gene, herein designated GAM GENE, on one or more GAM200 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3134] It is yet further appreciated that specific functions, and accordingly utilities, of GAM200 correlate with, and may

be deduced from, the identity of the target genes which GAM200 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3135] Nucleotide sequences of the GAM200 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM200 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM200 are further described hereinbelow with reference to Table Table1.

[3136] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM200 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3137] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 201 (GAM201) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3138] GAM201 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM201 was detected is described hereinabove with reference to Figs. 2-8.

[3139] GAM201 gene, herein designated GAM GENE, and GAM201 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3140] GAM201 gene, herein designated GAM GENE, encodes a GAM201 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM201 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM201 precursor RNA is designated SEQ ID:174, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:174 is located at position 29248816 relative to contig NT_007819.11, on chromosome 7.

[3141] GAM201 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3142] An enzyme complex designated DICER COMPLEX, dices the GAM201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM201 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM201 RNA is designated SEQ ID:1850, and is provided hereinbelow with reference to the sequence listing part.

[3143] GAM201 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM201 target RNA, herein designated GAM TARGET RNA. GAM201 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3144] GAM201 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM201 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM201 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM201 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM201 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3145] The complementary binding of GAM201 RNA, herein designated GAM RNA, to target binding sites on GAM201 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM201 target RNA, herein designated GAM TARGET RNA, into GAM201 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3146] It is appreciated that GAM201 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM201 target genes. The mRNA of each one of this plurality of GAM201 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM201 RNA, herein designated GAM RNA, and which when bound by GAM201 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM201 target proteins.

[3147] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM201 gene, herein designated GAM GENE, on one or more GAM201 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3148] It is yet further appreciated that specific functions, and accordingly utilities, of GAM201 correlate with, and may be deduced from, the identity of the target genes which GAM201 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3149] Nucleotide sequences of the GAM201 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM201 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM201 are further described hereinbelow with reference to Table Table1.

[3150] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM201 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3151] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 202 (GAM202) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3152] GAM202 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM202 was detected is described hereinabove with reference to Figs. 2-8.

[3153] GAM202 gene, herein designated GAM GENE, and GAM202 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3154] GAM202 gene, herein designated GAM GENE, encodes a GAM202 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM202 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM202 precursor RNA is desig-

nated SEQ ID:175, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:175 is located at position 2349685 relative to contig NT_021907.13, on chromosome 1.

[3155] GAM202 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3156] An enzyme complex designated DICER COMPLEX, dices the GAM202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM202 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM202 RNA is designated SEQ ID:1851, and is provided hereinbelow with reference to the sequence listing part.

[3157] GAM202 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM202 target RNA, herein designated GAM TARGET RNA. GAM202 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3158] GAM202 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM202 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM202 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM202 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM202 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3159] The complementary binding of GAM202 RNA, herein designated GAM RNA, to target binding sites on GAM202 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM202 target RNA, herein designated GAM TARGET RNA, into GAM202 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3160] It is appreciated that GAM202 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM202 target genes. The mRNA of each one of this plurality of GAM202 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM202 RNA, herein designated GAM RNA, and which when bound by GAM202 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM202 target proteins.

[3161] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM202 gene, herein designated GAM GENE, on one or more GAM202 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3162] It is yet further appreciated that specific functions, and accordingly utilities, of GAM202 correlate with, and may be deduced from, the identity of the target genes which GAM202 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3163] Nucleotide sequences of the GAM202 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM202 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM202 are further described hereinbelow with reference to Table Table1.

[3164] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM202 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3165] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 203 (GAM203) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3166] GAM203 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM203 was detected is described hereinabove with reference to Figs. 2-8.

[3167] GAM203 gene, herein designated GAM GENE, and GAM203 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3168] GAM203 gene, herein designated GAM GENE, encodes a GAM203 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM203 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM203 precursor RNA is designated SEQ ID:176, and is provided hereinbelow with reference to the sequence listing part.

[3169] GAM203 has 9 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[3170] SEQ ID:98499 detected in mouse EST Accession AA120179.1.

[3171] SEQ ID:98500 detected in mouse EST Accession AA067809.1.

[3172] SEQ ID:98501 detected in mouse EST Accession BE309522.1.

[3173] SEQ ID:98502 detected in mouse EST Accession AI226829.1.

[3174] SEQ ID:98503 detected in mouse EST Accession AI325803.1.

[3175] SEQ ID:98504 detected in mouse EST Accession BE915479.1.

[3176] SEQ ID:98505 detected in mouse EST Accession AI892495.1.

[3177] SEQ ID:98506 detected in mouse EST Accession AI314077.1.

[3178] SEQ ID:98507 detected in mouse EST Accession BI102267.1.

[3179] GAM203 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3180] An enzyme complex designated DICER COMPLEX, dices

the GAM203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM203 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM203 RNA is designated SEQ ID:1852, and is provided hereinbelow with reference to the sequence listing part.

[3181] GAM203 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM203 target RNA, herein designated GAM TARGET RNA. GAM203 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3182] GAM203 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM203 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM203

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM203 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM203 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3183] The complementary binding of GAM203 RNA, herein designated GAM RNA, to target binding sites on GAM203 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM203 target RNA, herein designated GAM TARGET RNA, into GAM203 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3184] It is appreciated that GAM203 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM203 target genes. The mRNA of each one of this plurality of GAM203 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM203 RNA, herein designated GAM RNA, and which when bound by GAM203 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM203 target proteins.

[3185] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM203 gene, herein designated GAM GENE, on one or more GAM203 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3186] It is yet further appreciated that specific functions, and accordingly utilities, of GAM203 correlate with, and may be deduced from, the identity of the target genes which GAM203 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3187] Nucleotide sequences of the GAM203 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM203 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM203 are further described hereinbelow with reference to Table Table1.

[3188] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM203 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3189] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 204 (GAM204) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3190] GAM204 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM204 was detected is described hereinabove with reference to Figs. 2-8.

[3191] GAM204 gene, herein designated GAM GENE, and GAM204 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3192] GAM204 gene, herein designated GAM GENE, encodes a GAM204 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM204 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM204 precursor RNA is designated SEQ ID:177, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:177 is located at position 23535227 relative to contig NT_033899.3, on chromosome 11.

[3193] GAM204 has 2 highly conserved, expressed mouse ho-

mologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[3194] SEQ ID:100069 detected in mouse EST Accession BE368829.1.

[3195] SEQ ID:100070 detected in mouse EST Accession BI714485.1.

[3196] GAM204 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3197] An enzyme complex designated DICER COMPLEX, dices the GAM204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM204 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM204 RNA is designated SEQ ID:1853, and is provided hereinbelow with reference to the sequence listing part.

[3198] GAM204 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM204 target RNA, herein designated GAM TARGET RNA. GAM204 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3199] GAM204 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM204 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM204 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM204 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM204 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3200] The complementary binding of GAM204 RNA, herein designated GAM RNA, to target binding sites on GAM204 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM204 target RNA, herein designated GAM TARGET RNA, into GAM204 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3201] It is appreciated that GAM204 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM204 target genes. The mRNA of each one of this plurality of GAM204 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM204 RNA, herein designated GAM RNA, and which when bound by GAM204 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM204 target proteins.

[3202] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM204 gene, herein designated GAM GENE, on one or more GAM204 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3203] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM204 correlate with, and may be deduced from, the identity of the target genes which GAM204 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3204] Nucleotide sequences of the GAM204 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM204 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM204 are further described hereinbelow with reference to Table Table1.

[3205] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM204 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3206] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 205 (GAM205) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3207] GAM205 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM205 was detected is described hereinabove with reference to Figs. 2-8.

[3208] GAM205 gene, herein designated GAM GENE, and GAM205 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3209] GAM205 gene, herein designated GAM GENE, encodes a GAM205 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM205 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM205 precursor RNA is designated SEQ ID:178, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:178 is located at position 2840900 relative to contig NT_004734.13, on chromosome 1.

[3210] GAM205 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3211] An enzyme complex designated DICER COMPLEX, dices the GAM205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM205 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM205 RNA is designated SEQ ID:1854, and is provided hereinbelow with reference to the sequence listing part.

[3212] GAM205 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM205 target RNA, herein designated GAM TARGET RNA.
GAM205 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[3213] GAM205 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM205 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM205 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM205 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM205 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3214] The complementary binding of GAM205 RNA, herein designated GAM RNA, to target binding sites on GAM205 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM205 target RNA, herein designated GAM TARGET RNA, into GAM205 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3215] It is appreciated that GAM205 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM205 target genes. The mRNA of each one of this plurality of GAM205 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM205 RNA, herein designated GAM RNA, and which when bound by GAM205 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM205 target proteins.

[3216] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM205 gene, herein designated GAM GENE, on one or more GAM205 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3217] It is yet further appreciated that specific functions, and accordingly utilities, of GAM205 correlate with, and may be deduced from, the identity of the target genes which GAM205 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3218] Nucleotide sequences of the GAM205 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM205 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM205 are further described hereinbelow with reference to Table Table1.

[3219] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM205 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3220] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 206 (GAM206) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3221] GAM206 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM206 was detected is described hereinabove with reference to Figs. 2-8.

[3222] GAM206 gene, herein designated GAM GENE, and GAM206 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3223] GAM206 gene, herein designated GAM GENE, encodes a GAM206 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM206 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM206 precursor RNA is designated SEQ ID:179, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:179 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[3224] GAM206 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3225] An enzyme complex designated DICER COMPLEX, dices the GAM206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM206 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM206 RNA is designated SEQ ID:1855, and is provided hereinbelow with reference to the sequence listing part.

[3226] GAM206 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM206 target RNA, herein designated GAM TARGET RNA. GAM206 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3227] GAM206 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM206 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM206 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM206 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM206 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3228] The complementary binding of GAM206 RNA, herein designated GAM RNA, to target binding sites on GAM206 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM206 target RNA, herein designated GAM TARGET RNA, into GAM206 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3229] It is appreciated that GAM206 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM206 target genes. The mRNA of each one of this plurality of GAM206 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM206 RNA, herein designated GAM RNA, and which when bound by

GAM206 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM206 target proteins.

[3230] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM206 gene, herein designated GAM GENE, on one or more GAM206 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3231] It is yet further appreciated that specific functions, and accordingly utilities, of GAM206 correlate with, and may be deduced from, the identity of the target genes which GAM206 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[3232] Nucleotide sequences of the GAM206 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM206 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM206 are further described hereinbelow with reference to Table Table1.

[3233] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM206 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3234] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 207 (GAM207) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3235] GAM207 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM207 was detected is described hereinabove

with reference to Figs. 2-8.

[3236] GAM207 gene, herein designated GAM GENE, and GAM207 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3237] GAM207 gene, herein designated GAM GENE, encodes a GAM207 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM207 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM207 precursor RNA is designated SEQ ID:180, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:180 is located at position 7678827 relative to contig NT_004852.13, on chromosome 1.

[3238] GAM207 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[3239] An enzyme complex designated DICER COMPLEX, dices the GAM207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM207 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM207 RNA is designated SEQ ID:1856, and is provided hereinbelow with reference to the sequence listing part.

[3240] GAM207 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM207 target RNA, herein designated GAM TARGET RNA.
GAM207 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3241] GAM207 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM207 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM207 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM207 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM207 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3242] The complementary binding of GAM207 RNA, herein designated GAM RNA, to target binding sites on GAM207 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM207 target RNA, herein desig-

nated GAM TARGET RNA, into GAM207 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3243] It is appreciated that GAM207 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM207 target genes. The mRNA of each one of this plurality of GAM207 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM207 RNA, herein designated GAM RNA, and which when bound by GAM207 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM207 target proteins.

[3244] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM207 gene, herein designated GAM GENE, on one or more GAM207 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3245] It is yet further appreciated that specific functions, and accordingly utilities, of GAM207 correlate with, and may be deduced from, the identity of the target genes which GAM207 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3246] Nucleotide sequences of the GAM207 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM207 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM207 are further described hereinbelow with reference to Table Table1.

[3247] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM207 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[3248] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 208 (GAM208) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3249] GAM208 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM208 was detected is described hereinabove with reference to Figs. 2-8.

[3250] GAM208 gene, herein designated GAM GENE, and GAM208 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3251] GAM208 gene, herein designated GAM GENE, encodes a GAM208 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM208 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM208 precursor RNA is designated SEQ ID:181, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:181 is located at position 1219777 relative to contig NT_007422.11, on chromosome 6.

[3252] GAM208 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3253] An enzyme complex designated DICER COMPLEX, dices the GAM208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM208 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM208 RNA is designated SEQ ID:1857, and is provided hereinbelow with reference to the sequence listing part.

[3254] GAM208 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM208 target RNA, herein designated GAM TARGET RNA. GAM208 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3255] GAM208 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM208 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM208 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM208 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM208

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3256] The complementary binding of GAM208 RNA, herein designated GAM RNA, to target binding sites on GAM208 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM208 target RNA, herein designated GAM TARGET RNA, into GAM208 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3257] It is appreciated that GAM208 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM208 target genes. The mRNA of each one of this plurality of GAM208 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM208 RNA, herein designated GAM RNA, and which when bound by GAM208 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM208 target proteins.

[3258] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM208 gene, herein designated GAM GENE, on one or more GAM208 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3259] It is yet further appreciated that specific functions, and accordingly utilities, of GAM208 correlate with, and may be deduced from, the identity of the target genes which GAM208 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3260] Nucleotide sequences of the GAM208 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM208 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM208 are further described hereinbelow with reference to Table Table1.

[3261] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM208 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3262] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 209 (GAM209) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3263] GAM209 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM209 was detected is described hereinabove with reference to Figs. 2-8.

[3264] GAM209 gene, herein designated GAM GENE, and GAM209 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[3265] GAM209 gene, herein designated GAM GENE, encodes a GAM209 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM209 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM209 precursor RNA is designated SEQ ID:182, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:182 is located at position 2071068 relative to contig NT_008183.13, on chromosome 8.

[3266] GAM209 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3267] An enzyme complex designated DICER COMPLEX, dices

the GAM209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM209 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM209 RNA is designated SEQ ID:1858, and is provided hereinbelow with reference to the sequence listing part.

[3268] GAM209 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM209 target RNA, herein designated GAM TARGET RNA. GAM209 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3269] GAM209 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM209 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM209

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM209 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM209 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3270] The complementary binding of GAM209 RNA, herein designated GAM RNA, to target binding sites on GAM209 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM209 target RNA, herein designated GAM TARGET RNA, into GAM209 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3271] It is appreciated that GAM209 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM209 target genes. The mRNA of each one of this plurality of GAM209 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM209 RNA, herein designated GAM RNA, and which when bound by GAM209 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM209 target proteins.

[3272] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM209 gene, herein designated GAM GENE, on one or more GAM209 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3273] It is yet further appreciated that specific functions, and accordingly utilities, of GAM209 correlate with, and may be deduced from, the identity of the target genes which GAM209 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3274] Nucleotide sequences of the GAM209 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM209 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM209 are further described hereinbelow with reference to Table Table1.

[3275] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM209 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3276] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 210 (GAM210) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3277] GAM210 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM210 was detected is described hereinabove with reference to Figs. 2-8.

[3278] GAM210 gene, herein designated GAM GENE, and GAM210 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3279] GAM210 gene, herein designated GAM GENE, encodes a GAM210 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM210 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM210 precursor RNA is designated SEQ ID:183, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:183 is located at position 678567 relative to contig NT_011362.7, on chromosome 20.

[3280] GAM210 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3281] An enzyme complex designated DICER COMPLEX, dices the GAM210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM210 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM210 RNA is designated SEQ ID:1859, and is provided hereinbelow with reference to the sequence listing part.

[3282] GAM210 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM210 target RNA, herein designated GAM TARGET RNA.

GAM210 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3283] GAM210 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM210 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM210 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM210 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM210 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3284] The complementary binding of GAM210 RNA, herein designated GAM RNA, to target binding sites on GAM210 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM210 target RNA, herein designated GAM TARGET RNA, into GAM210 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3285] It is appreciated that GAM210 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM210 target genes. The mRNA of each one of this plurality of GAM210 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM210 RNA, herein designated GAM RNA, and which when bound by GAM210 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM210 target proteins.

[3286] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM210 gene, herein designated GAM GENE, on one or more GAM210 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3287] It is yet further appreciated that specific functions, and accordingly utilities, of GAM210 correlate with, and may be deduced from, the identity of the target genes which GAM210 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3288] Nucleotide sequences of the GAM210 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM210 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM210 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM210 are further described hereinbelow with reference to Table Table1.

[3289] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM210 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3290] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 211 (GAM211) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3291] GAM211 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM211 was detected is described hereinabove with reference to Figs. 2-8.

[3292] GAM211 gene, herein designated GAM GENE, and GAM211 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3293] GAM211 gene, herein designated GAM GENE, encodes a GAM211 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM211 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM211 precursor RNA is designated SEQ ID:184, and is provided hereinbelow with reference to the sequence listing part.

[3294] GAM211 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3295] An enzyme complex designated DICER COMPLEX, dices the GAM211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM211 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM211 RNA is designated SEQ ID:1860, and is provided hereinbelow with reference to the sequence listing part.

[3296] GAM211 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM211 target RNA, herein designated GAM TARGET RNA. GAM211 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3297] GAM211 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM211 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM211 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM211 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM211 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3298] The complementary binding of GAM211 RNA, herein designated GAM RNA, to target binding sites on GAM211 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM211 target RNA, herein designated GAM TARGET RNA, into GAM211 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3299] It is appreciated that GAM211 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM211 target genes. The mRNA of each one of this plurality of GAM211 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM211 RNA, herein designated GAM RNA, and which when bound by GAM211 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM211 target proteins.

[3300] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM211 gene, herein designated GAM GENE, on one or more GAM211 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3301] It is yet further appreciated that specific functions, and accordingly utilities, of GAM211 correlate with, and may

be deduced from, the identity of the target genes which GAM211 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3302] Nucleotide sequences of the GAM211 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM211 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM211 are further described hereinbelow with reference to Table Table1.

[3303] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM211 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3304] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 212 (GAM212) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3305] GAM212 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM212 was detected is described hereinabove with reference to Figs. 2-8.

[3306] GAM212 gene, herein designated GAM GENE, and GAM212 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3307] GAM212 gene, herein designated GAM GENE, encodes a GAM212 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM212 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM212 precursor RNA is designated SEQ ID:185, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:185 is located at position 8019650 relative to contig NT_022171.11, on chromosome 2.

[3308] GAM212 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3309] An enzyme complex designated DICER COMPLEX, dices the GAM212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM212 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM212 RNA is designated SEQ ID:1861, and is provided hereinbelow with reference to the sequence listing part.

[3310] GAM212 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM212 target RNA, herein designated GAM TARGET RNA. GAM212 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3311] GAM212 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM212 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM212 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM212 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM212 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3312] The complementary binding of GAM212 RNA, herein designated GAM RNA, to target binding sites on GAM212 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM212 target RNA, herein designated GAM TARGET RNA, into GAM212 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3313] It is appreciated that GAM212 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM212 target genes. The mRNA of each one of this plurality of GAM212 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM212 RNA, herein designated GAM RNA, and which when bound by GAM212 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM212 target proteins.

[3314] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM212 gene, herein designated GAM GENE, on one or more GAM212 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3315] It is yet further appreciated that specific functions, and accordingly utilities, of GAM212 correlate with, and may be deduced from, the identity of the target genes which GAM212 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3316] Nucleotide sequences of the GAM212 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM212 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM212 are further described hereinbelow with reference to Table Table1.

[3317] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM212 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3318] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 213 (GAM213) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3319] GAM213 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM213 was detected is described hereinabove with reference to Figs. 2-8.

[3320] GAM213 gene, herein designated GAM GENE, and GAM213 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3321] GAM213 gene, herein designated GAM GENE, encodes a GAM213 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM213 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM213 precursor RNA is desig-

nated SEQ ID:186, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:186 is located at position 19527606 relative to contig NT_007933.10, on chromosome 7.

[3322] GAM213 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3323] An enzyme complex designated DICER COMPLEX, dices the GAM213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM213 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM213 RNA is designated SEQ ID:1862, and is provided hereinbelow with reference to the sequence listing part.

[3324] GAM213 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM213 target RNA, herein designated GAM TARGET RNA. GAM213 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3325] GAM213 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM213 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM213 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM213 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM213 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3326] The complementary binding of GAM213 RNA, herein designated GAM RNA, to target binding sites on GAM213 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM213 target RNA, herein designated GAM TARGET RNA, into GAM213 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3327] It is appreciated that GAM213 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM213 target genes. The mRNA of each one of this plurality of GAM213 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM213 RNA, herein designated GAM RNA, and which when bound by GAM213 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM213 target proteins.

[3328] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM213 gene, herein designated GAM GENE, on one or more GAM213 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3329] It is yet further appreciated that specific functions, and accordingly utilities, of GAM213 correlate with, and may be deduced from, the identity of the target genes which GAM213 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3330] Nucleotide sequences of the GAM213 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM213 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM213 are further described hereinbelow with reference to Table Table1.

[3331] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM213 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3332] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 214 (GAM214) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3333] GAM214 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM214 was detected is described hereinabove with reference to Figs. 2-8.

[3334] GAM214 gene, herein designated GAM GENE, and GAM214 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3335] GAM214 gene, herein designated GAM GENE, encodes a GAM214 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM214 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM214 precursor RNA is designated SEQ ID:187, and is provided hereinbelow with reference to the sequence listing part.

[3336] GAM214 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3337] An enzyme complex designated DICER COMPLEX, dices

the GAM214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM214 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM214 RNA is designated SEQ ID:1863, and is provided hereinbelow with reference to the sequence listing part.

[3338] GAM214 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM214 target RNA, herein designated GAM TARGET RNA. GAM214 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3339] GAM214 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM214 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM214

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM214 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM214 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3340] The complementary binding of GAM214 RNA, herein designated GAM RNA, to target binding sites on GAM214 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM214 target RNA, herein designated GAM TARGET RNA, into GAM214 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3341] It is appreciated that GAM214 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM214 target genes. The mRNA of each one of this plurality of GAM214 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM214 RNA, herein designated GAM RNA, and which when bound by GAM214 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM214 target proteins.

[3342] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM214 gene, herein designated GAM GENE, on one or more GAM214 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3343] It is yet further appreciated that specific functions, and accordingly utilities, of GAM214 correlate with, and may be deduced from, the identity of the target genes which GAM214 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3344] Nucleotide sequences of the GAM214 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM214 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM214 are further described hereinbelow with reference to Table Table1.

[3345] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM214 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3346] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 215 (GAM215) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3347] GAM215 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM215 was detected is described hereinabove with reference to Figs. 2-8.

[3348] GAM215 gene, herein designated GAM GENE, and GAM215 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3349] GAM215 gene, herein designated GAM GENE, encodes a GAM215 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM215 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM215 precursor RNA is designated SEQ ID:188, and is provided hereinbelow with reference to the sequence listing part.

[3350] GAM215 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3351] An enzyme complex designated DICER COMPLEX, dices the GAM215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM215 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM215 RNA is designated SEQ ID:1864, and is provided hereinbelow with reference to the sequence listing part.

[3352] GAM215 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM215 target RNA, herein designated GAM TARGET RNA. GAM215 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3353] GAM215 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM215 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM215 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM215 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM215 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3354] The complementary binding of GAM215 RNA, herein designated GAM RNA, to target binding sites on GAM215 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM215 target RNA, herein designated GAM TARGET RNA, into GAM215 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3355] It is appreciated that GAM215 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM215 target genes. The mRNA of each one of this plurality of GAM215 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM215 RNA, herein designated GAM RNA, and which when bound by GAM215 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM215 target proteins.

[3356] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM215 gene, herein designated GAM GENE, on one or more GAM215 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3357] It is yet further appreciated that specific functions, and accordingly utilities, of GAM215 correlate with, and may be deduced from, the identity of the target genes which GAM215 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3358] Nucleotide sequences of the GAM215 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM215 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM215 are further described hereinbelow with reference to Table Table1.

[3359] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM215 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3360] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 216 (GAM216) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3361] GAM216 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM216 was detected is described hereinabove with reference to Figs. 2-8.

[3362] GAM216 gene, herein designated GAM GENE, and GAM216 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3363] GAM216 gene, herein designated GAM GENE, encodes a GAM216 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM216 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM216 precursor RNA is designated SEQ ID:189, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:189 is located at position 11191842 relative to contig NT_005403.11, on chromosome 2.

[3364] GAM216 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3365] An enzyme complex designated DICER COMPLEX, dices the GAM216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM216 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM216 RNA is designated SEQ ID:1865, and is provided hereinbelow with reference to the sequence listing part.

[3366] GAM216 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM216 target RNA, herein designated GAM TARGET RNA. GAM216 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3367] GAM216 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM216 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM216 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM216 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM216 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3368] The complementary binding of GAM216 RNA, herein designated GAM RNA, to target binding sites on GAM216 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM216 target RNA, herein designated GAM TARGET RNA, into GAM216 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3369] It is appreciated that GAM216 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM216 target genes. The mRNA of each one of this plurality of GAM216 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM216 RNA, herein designated GAM RNA, and which when bound by GAM216 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM216 target proteins.

[3370] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM216 gene, herein designated GAM GENE, on one or more GAM216 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3371] It is yet further appreciated that specific functions, and accordingly utilities, of GAM216 correlate with, and may

be deduced from, the identity of the target genes which GAM216 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3372] Nucleotide sequences of the GAM216 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM216 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM216 are further described hereinbelow with reference to Table Table1.

[3373] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM216 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3374] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 217 (GAM217) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3375] GAM217 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM217 was detected is described hereinabove with reference to Figs. 2-8.

[3376] GAM217 gene, herein designated GAM GENE, and GAM217 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3377] GAM217 gene, herein designated GAM GENE, encodes a GAM217 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM217 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM217 precursor RNA is designated SEQ ID:190, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:190 is located at position 3678798 relative to contig NT_011651.11, on chromosome X.

[3378] GAM217 has 22 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[3379] SEQ ID:98387 detected in mouse EST Accession

W15061.1.

[3380] SEQ ID:98388 detected in mouse EST Accession AA038233.1.

[3381] SEQ ID:98389 detected in mouse EST Accession BE332467.1.

[3382] SEQ ID:98390 detected in mouse EST Accession AW741588.1.

[3383] SEQ ID:98391 detected in mouse EST Accession AA475709.1.

[3384] SEQ ID:98392 detected in mouse EST Accession BF658964.1.

[3385] SEQ ID:98393 detected in mouse EST Accession BG144466.1.

[3386] SEQ ID:98394 detected in mouse EST Accession AW541983.1.

[3387] SEQ ID:98395 detected in mouse EST Accession AI197014.1.

[3388] SEQ ID:98396 detected in mouse EST Accession BE335021.1.

[3389] SEQ ID:98397 detected in mouse EST Accession AW519570.1.

[3390] SEQ ID:98398 detected in mouse EST Accession BE332629.1.

[3391] SEQ ID:98399 detected in mouse EST Accession BF682079.1.

[3392] SEQ ID:98400 detected in mouse EST Accession AW744769.1.

[3393] SEQ ID:98401 detected in mouse EST Accession BB728526.1.

[3394] SEQ ID:98402 detected in mouse EST Accession BE946172.1.

[3395] SEQ ID:98403 detected in mouse EST Accession AI152617.1.

[3396] SEQ ID:98404 detected in mouse EST Accession AI875523.1.

[3397] SEQ ID:98405 detected in mouse EST Accession BB667985.1.

[3398] SEQ ID:98406 detected in mouse EST Accession W15842.1.

[3399] SEQ ID:98408 detected in mouse EST Accession AI326808.1.

[3400] SEQ ID:98409 detected in mouse EST Accession BG143442.1.

[3401] GAM217 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3402] An enzyme complex designated DICER COMPLEX, dices the GAM217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM217 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM217 RNA is designated SEQ ID:1866, and is provided hereinbelow with reference to the sequence listing part.

[3403] GAM217 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM217 target RNA, herein designated GAM TARGET RNA. GAM217 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3404] GAM217 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM217 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM217 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM217 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM217 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3405] The complementary binding of GAM217 RNA, herein designated GAM RNA, to target binding sites on GAM217 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM217 target RNA, herein designated GAM TARGET RNA, into GAM217 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3406] It is appreciated that GAM217 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM217 target genes. The mRNA of each one of this plurality of GAM217 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM217 RNA, herein designated GAM RNA, and which when bound by GAM217 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM217 target proteins.

[3407] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM217 gene, herein designated GAM GENE, on one or more GAM217 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3408] It is yet further appreciated that specific functions, and accordingly utilities, of GAM217 correlate with, and may be deduced from, the identity of the target genes which GAM217 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3409] Nucleotide sequences of the GAM217 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM217 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM217 are further described hereinbelow with reference to Table Table1.

[3410] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM217 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3411] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 218 (GAM218) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3412] GAM218 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM218 was detected is described hereinabove with reference to Figs. 2-8.

[3413] GAM218 gene, herein designated GAM GENE, and GAM218 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3414] GAM218 gene, herein designated GAM GENE, encodes a GAM218 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM218 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM218 precursor RNA is designated SEQ ID:191, and is provided hereinbelow with reference to the sequence listing part.

[3415] GAM218 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3416] An enzyme complex designated DICER COMPLEX, dices the GAM218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM218 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM218 RNA is designated SEQ ID:1867, and is provided hereinbelow with reference to the sequence listing part.

[3417] GAM218 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM218 target RNA, herein designated GAM TARGET RNA. GAM218 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3418] GAM218 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM218 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM218 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM218 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM218 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3419] The complementary binding of GAM218 RNA, herein designated GAM RNA, to target binding sites on GAM218 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM218 target RNA, herein designated GAM TARGET RNA, into GAM218 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3420] It is appreciated that GAM218 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM218 target genes. The mRNA of each one of this plurality of GAM218 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM218 RNA, herein designated GAM RNA, and which when bound by

GAM218 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM218 target proteins.

[3421] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM218 gene, herein designated GAM GENE, on one or more GAM218 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3422] It is yet further appreciated that specific functions, and accordingly utilities, of GAM218 correlate with, and may be deduced from, the identity of the target genes which GAM218 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[3423] Nucleotide sequences of the GAM218 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM218 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM218 are further described hereinbelow with reference to Table Table1.

[3424] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM218 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3425] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 219 (GAM219) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3426] GAM219 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM219 was detected is described hereinabove

with reference to Figs. 2-8.

[3427] GAM219 gene, herein designated GAM GENE, and GAM219 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3428] GAM219 gene, herein designated GAM GENE, encodes a GAM219 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM219 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM219 precursor RNA is designated SEQ ID:192, and is provided hereinbelow with reference to the sequence listing part.

[3429] GAM219 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3430] An enzyme complex designated DICER COMPLEX, dices the GAM219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM219 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM219 RNA is designated SEQ ID:1868, and is provided hereinbelow with reference to the sequence listing part.

[3431] GAM219 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM219 target RNA, herein designated GAM TARGET RNA. GAM219 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3432] GAM219 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM219 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM219 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM219 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM219 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3433] The complementary binding of GAM219 RNA, herein designated GAM RNA, to target binding sites on GAM219 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM219 target RNA, herein designated GAM TARGET RNA, into GAM219 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[3434] It is appreciated that GAM219 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM219 target genes. The mRNA of each one of this plurality of GAM219 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM219 RNA, herein designated GAM RNA, and which when bound by GAM219 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM219 target proteins.

[3435] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM219 gene, herein designated GAM GENE, on one or more GAM219 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3436] It is yet further appreciated that specific functions, and accordingly utilities, of GAM219 correlate with, and may be deduced from, the identity of the target genes which GAM219 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3437] Nucleotide sequences of the GAM219 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM219 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM219 are further described hereinbelow with reference to Table Table1.

[3438] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM219 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3439] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 220 (GAM220) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3440] GAM220 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM220 was detected is described hereinabove with reference to Figs. 2-8.

[3441] GAM220 gene, herein designated GAM GENE, and GAM220 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3442] GAM220 gene, herein designated GAM GENE, encodes a GAM220 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM220 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM220 precursor RNA is designated SEQ ID:193, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:193 is located at position 11649962 relative to contig NT_004668.13, on chromosome 1.

[3443] GAM220 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3444] An enzyme complex designated DICER COMPLEX, dices the GAM220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM220 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM220 RNA is designated SEQ ID:1869, and is provided hereinbelow with reference to the sequence listing part.

[3445] GAM220 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM220

target RNA, herein designated GAM TARGET RNA.

GAM220 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3446] GAM220 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM220 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM220 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM220 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM220 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3447] The complementary binding of GAM220 RNA, herein designated GAM RNA, to target binding sites on GAM220 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM220 target RNA, herein designated GAM TARGET RNA, into GAM220 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3448] It is appreciated that GAM220 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM220 target genes. The mRNA of each one of this plurality of GAM220 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM220 RNA, herein designated GAM RNA, and which when bound by GAM220 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM220 target proteins.

[3449] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM220 gene, herein designated GAM GENE, on one or more GAM220 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3450] It is yet further appreciated that specific functions, and accordingly utilities, of GAM220 correlate with, and may be deduced from, the identity of the target genes which GAM220 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3451] Nucleotide sequences of the GAM220 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM220 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM220 are further described hereinbelow with reference to Table Table1.

[3452] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM220 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3453] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 221 (GAM221) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3454] GAM221 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM221 was detected is described hereinabove with reference to Figs. 2-8.

[3455] GAM221 gene, herein designated GAM GENE, and GAM221 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3456] GAM221 gene, herein designated GAM GENE, encodes a

GAM221 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM221 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM221 precursor RNA is designated SEQ ID:194, and is provided hereinbelow with reference to the sequence listing part.

[3457] GAM221 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3458] An enzyme complex designated DICER COMPLEX, dices the GAM221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM221 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM221 RNA is designated SEQ ID:1870, and is provided hereinbelow with reference to the sequence listing part.

[3459] GAM221 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM221 target RNA, herein designated GAM TARGET RNA. GAM221 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3460] GAM221 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM221 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM221 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM221 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM221 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3461] The complementary binding of GAM221 RNA, herein designated GAM RNA, to target binding sites on GAM221 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM221 target RNA, herein designated GAM TARGET RNA, into GAM221 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3462] It is appreciated that GAM221 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM221 target genes. The mRNA of each one of this plurality of GAM221 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM221 RNA, herein designated GAM RNA, and which when bound by GAM221 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM221 target proteins.

[3463] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM221 gene, herein designated GAM GENE, on one or more GAM221 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3464] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM221 correlate with, and may be deduced from, the identity of the target genes which GAM221 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3465] Nucleotide sequences of the GAM221 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM221 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM221 are further described hereinbelow with reference to Table Table1.

[3466] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM221 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3467] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 222 (GAM222) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3468] GAM222 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM222 was detected is described hereinabove with reference to Figs. 2-8.

[3469] GAM222 gene, herein designated GAM GENE, and GAM222 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3470] GAM222 gene, herein designated GAM GENE, encodes a GAM222 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM222 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM222 precursor RNA is designated SEQ ID:195, and is provided hereinbelow with reference to the sequence listing part.

[3471] GAM222 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3472] An enzyme complex designated DICER COMPLEX, dices the GAM222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM222 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM222 RNA is designated SEQ ID:1871, and is provided hereinbelow with reference to the sequence listing part.

[3473] GAM222 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM222 target RNA, herein designated GAM TARGET RNA. GAM222 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3474] GAM222 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM222 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM222 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM222 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM222 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3475] The complementary binding of GAM222 RNA, herein designated GAM RNA, to target binding sites on GAM222 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM222 target RNA, herein designated GAM TARGET RNA, into GAM222 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3476] It is appreciated that GAM222 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM222 target genes. The mRNA of each one of this plurality of GAM222 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM222 RNA, herein designated GAM RNA, and which when bound by GAM222 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM222 target proteins.

[3477] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM222 gene, herein designated GAM GENE, on one or more GAM222 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3478] It is yet further appreciated that specific functions, and accordingly utilities, of GAM222 correlate with, and may be deduced from, the identity of the target genes which GAM222 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3479] Nucleotide sequences of the GAM222 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM222 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM222 are further described hereinbelow with reference to Table Table1.

[3480] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM222 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3481] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 223 (GAM223) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3482] GAM223 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM223 was detected is described hereinabove with reference to Figs. 2-8.

[3483] GAM223 gene, herein designated GAM GENE, and GAM223 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3484] GAM223 gene, herein designated GAM GENE, encodes a GAM223 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM223 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM223 precursor RNA is designated SEQ ID:196, and is provided hereinbelow with refer-

ence to the sequence listing part.

[3485] GAM223 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3486] An enzyme complex designated DICER COMPLEX, dices the GAM223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM223 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM223 RNA is designated SEQ ID:1872, and is provided hereinbelow with reference to the sequence listing part.

[3487] GAM223 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM223 target RNA, herein designated GAM TARGET RNA.

GAM223 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3488] GAM223 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM223 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM223 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM223 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM223 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3489] The complementary binding of GAM223 RNA, herein designated GAM RNA, to target binding sites on GAM223 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM223 target RNA, herein designated GAM TARGET RNA, into GAM223 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3490] It is appreciated that GAM223 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM223 target genes. The mRNA of each one of this plurality of GAM223 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM223 RNA, herein designated GAM RNA, and which when bound by GAM223 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM223 target proteins.

[3491] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM223 gene, herein designated GAM GENE, on one or more GAM223 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3492] It is yet further appreciated that specific functions, and accordingly utilities, of GAM223 correlate with, and may be deduced from, the identity of the target genes which GAM223 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3493] Nucleotide sequences of the GAM223 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM223 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM223 are further described hereinbelow with reference to Table Table1.

[3494] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM223 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3495] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 224 (GAM224) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3496] GAM224 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM224 was detected is described hereinabove with reference to Figs. 2-8.

[3497] GAM224 gene, herein designated GAM GENE, and GAM224 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3498] GAM224 gene, herein designated GAM GENE, encodes a GAM224 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM224 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM224 precursor RNA is designated SEQ ID:197, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:197 is located at position 2349675 relative to contig NT_021907.13, on chromosome 1.

[3499] GAM224 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3500] An enzyme complex designated DICER COMPLEX, dices the GAM224 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM224 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM224 RNA is designated SEQ ID:1873, and is provided hereinbelow with reference to the sequence listing part.

[3501] GAM224 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM224 target RNA, herein designated GAM TARGET RNA. GAM224 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3502] GAM224 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM224 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM224 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM224 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM224 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3503] The complementary binding of GAM224 RNA, herein designated GAM RNA, to target binding sites on GAM224 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM224 target RNA, herein designated GAM TARGET RNA, into GAM224 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3504] It is appreciated that GAM224 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM224 target genes. The mRNA of each one of this plurality of GAM224 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM224 RNA, herein designated GAM RNA, and which when bound by GAM224 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM224 target proteins.

[3505] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM224 gene, herein designated GAM GENE, on one or more GAM224 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3506] It is yet further appreciated that specific functions, and accordingly utilities, of GAM224 correlate with, and may be deduced from, the identity of the target genes which GAM224 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3507] Nucleotide sequences of the GAM224 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM224 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM224 are further described hereinbelow with reference to Table Table1.

[3508] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM224 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3509] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

225 (GAM225) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3510] GAM225 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM225 was detected is described hereinabove with reference to Figs. 2-8.

[3511] GAM225 gene, herein designated GAM GENE, and GAM225 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3512] GAM225 gene, herein designated GAM GENE, encodes a GAM225 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM225 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM225 precursor RNA is designated SEQ ID:198, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:198 is located at position 24197241 relative to contig NT_007933.10, on chromosome 7.

[3513] GAM225 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide se-

quence of which is similar to the nucleotide sequence of SEQ ID:99446, which mouse homolog is detected in mouse EST accession AA260986.1.

[3514] GAM225 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3515] An enzyme complex designated DICER COMPLEX, dices the GAM225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM225 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM225 RNA is designated SEQ ID:1874, and is provided

hereinbelow with reference to the sequence listing part.

[3516] GAM225 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM225 target RNA, herein designated GAM TARGET RNA.
GAM225 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3517] GAM225 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM225 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM225 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM225 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM225 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3518] The complementary binding of GAM225 RNA, herein designated GAM RNA, to target binding sites on GAM225 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM225 target RNA, herein designated GAM TARGET RNA, into GAM225 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3519] It is appreciated that GAM225 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM225 target genes. The mRNA of each one of this plurality of GAM225 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM225 RNA, herein designated GAM RNA, and which when bound by GAM225 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM225 tar-

get proteins.

[3520] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM225 gene, herein designated GAM GENE, on one or more GAM225 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3521] It is yet further appreciated that specific functions, and accordingly utilities, of GAM225 correlate with, and may be deduced from, the identity of the target genes which GAM225 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3522] Nucleotide sequences of the GAM225 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM225 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM225 are further described hereinbelow with reference to Table Table1.

[3523] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM225 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3524] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 226 (GAM226) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3525] GAM226 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM226 was detected is described hereinabove with reference to Figs. 2-8.

[3526] GAM226 gene, herein designated GAM GENE, and

GAM226 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3527] GAM226 gene, herein designated GAM GENE, encodes a GAM226 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM226 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM226 precursor RNA is designated SEQ ID:199, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:199 is located at position 1089589 relative to contig NT_011295.8, on chromosome 19.

[3528] GAM226 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3529] An enzyme complex designated DICER COMPLEX, dices the GAM226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM226 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM226 RNA is designated SEQ ID:1875, and is provided hereinbelow with reference to the sequence listing part.

[3530] GAM226 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM226 target RNA, herein designated GAM TARGET RNA. GAM226 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3531] GAM226 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM226 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM226 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM226 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM226 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3532] The complementary binding of GAM226 RNA, herein designated GAM RNA, to target binding sites on GAM226 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM226 target RNA, herein designated GAM TARGET RNA, into GAM226 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[3533] It is appreciated that GAM226 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM226 target genes. The mRNA of each one of this plurality of GAM226 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM226 RNA, herein designated GAM RNA, and which when bound by GAM226 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM226 target proteins.

[3534] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM226 gene, herein designated GAM GENE, on one or more GAM226 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3535] It is yet further appreciated that specific functions, and accordingly utilities, of GAM226 correlate with, and may be deduced from, the identity of the target genes which GAM226 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3536] Nucleotide sequences of the GAM226 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM226 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM226 are further described hereinbelow with reference to Table Table1.

[3537] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM226 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3538] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 227 (GAM227) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3539] GAM227 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM227 was detected is described hereinabove with reference to Figs. 2-8.

[3540] GAM227 gene, herein designated GAM GENE, and GAM227 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3541] GAM227 gene, herein designated GAM GENE, encodes a GAM227 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM227 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM227 precursor RNA is designated SEQ ID:200, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:200 is located at position 10450332 relative to contig NT_007758.8, on chromosome 7.

[3542] GAM227 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3543] An enzyme complex designated DICER COMPLEX, dices the GAM227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM227 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM227 RNA is designated SEQ ID:1876, and is provided hereinbelow with reference to the sequence listing part.

[3544] GAM227 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM227

target RNA, herein designated GAM TARGET RNA.

GAM227 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3545] GAM227 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM227 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM227 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM227 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM227 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3546] The complementary binding of GAM227 RNA, herein designated GAM RNA, to target binding sites on GAM227 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM227 target RNA, herein designated GAM TARGET RNA, into GAM227 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3547] It is appreciated that GAM227 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM227 target genes. The mRNA of each one of this plurality of GAM227 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM227 RNA, herein designated GAM RNA, and which when bound by GAM227 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM227 target proteins.

[3548] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM227 gene, herein designated GAM GENE, on one or more GAM227 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3549] It is yet further appreciated that specific functions, and accordingly utilities, of GAM227 correlate with, and may be deduced from, the identity of the target genes which GAM227 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3550] Nucleotide sequences of the GAM227 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM227 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM227 are further described hereinbelow with reference to Table Table1.

[3551] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM227 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3552] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 228 (GAM228) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3553] GAM228 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM228 was detected is described hereinabove with reference to Figs. 2-8.

[3554] GAM228 gene, herein designated GAM GENE, and GAM228 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3555] GAM228 gene, herein designated GAM GENE, encodes a

GAM228 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM228 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM228 precursor RNA is designated SEQ ID:201, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:201 is located at position 26076943 relative to contig NT_005403.11, on chromosome 2.

[3556] GAM228 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3557] An enzyme complex designated DICER COMPLEX, dices the GAM228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM228 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM228 RNA is designated SEQ ID:1877, and is provided hereinbelow with reference to the sequence listing part.

[3558] GAM228 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM228 target RNA, herein designated GAM TARGET RNA. GAM228 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3559] GAM228 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM228 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM228 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM228 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM228 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3560] The complementary binding of GAM228 RNA, herein designated GAM RNA, to target binding sites on GAM228 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM228 target RNA, herein designated GAM TARGET RNA, into GAM228 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3561] It is appreciated that GAM228 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM228 target genes. The mRNA of each one of this plurality of GAM228 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM228 RNA, herein designated GAM RNA, and which when bound by GAM228 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM228 target proteins.

[3562] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM228 gene, herein designated GAM GENE, on one or more GAM228 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[3563] It is yet further appreciated that specific functions, and accordingly utilities, of GAM228 correlate with, and may be deduced from, the identity of the target genes which GAM228 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3564] Nucleotide sequences of the GAM228 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM228 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM228 are further described hereinbelow with reference to Table Table1.

[3565] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM228 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3566] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 229 (GAM229) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[3567] GAM229 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM229 was detected is described hereinabove with reference to Figs. 2-8.

[3568] GAM229 gene, herein designated GAM GENE, and GAM229 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3569] GAM229 gene, herein designated GAM GENE, encodes a GAM229 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM229 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM229 precursor RNA is designated SEQ ID:202, and is provided hereinbelow with reference to the sequence listing part.

[3570] GAM229 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3571] An enzyme complex designated DICER COMPLEX, dices the GAM229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM229 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM229 RNA is designated SEQ ID:1878, and is provided hereinbelow with reference to the sequence listing part.

[3572] GAM229 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM229 target RNA, herein designated GAM TARGET RNA.
GAM229 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[3573] GAM229 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM229 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM229 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM229 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM229 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3574] The complementary binding of GAM229 RNA, herein designated GAM RNA, to target binding sites on GAM229 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM229 target RNA, herein designated GAM TARGET RNA, into GAM229 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3575] It is appreciated that GAM229 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM229 target genes. The mRNA of each one of this plurality of GAM229 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM229 RNA, herein designated GAM RNA, and which when bound by GAM229 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM229 target proteins.

[3576] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM229 gene, herein designated GAM GENE, on one or more GAM229 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3577] It is yet further appreciated that specific functions, and accordingly utilities, of GAM229 correlate with, and may be deduced from, the identity of the target genes which GAM229 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3578] Nucleotide sequences of the GAM229 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM229 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM229 are further described hereinbelow with reference to Table Table1.

[3579] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM229 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3580] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 230 (GAM230) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3581] GAM230 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM230 was detected is described hereinabove with reference to Figs. 2-8.

[3582] GAM230 gene, herein designated GAM GENE, and GAM230 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3583] GAM230 gene, herein designated GAM GENE, encodes a GAM230 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM230 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM230 precursor RNA is designated SEQ ID:203, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:203 is located at position 2825713 relative to contig NT_008902.13, on chromosome 10.

[3584] GAM230 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3585] An enzyme complex designated DICER COMPLEX, dices the GAM230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM230 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM230 RNA is designated SEQ ID:1879, and is provided hereinbelow with reference to the sequence listing part.

[3586] GAM230 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM230 target RNA, herein designated GAM TARGET RNA. GAM230 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3587] GAM230 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM230 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM230 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM230 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM230 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3588] The complementary binding of GAM230 RNA, herein designated GAM RNA, to target binding sites on GAM230 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM230 target RNA, herein designated GAM TARGET RNA, into GAM230 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3589] It is appreciated that GAM230 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM230 target genes. The mRNA of each one of this plurality of GAM230 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM230 RNA, herein designated GAM RNA, and which when bound by

GAM230 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM230 target proteins.

[3590] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM230 gene, herein designated GAM GENE, on one or more GAM230 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3591] It is yet further appreciated that specific functions, and accordingly utilities, of GAM230 correlate with, and may be deduced from, the identity of the target genes which GAM230 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[3592] Nucleotide sequences of the GAM230 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM230 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM230 are further described hereinbelow with reference to Table Table1.

[3593] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM230 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3594] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 231 (GAM231) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3595] GAM231 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM231 was detected is described hereinabove

with reference to Figs. 2-8.

[3596] GAM231 gene, herein designated GAM GENE, and GAM231 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3597] GAM231 gene, herein designated GAM GENE, encodes a GAM231 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM231 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM231 precursor RNA is designated SEQ ID:204, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:204 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[3598] GAM231 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[3599] An enzyme complex designated DICER COMPLEX, dices the GAM231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM231 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM231 RNA is designated SEQ ID:1880, and is provided hereinbelow with reference to the sequence listing part.

[3600] GAM231 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM231 target RNA, herein designated GAM TARGET RNA.
GAM231 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3601] GAM231 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM231 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM231 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM231 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM231 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3602] The complementary binding of GAM231 RNA, herein designated GAM RNA, to target binding sites on GAM231 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM231 target RNA, herein desig-

nated GAM TARGET RNA, into GAM231 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3603] It is appreciated that GAM231 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM231 target genes. The mRNA of each one of this plurality of GAM231 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM231 RNA, herein designated GAM RNA, and which when bound by GAM231 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM231 target proteins.

[3604] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM231 gene, herein designated GAM GENE, on one or more GAM231 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3605] It is yet further appreciated that specific functions, and accordingly utilities, of GAM231 correlate with, and may be deduced from, the identity of the target genes which GAM231 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3606] Nucleotide sequences of the GAM231 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM231 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM231 are further described hereinbelow with reference to Table Table1.

[3607] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM231 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[3608] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 233 (GAM233) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3609] GAM233 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM233 was detected is described hereinabove with reference to Figs. 2-8.

[3610] GAM233 gene, herein designated GAM GENE, and GAM233 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3611] GAM233 gene, herein designated GAM GENE, encodes a GAM233 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM233 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM233 precursor RNA is designated SEQ ID:205, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:205 is located at position 17488489 relative to contig NT_011520.8, on chromosome 22.

[3612] GAM233 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3613] An enzyme complex designated DICER COMPLEX, dices the GAM233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM233 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM233 RNA is designated SEQ ID:1881, and is provided hereinbelow with reference to the sequence listing part.

[3614] GAM233 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM233 target RNA, herein designated GAM TARGET RNA. GAM233 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3615] GAM233 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM233 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM233 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM233 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM233

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3616] The complementary binding of GAM233 RNA, herein designated GAM RNA, to target binding sites on GAM233 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM233 target RNA, herein designated GAM TARGET RNA, into GAM233 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3617] It is appreciated that GAM233 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM233 target genes. The mRNA of each one of this plurality of GAM233 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM233 RNA, herein designated GAM RNA, and which when bound by GAM233 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM233 target proteins.

[3618] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM233 gene, herein designated GAM GENE, on one or more GAM233 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3619] It is yet further appreciated that specific functions, and accordingly utilities, of GAM233 correlate with, and may be deduced from, the identity of the target genes which GAM233 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3620] Nucleotide sequences of the GAM233 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM233 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM233 are further described hereinbelow with reference to Table Table1.

[3621] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM233 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3622] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 234 (GAM234) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3623] GAM234 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM234 was detected is described hereinabove with reference to Figs. 2-8.

[3624] GAM234 gene, herein designated GAM GENE, and GAM234 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[3625] GAM234 gene, herein designated GAM GENE, encodes a GAM234 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM234 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM234 precursor RNA is designated SEQ ID:206, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:206 is located at position 10716414 relative to contig NT_033899.3, on chromosome 11.

[3626] GAM234 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3627] An enzyme complex designated DICER COMPLEX, dices

the GAM234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM234 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM234 RNA is designated SEQ ID:1882, and is provided hereinbelow with reference to the sequence listing part.

[3628] GAM234 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM234 target RNA, herein designated GAM TARGET RNA. GAM234 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3629] GAM234 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM234 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM234

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM234 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM234 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3630] The complementary binding of GAM234 RNA, herein designated GAM RNA, to target binding sites on GAM234 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM234 target RNA, herein designated GAM TARGET RNA, into GAM234 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3631] It is appreciated that GAM234 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM234 target genes. The mRNA of each one of this plurality of GAM234 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM234 RNA, herein designated GAM RNA, and which when bound by GAM234 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM234 target proteins.

[3632] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM234 gene, herein designated GAM GENE, on one or more GAM234 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3633] It is yet further appreciated that specific functions, and accordingly utilities, of GAM234 correlate with, and may be deduced from, the identity of the target genes which GAM234 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3634] Nucleotide sequences of the GAM234 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM234 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM234 are further described hereinbelow with reference to Table Table1.

[3635] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM234 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3636] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 235 (GAM235) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3637] GAM235 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM235 was detected is described hereinabove with reference to Figs. 2-8.

[3638] GAM235 gene, herein designated GAM GENE, and GAM235 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3639] GAM235 gene, herein designated GAM GENE, encodes a GAM235 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM235 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM235 precursor RNA is designated SEQ ID:207, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:207 is located at position 8666480 relative to contig NT_026437.9, on chromosome 14.

[3640] GAM235 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3641] An enzyme complex designated DICER COMPLEX, dices the GAM235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM235 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM235 RNA is designated SEQ ID:1883, and is provided hereinbelow with reference to the sequence listing part.

[3642] GAM235 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM235 target RNA, herein designated GAM TARGET RNA.

GAM235 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3643] GAM235 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM235 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM235 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM235 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM235 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3644] The complementary binding of GAM235 RNA, herein designated GAM RNA, to target binding sites on GAM235 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM235 target RNA, herein designated GAM TARGET RNA, into GAM235 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3645] It is appreciated that GAM235 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM235 target genes. The mRNA of each one of this plurality of GAM235 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM235 RNA, herein designated GAM RNA, and which when bound by GAM235 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM235 target proteins.

[3646] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM235 gene, herein designated GAM GENE, on one or more GAM235 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3647] It is yet further appreciated that specific functions, and accordingly utilities, of GAM235 correlate with, and may be deduced from, the identity of the target genes which GAM235 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3648] Nucleotide sequences of the GAM235 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM235 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM235 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM235 are further described hereinbelow with reference to Table Table1.

[3649] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM235 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3650] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 236 (GAM236) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3651] GAM236 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM236 was detected is described hereinabove with reference to Figs. 2-8.

[3652] GAM236 gene, herein designated GAM GENE, and GAM236 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3653] GAM236 gene, herein designated GAM GENE, encodes a GAM236 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM236 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM236 precursor RNA is designated SEQ ID:208, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:208 is located at position 9320626 relative to contig NT_033944.3, on chromosome 6.

[3654] GAM236 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3655] An enzyme complex designated DICER COMPLEX, dices the GAM236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM236 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM236 RNA is designated SEQ ID:1884, and is provided hereinbelow with reference to the sequence listing part.

[3656] GAM236 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM236 target RNA, herein designated GAM TARGET RNA. GAM236 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3657] GAM236 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM236 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM236 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM236 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM236 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3658] The complementary binding of GAM236 RNA, herein designated GAM RNA, to target binding sites on GAM236 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM236 target RNA, herein designated GAM TARGET RNA, into GAM236 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3659] It is appreciated that GAM236 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM236 target genes. The mRNA of each one of this plu-

rality of GAM236 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM236 RNA, herein designated GAM RNA, and which when bound by GAM236 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM236 target proteins.

[3660] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM236 gene, herein designated GAM GENE, on one or more GAM236 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3661] It is yet further appreciated that specific functions, and accordingly utilities, of GAM236 correlate with, and may be deduced from, the identity of the target genes which GAM236 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3662] Nucleotide sequences of the GAM236 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM236 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM236 are further described hereinbelow with reference to Table Table1.

[3663] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM236 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3664] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 237 (GAM237) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[3665] GAM237 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM237 was detected is described hereinabove with reference to Figs. 2-8.

[3666] GAM237 gene, herein designated GAM GENE, and GAM237 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3667] GAM237 gene, herein designated GAM GENE, encodes a GAM237 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM237 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM237 precursor RNA is designated SEQ ID:209, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:209 is located at position 10450330 relative to contig NT_007758.8, on chromosome 7.

[3668] GAM237 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3669] An enzyme complex designated DICER COMPLEX, dices the GAM237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM237 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM237 RNA is designated SEQ ID:1885, and is provided hereinbelow with reference to the sequence listing part.

[3670] GAM237 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM237 target RNA, herein designated GAM TARGET RNA. GAM237 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3671] GAM237 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM237 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM237 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM237 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM237 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3672] The complementary binding of GAM237 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM237 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM237 target RNA, herein designated GAM TARGET RNA, into GAM237 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3673] It is appreciated that GAM237 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM237 target genes. The mRNA of each one of this plurality of GAM237 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM237 RNA, herein designated GAM RNA, and which when bound by GAM237 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM237 target proteins.

[3674] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM237 gene, herein designated GAM GENE, on one or more GAM237 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3675] It is yet further appreciated that specific functions, and accordingly utilities, of GAM237 correlate with, and may be deduced from, the identity of the target genes which GAM237 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3676] Nucleotide sequences of the GAM237 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM237 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM237 are further described hereinbelow with reference to Table Table1.

[3677] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM237 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3678] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 238 (GAM238) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3679] GAM238 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM238 was detected is described hereinabove with reference to Figs. 2-8.

[3680] GAM238 gene, herein designated GAM GENE, and GAM238 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3681] GAM238 gene, herein designated GAM GENE, encodes a GAM238 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM238 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM238 precursor RNA is designated SEQ ID:210, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:210 is located at position 134281 relative to contig NT_008127.12, on chromosome 8.

[3682] GAM238 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3683] An enzyme complex designated DICER COMPLEX, dices the GAM238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM238 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM238 RNA is designated SEQ ID:1886, and is provided hereinbelow with reference to the sequence listing part.

[3684] GAM238 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM238 target RNA, herein designated GAM TARGET RNA. GAM238 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3685] GAM238 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM238 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM238 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM238 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM238 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3686] The complementary binding of GAM238 RNA, herein designated GAM RNA, to target binding sites on GAM238 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM238 target RNA, herein designated GAM TARGET RNA, into GAM238 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3687] It is appreciated that GAM238 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM238 target genes. The mRNA of each one of this plurality of GAM238 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM238 RNA,

herein designated GAM RNA, and which when bound by GAM238 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM238 target proteins.

[3688] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM238 gene, herein designated GAM GENE, on one or more GAM238 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3689] It is yet further appreciated that specific functions, and accordingly utilities, of GAM238 correlate with, and may be deduced from, the identity of the target genes which

GAM238 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3690] Nucleotide sequences of the GAM238 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM238 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM238 are further described hereinbelow with reference to Table Table1.

[3691] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM238 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3692] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 239 (GAM239) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3693] GAM239 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM239 was detected is described hereinabove with reference to Figs. 2-8.

[3694] GAM239 gene, herein designated GAM GENE, and GAM239 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3695] GAM239 gene, herein designated GAM GENE, encodes a GAM239 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM239 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM239 precursor RNA is designated SEQ ID:211, and is provided hereinbelow with reference to the sequence listing part.

[3696] GAM239 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[3697] An enzyme complex designated DICER COMPLEX, dices the GAM239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM239 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM239 RNA is designated SEQ ID:1887, and is provided hereinbelow with reference to the sequence listing part.

[3698] GAM239 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM239 target RNA, herein designated GAM TARGET RNA. GAM239 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3699] GAM239 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM239 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM239 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM239 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM239 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3700] The complementary binding of GAM239 RNA, herein designated GAM RNA, to target binding sites on GAM239 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM239 target RNA, herein designated GAM TARGET RNA, into GAM239 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3701] It is appreciated that GAM239 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM239 target genes. The mRNA of each one of this plurality of GAM239 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM239 RNA, herein designated GAM RNA, and which when bound by GAM239 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM239 target proteins.

[3702] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM239 gene, herein designated GAM GENE, on one or more GAM239 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3703] It is yet further appreciated that specific functions, and accordingly utilities, of GAM239 correlate with, and may be deduced from, the identity of the target genes which GAM239 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3704] Nucleotide sequences of the GAM239 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM239 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM239 are further described hereinbelow with reference to Table Table1.

[3705] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM239 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3706] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 240 (GAM240) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3707] GAM240 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM240 was detected is described hereinabove with reference to Figs. 2-8.

[3708] GAM240 gene, herein designated GAM GENE, and GAM240 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3709] GAM240 gene, herein designated GAM GENE, encodes a GAM240 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM240 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM240 precursor RNA is designated SEQ ID:212, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:212 is located at position 387404 relative to contig

NT_022508.11, on chromosome 3.

[3710] GAM240 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3711] An enzyme complex designated DICER COMPLEX, dices the GAM240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM240 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM240 RNA is designated SEQ ID:1888, and is provided hereinbelow with reference to the sequence listing part.

[3712] GAM240 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM240 target RNA, herein designated GAM TARGET RNA.

GAM240 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3713] GAM240 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM240 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM240 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM240 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM240 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3714] The complementary binding of GAM240 RNA, herein designated GAM RNA, to target binding sites on GAM240 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM240 target RNA, herein designated GAM TARGET RNA, into GAM240 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3715] It is appreciated that GAM240 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM240 target genes. The mRNA of each one of this plurality of GAM240 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM240 RNA, herein designated GAM RNA, and which when bound by GAM240 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM240 target proteins.

[3716] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM240 gene, herein designated GAM GENE, on one or more GAM240 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3717] It is yet further appreciated that specific functions, and accordingly utilities, of GAM240 correlate with, and may be deduced from, the identity of the target genes which GAM240 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3718] Nucleotide sequences of the GAM240 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM240 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM240 are further described hereinbelow with reference to Table Table1.

[3719] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM240 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3720] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 241 (GAM241) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3721] GAM241 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM241 was detected is described hereinabove with reference to Figs. 2-8.

[3722] GAM241 gene, herein designated GAM GENE, and GAM241 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3723] GAM241 gene, herein designated GAM GENE, encodes a GAM241 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM241 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM241 precursor RNA is designated SEQ ID:213, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:213 is located at position 2349689 relative to contig NT_021907.13, on chromosome 1.

[3724] GAM241 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3725] An enzyme complex designated DICER COMPLEX, dices the GAM241 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM241 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM241 RNA is designated SEQ ID:1889, and is provided hereinbelow with reference to the sequence listing part.

[3726] GAM241 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM241 target RNA, herein designated GAM TARGET RNA. GAM241 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3727] GAM241 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM241 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM241 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM241 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM241 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3728] The complementary binding of GAM241 RNA, herein designated GAM RNA, to target binding sites on GAM241 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM241 target RNA, herein designated GAM TARGET RNA, into GAM241 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3729] It is appreciated that GAM241 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM241 target genes. The mRNA of each one of this plurality of GAM241 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM241 RNA, herein designated GAM RNA, and which when bound by GAM241 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM241 target proteins.

[3730] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM241 gene, herein designated GAM GENE, on one or more GAM241 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3731] It is yet further appreciated that specific functions, and accordingly utilities, of GAM241 correlate with, and may be deduced from, the identity of the target genes which GAM241 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3732] Nucleotide sequences of the GAM241 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM241 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM241 are further described hereinbelow with reference to Table Table1.

[3733] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM241 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3734] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

242 (GAM242) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3735] GAM242 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM242 was detected is described hereinabove with reference to Figs. 2-8.

[3736] GAM242 gene, herein designated GAM GENE, and GAM242 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3737] GAM242 gene, herein designated GAM GENE, encodes a GAM242 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM242 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM242 precursor RNA is designated SEQ ID:214, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:214 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[3738] GAM242 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM242 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3739] An enzyme complex designated DICER COMPLEX, dices the GAM242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM242 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM242 RNA is designated SEQ ID:1890, and is provided hereinbelow with reference to the sequence listing part.

[3740] GAM242 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM242 target RNA, herein designated GAM TARGET RNA. GAM242 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3741] GAM242 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM242 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM242 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM242 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM242 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[3742] The complementary binding of GAM242 RNA, herein designated GAM RNA, to target binding sites on GAM242 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM242 target RNA, herein designated GAM TARGET RNA, into GAM242 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3743] It is appreciated that GAM242 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM242 target genes. The mRNA of each one of this plurality of GAM242 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM242 RNA, herein designated GAM RNA, and which when bound by GAM242 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM242 target proteins.

[3744] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM242 gene, herein designated GAM GENE, on one or

more GAM242 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3745] It is yet further appreciated that specific functions, and accordingly utilities, of GAM242 correlate with, and may be deduced from, the identity of the target genes which GAM242 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3746] Nucleotide sequences of the GAM242 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM242 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM242 are further de-

scribed hereinbelow with reference to Table Table1.

[3747] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM242 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3748] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 243 (GAM243) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3749] GAM243 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM243 was detected is described hereinabove with reference to Figs. 2-8.

[3750] GAM243 gene, herein designated GAM GENE, and GAM243 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3751] GAM243 gene, herein designated GAM GENE, encodes a GAM243 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM243 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM243 precursor RNA is designated SEQ ID:215, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:215 is located at position 1069676 relative to contig NT_007741.10, on chromosome 7.

[3752] GAM243 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3753] An enzyme complex designated DICER COMPLEX, dices the GAM243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM243 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM243 RNA is designated SEQ ID:1891, and is provided hereinbelow with reference to the sequence listing part.

[3754] GAM243 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM243 target RNA, herein designated GAM TARGET RNA. GAM243 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3755] GAM243 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM243 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM243 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM243 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM243 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3756] The complementary binding of GAM243 RNA, herein designated GAM RNA, to target binding sites on GAM243 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM243 target RNA, herein designated GAM TARGET RNA, into GAM243 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3757] It is appreciated that GAM243 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM243 target genes. The mRNA of each one of this plurality of GAM243 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM243 RNA, herein designated GAM RNA, and which when bound by GAM243 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM243 target proteins.

[3758] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM243 gene, herein designated GAM GENE, on one or more GAM243 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3759] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM243 correlate with, and may be deduced from, the identity of the target genes which GAM243 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3760] Nucleotide sequences of the GAM243 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM243 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM243 are further described hereinbelow with reference to Table Table1.

[3761] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM243 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3762] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 244 (GAM244) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3763] GAM244 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM244 was detected is described hereinabove with reference to Figs. 2-8.

[3764] GAM244 gene, herein designated GAM GENE, and GAM244 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3765] GAM244 gene, herein designated GAM GENE, encodes a GAM244 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM244 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM244 precursor RNA is designated SEQ ID:216, and is provided hereinbelow with reference to the sequence listing part.

[3766] GAM244 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3767] An enzyme complex designated DICER COMPLEX, dices the GAM244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM244 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM244 RNA is designated SEQ ID:1892, and is provided hereinbelow with reference to the sequence listing part.

[3768] GAM244 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM244 target RNA, herein designated GAM TARGET RNA. GAM244 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3769] GAM244 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM244 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM244 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM244 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM244 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3770] The complementary binding of GAM244 RNA, herein designated GAM RNA, to target binding sites on GAM244 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM244 target RNA, herein designated GAM TARGET RNA, into GAM244 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3771] It is appreciated that GAM244 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM244 target genes. The mRNA of each one of this plurality of GAM244 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM244 RNA, herein designated GAM RNA, and which when bound by GAM244 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM244 target proteins.

[3772] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM244 gene, herein designated GAM GENE, on one or more GAM244 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3773] It is yet further appreciated that specific functions, and accordingly utilities, of GAM244 correlate with, and may be deduced from, the identity of the target genes which GAM244 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3774] Nucleotide sequences of the GAM244 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM244 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM244 are further described hereinbelow with reference to Table Table1.

[3775] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM244 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3776] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 245 (GAM245) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3777] GAM245 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM245 was detected is described hereinabove with reference to Figs. 2-8.

[3778] GAM245 gene, herein designated GAM GENE, and GAM245 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3779] GAM245 gene, herein designated GAM GENE, encodes a GAM245 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM245 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM245 precursor RNA is designated SEQ ID:217, and is provided hereinbelow with refer-

ence to the sequence listing part.

[3780] GAM245 has 17 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[3781] SEQ ID:99217 detected in mouse EST Accession AL364580.1.

[3782] SEQ ID:99218 detected in mouse EST Accession AA670995.1.

[3783] SEQ ID:99219 detected in mouse EST Accession BE310323.1.

[3784] SEQ ID:99220 detected in mouse EST Accession W81953.1.

[3785] SEQ ID:99221 detected in mouse EST Accession AA168282.1.

[3786] SEQ ID:99222 detected in mouse EST Accession AA968124.1.

[3787] SEQ ID:99223 detected in mouse EST Accession AI892667.1.

[3788] SEQ ID:99224 detected in mouse EST Accession BI646213.1.

[3789] SEQ ID:99225 detected in mouse EST Accession

BI650187.1.

[3790] SEQ ID:99226 detected in mouse EST Accession BI686558.1.

[3791] SEQ ID:99227 detected in mouse EST Accession BI414768.1.

[3792] SEQ ID:99228 detected in mouse EST Accession BI408030.1.

[3793] SEQ ID:99229 detected in mouse EST Accession BF785049.1.

[3794] SEQ ID:99230 detected in mouse EST Accession BE913515.1.

[3795] SEQ ID:99231 detected in mouse EST Accession BI697701.1.

[3796] SEQ ID:99232 detected in mouse EST Accession BG863165.1.

[3797] SEQ ID:99233 detected in mouse EST Accession BG975985.1.

[3798] GAM245 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3799] An enzyme complex designated DICER COMPLEX, dices the GAM245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM245 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM245 RNA is designated SEQ ID:1893, and is provided hereinbelow with reference to the sequence listing part.

[3800] GAM245 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM245 target RNA, herein designated GAM TARGET RNA. GAM245 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3801] GAM245 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM245 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM245 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM245 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM245 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3802] The complementary binding of GAM245 RNA, herein designated GAM RNA, to target binding sites on GAM245 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM245 target RNA, herein designated GAM TARGET RNA, into GAM245 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3803] It is appreciated that GAM245 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM245 target genes. The mRNA of each one of this plurality of GAM245 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM245 RNA, herein designated GAM RNA, and which when bound by GAM245 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM245 target proteins.

[3804] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM245 gene, herein designated GAM GENE, on one or more GAM245 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3805] It is yet further appreciated that specific functions, and accordingly utilities, of GAM245 correlate with, and may be deduced from, the identity of the target genes which GAM245 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3806] Nucleotide sequences of the GAM245 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM245 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM245 are further described hereinbelow with reference to Table Table1.

[3807] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM245 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3808] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 246 (GAM246) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3809] GAM246 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM246 was detected is described hereinabove with reference to Figs. 2-8.

[3810] GAM246 gene, herein designated GAM GENE, and GAM246 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3811] GAM246 gene, herein designated GAM GENE, encodes a GAM246 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM246 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM246 precursor RNA is desig-

nated SEQ ID:218, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:218 is located at position 881711 relative to contig NT_024812.8, on chromosome 16.

[3812] GAM246 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3813] An enzyme complex designated DICER COMPLEX, dices the GAM246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM246 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM246 RNA is designated SEQ ID:1894, and is provided hereinbelow with reference to the sequence listing part.

[3814] GAM246 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM246 target RNA, herein designated GAM TARGET RNA. GAM246 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3815] GAM246 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM246 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM246 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM246 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM246 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3816] The complementary binding of GAM246 RNA, herein designated GAM RNA, to target binding sites on GAM246 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM246 target RNA, herein designated GAM TARGET RNA, into GAM246 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3817] It is appreciated that GAM246 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM246 target genes. The mRNA of each one of this plurality of GAM246 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM246 RNA, herein designated GAM RNA, and which when bound by GAM246 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM246 target proteins.

[3818] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM246 gene, herein designated GAM GENE, on one or more GAM246 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3819] It is yet further appreciated that specific functions, and accordingly utilities, of GAM246 correlate with, and may be deduced from, the identity of the target genes which GAM246 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3820] Nucleotide sequences of the GAM246 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM246 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM246 are further described hereinbelow with reference to Table Table1.

[3821] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM246 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3822] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 247 (GAM247) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3823] GAM247 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM247 was detected is described hereinabove with reference to Figs. 2-8.

[3824] GAM247 gene, herein designated GAM GENE, and GAM247 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3825] GAM247 gene, herein designated GAM GENE, encodes a GAM247 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM247 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM247 precursor RNA is designated SEQ ID:219, and is provided hereinbelow with reference to the sequence listing part.

[3826] GAM247 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3827] An enzyme complex designated DICER COMPLEX, dices

the GAM247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM247 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM247 RNA is designated SEQ ID:1895, and is provided hereinbelow with reference to the sequence listing part.

[3828] GAM247 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM247 target RNA, herein designated GAM TARGET RNA. GAM247 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3829] GAM247 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM247 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM247

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM247 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM247 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3830] The complementary binding of GAM247 RNA, herein designated GAM RNA, to target binding sites on GAM247 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM247 target RNA, herein designated GAM TARGET RNA, into GAM247 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3831] It is appreciated that GAM247 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM247 target genes. The mRNA of each one of this plurality of GAM247 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM247 RNA, herein designated GAM RNA, and which when bound by GAM247 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM247 target proteins.

[3832] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM247 gene, herein designated GAM GENE, on one or more GAM247 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3833] It is yet further appreciated that specific functions, and accordingly utilities, of GAM247 correlate with, and may be deduced from, the identity of the target genes which GAM247 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3834] Nucleotide sequences of the GAM247 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM247 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM247 are further described hereinbelow with reference to Table Table1.

[3835] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM247 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3836] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 248 (GAM248) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3837] GAM248 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM248 was detected is described hereinabove with reference to Figs. 2-8.

[3838] GAM248 gene, herein designated GAM GENE, and GAM248 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3839] GAM248 gene, herein designated GAM GENE, encodes a GAM248 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM248 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM248 precursor RNA is designated SEQ ID:220, and is provided hereinbelow with reference to the sequence listing part.

[3840] GAM248 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3841] An enzyme complex designated DICER COMPLEX, dices the GAM248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM248 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM248 RNA is designated SEQ ID:1896, and is provided hereinbelow with reference to the sequence listing part.

[3842] GAM248 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM248 target RNA, herein designated GAM TARGET RNA. GAM248 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3843] GAM248 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM248 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM248 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM248 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM248 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3844] The complementary binding of GAM248 RNA, herein designated GAM RNA, to target binding sites on GAM248 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM248 target RNA, herein designated GAM TARGET RNA, into GAM248 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3845] It is appreciated that GAM248 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM248 target genes. The mRNA of each one of this plurality of GAM248 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM248 RNA, herein designated GAM RNA, and which when bound by GAM248 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM248 target proteins.

[3846] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM248 gene, herein designated GAM GENE, on one or more GAM248 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3847] It is yet further appreciated that specific functions, and accordingly utilities, of GAM248 correlate with, and may be deduced from, the identity of the target genes which GAM248 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3848] Nucleotide sequences of the GAM248 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM248 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM248 are further described hereinbelow with reference to Table Table1.

[3849] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM248 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3850] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 249 (GAM249) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3851] GAM249 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM249 was detected is described hereinabove with reference to Figs. 2-8.

[3852] GAM249 gene, herein designated GAM GENE, and GAM249 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3853] GAM249 gene, herein designated GAM GENE, encodes a GAM249 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM249 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM249 precursor RNA is designated SEQ ID:221, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:221 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[3854] GAM249 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3855] An enzyme complex designated DICER COMPLEX, dices the GAM249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM249 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM249 RNA is designated SEQ ID:1897, and is provided hereinbelow with reference to the sequence listing part.

[3856] GAM249 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM249 target RNA, herein designated GAM TARGET RNA. GAM249 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3857] GAM249 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM249 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM249 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM249 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM249 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3858] The complementary binding of GAM249 RNA, herein designated GAM RNA, to target binding sites on GAM249 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM249 target RNA, herein designated GAM TARGET RNA, into GAM249 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3859] It is appreciated that GAM249 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM249 target genes. The mRNA of each one of this plurality of GAM249 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM249 RNA, herein designated GAM RNA, and which when bound by GAM249 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM249 target proteins.

[3860] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM249 gene, herein designated GAM GENE, on one or more GAM249 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3861] It is yet further appreciated that specific functions, and accordingly utilities, of GAM249 correlate with, and may

be deduced from, the identity of the target genes which GAM249 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3862] Nucleotide sequences of the GAM249 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM249 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM249 are further described hereinbelow with reference to Table Table1.

[3863] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM249 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3864] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 250 (GAM250) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3865] GAM250 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM250 was detected is described hereinabove with reference to Figs. 2-8.

[3866] GAM250 gene, herein designated GAM GENE, and GAM250 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3867] GAM250 gene, herein designated GAM GENE, encodes a GAM250 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM250 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM250 precursor RNA is designated SEQ ID:222, and is provided hereinbelow with reference to the sequence listing part.

[3868] GAM250 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[3869] An enzyme complex designated DICER COMPLEX, dices the GAM250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM250 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM250 RNA is designated SEQ ID:1898, and is provided hereinbelow with reference to the sequence listing part.

[3870] GAM250 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM250 target RNA, herein designated GAM TARGET RNA.
GAM250 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3871] GAM250 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM250 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM250 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM250 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM250 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3872] The complementary binding of GAM250 RNA, herein designated GAM RNA, to target binding sites on GAM250 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM250 target RNA, herein desig-

nated GAM TARGET RNA, into GAM250 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3873] It is appreciated that GAM250 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM250 target genes. The mRNA of each one of this plurality of GAM250 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM250 RNA, herein designated GAM RNA, and which when bound by GAM250 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM250 target proteins.

[3874] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM250 gene, herein designated GAM GENE, on one or more GAM250 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3875] It is yet further appreciated that specific functions, and accordingly utilities, of GAM250 correlate with, and may be deduced from, the identity of the target genes which GAM250 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3876] Nucleotide sequences of the GAM250 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM250 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM250 are further described hereinbelow with reference to Table Table1.

[3877] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM250 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[3878] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 251 (GAM251) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3879] GAM251 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM251 was detected is described hereinabove with reference to Figs. 2-8.

[3880] GAM251 gene, herein designated GAM GENE, and GAM251 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3881] GAM251 gene, herein designated GAM GENE, encodes a GAM251 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM251 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM251 precursor RNA is designated SEQ ID:223, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:223 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[3882] GAM251 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[3883] SEQ ID:99749 detected in mouse EST Accession AA144533.1.

[3884] SEQ ID:99750 detected in mouse EST Accession AA671455.1.

[3885] SEQ ID:99751 detected in mouse EST Accession AW824753.1.

[3886] SEQ ID:99752 detected in mouse EST Accession BE943987.1.

[3887] SEQ ID:99753 detected in mouse EST Accession BE691447.1.

[3888] SEQ ID:99754 detected in mouse EST Accession BE691413.1.

[3889] SEQ ID:99755 detected in mouse EST Accession BG808025.1.

[3890] SEQ ID:99756 detected in mouse EST Accession BG808010.1.

[3891] SEQ ID:99757 detected in mouse EST Accession BG807850.1.

[3892] SEQ ID:99758 detected in mouse EST Accession BG805970.1.

[3893] SEQ ID:99759 detected in mouse EST Accession BG145596.1.

[3894] SEQ ID:99760 detected in mouse EST Accession BE692802.1.

[3895] SEQ ID:99761 detected in mouse EST Accession BB609859.1.

[3896] SEQ ID:99762 detected in mouse EST Accession AW208601.1.

[3897] SEQ ID:99768 detected in mouse EST Accession BB610842.1.

[3898] GAM251 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[3899] An enzyme complex designated DICER COMPLEX, dices the GAM251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM251 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM251 RNA is designated SEQ ID:1899, and is provided hereinbelow with reference to the sequence listing part.

[3900] GAM251 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM251 target RNA, herein designated GAM TARGET RNA. GAM251 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3901] GAM251 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM251 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM251 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM251 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM251 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3902] The complementary binding of GAM251 RNA, herein designated GAM RNA, to target binding sites on GAM251 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM251 target RNA, herein designated GAM TARGET RNA, into GAM251 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3903] It is appreciated that GAM251 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM251 target genes. The mRNA of each one of this plurality of GAM251 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM251 RNA, herein designated GAM RNA, and which when bound by GAM251 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM251 target proteins.

[3904] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM251 gene, herein designated GAM GENE, on one or more GAM251 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3905] It is yet further appreciated that specific functions, and accordingly utilities, of GAM251 correlate with, and may be deduced from, the identity of the target genes which GAM251 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3906] Nucleotide sequences of the GAM251 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM251 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM251 are further described hereinbelow with reference to Table Table1.

[3907] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM251 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3908] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 252 (GAM252) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3909] GAM252 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM252 was detected is described hereinabove with reference to Figs. 2-8.

[3910] GAM252 gene, herein designated GAM GENE, and GAM252 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3911] GAM252 gene, herein designated GAM GENE, encodes a GAM252 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM252 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM252 precursor RNA is designated SEQ ID:224, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:224 is located at position 5877318 relative to con-

tig NT_023935.13, on chromosome 9.

[3912] GAM252 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99176, which mouse homolog is detected in mouse EST accession AA881786.1.

[3913] GAM252 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3914] An enzyme complex designated DICER COMPLEX, dices the GAM252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM252 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 96%) nucleotide sequence of GAM252 RNA is designated SEQ ID:1900, and is provided hereinbelow with reference to the sequence listing part.

[3915] GAM252 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM252 target RNA, herein designated GAM TARGET RNA. GAM252 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3916] GAM252 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM252 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM252 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM252 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM252 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3917] The complementary binding of GAM252 RNA, herein designated GAM RNA, to target binding sites on GAM252 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM252 target RNA, herein designated GAM TARGET RNA, into GAM252 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3918] It is appreciated that GAM252 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM252 target genes. The mRNA of each one of this plurality of GAM252 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM252 RNA,

herein designated GAM RNA, and which when bound by GAM252 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM252 target proteins.

[3919] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM252 gene, herein designated GAM GENE, on one or more GAM252 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3920] It is yet further appreciated that specific functions, and accordingly utilities, of GAM252 correlate with, and may be deduced from, the identity of the target genes which

GAM252 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3921] Nucleotide sequences of the GAM252 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM252 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM252 are further described hereinbelow with reference to Table Table1.

[3922] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM252 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3923] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 253 (GAM253) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3924] GAM253 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM253 was detected is described hereinabove with reference to Figs. 2-8.

[3925] GAM253 gene, herein designated GAM GENE, and GAM253 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3926] GAM253 gene, herein designated GAM GENE, encodes a GAM253 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM253 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM253 precursor RNA is designated SEQ ID:225, and is provided hereinbelow with reference to the sequence listing part.

[3927] GAM253 has 5 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[3928] SEQ ID:98466 detected in mouse EST Accession AA611182.1.

[3929] SEQ ID:98467 detected in mouse EST Accession BF452989.1.

[3930] SEQ ID:98469 detected in mouse EST Accession BF141241.1.

[3931] SEQ ID:98478 detected in mouse EST Accession AI019032.1.

[3932] SEQ ID:98479 detected in mouse EST Accession BE850845.1.

[3933] GAM253 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3934] An enzyme complex designated DICER COMPLEX, dices the GAM253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM253 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM253 RNA is designated SEQ ID:1901, and is provided hereinbelow with reference to the sequence listing part.

[3935] GAM253 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM253 target RNA, herein designated GAM TARGET RNA. GAM253 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3936] GAM253 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM253 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM253 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM253 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM253 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3937] The complementary binding of GAM253 RNA, herein designated GAM RNA, to target binding sites on GAM253 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM253 target RNA, herein designated GAM TARGET RNA, into GAM253 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3938] It is appreciated that GAM253 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM253 target genes. The mRNA of each one of this plurality of GAM253 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM253 RNA,

herein designated GAM RNA, and which when bound by GAM253 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM253 target proteins.

[3939] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM253 gene, herein designated GAM GENE, on one or more GAM253 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3940] It is yet further appreciated that specific functions, and accordingly utilities, of GAM253 correlate with, and may be deduced from, the identity of the target genes which

GAM253 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3941] Nucleotide sequences of the GAM253 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM253 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM253 are further described hereinbelow with reference to Table Table1.

[3942] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM253 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3943] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 254 (GAM254) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3944] GAM254 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM254 was detected is described hereinabove with reference to Figs. 2-8.

[3945] GAM254 gene, herein designated GAM GENE, and GAM254 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3946] GAM254 gene, herein designated GAM GENE, encodes a GAM254 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM254 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM254 precursor RNA is designated SEQ ID:226, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:226 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[3947] GAM254 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3948] An enzyme complex designated DICER COMPLEX, dices the GAM254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM254 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM254 RNA is designated SEQ ID:1902, and is provided hereinbelow with reference to the sequence listing part.

[3949] GAM254 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM254 target RNA, herein designated GAM TARGET RNA. GAM254 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3950] GAM254 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM254 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM254 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM254 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM254 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3951] The complementary binding of GAM254 RNA, herein designated GAM RNA, to target binding sites on GAM254 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM254 target RNA, herein designated GAM TARGET RNA, into GAM254 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3952] It is appreciated that GAM254 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM254 target genes. The mRNA of each one of this plurality of GAM254 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM254 RNA, herein designated GAM RNA, and which when bound by GAM254 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM254 target proteins.

[3953] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM254 gene, herein designated GAM GENE, on one or more GAM254 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3954] It is yet further appreciated that specific functions, and accordingly utilities, of GAM254 correlate with, and may be deduced from, the identity of the target genes which GAM254 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3955] Nucleotide sequences of the GAM254 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM254 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM254 are further described hereinbelow with reference to Table Table1.

[3956] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM254 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3957] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 255 (GAM255) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3958] GAM255 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM255 was detected is described hereinabove with reference to Figs. 2-8.

[3959] GAM255 gene, herein designated GAM GENE, and GAM255 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3960] GAM255 gene, herein designated GAM GENE, encodes a GAM255 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM255 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM255 precursor RNA is designated SEQ ID:227, and is provided hereinbelow with refer-

ence to the sequence listing part.

[3961] GAM255 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3962] An enzyme complex designated DICER COMPLEX, dices the GAM255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM255 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM255 RNA is designated SEQ ID:1903, and is provided hereinbelow with reference to the sequence listing part.

[3963] GAM255 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM255 target RNA, herein designated GAM TARGET RNA.

GAM255 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3964] GAM255 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM255 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM255 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM255 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM255 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3965] The complementary binding of GAM255 RNA, herein designated GAM RNA, to target binding sites on GAM255 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM255 target RNA, herein designated GAM TARGET RNA, into GAM255 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3966] It is appreciated that GAM255 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM255 target genes. The mRNA of each one of this plurality of GAM255 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM255 RNA, herein designated GAM RNA, and which when bound by GAM255 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM255 target proteins.

[3967] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM255 gene, herein designated GAM GENE, on one or more GAM255 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3968] It is yet further appreciated that specific functions, and accordingly utilities, of GAM255 correlate with, and may be deduced from, the identity of the target genes which GAM255 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3969] Nucleotide sequences of the GAM255 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM255 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM255 are further described hereinbelow with reference to Table Table1.

[3970] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM255 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3971] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 256 (GAM256) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3972] GAM256 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM256 was detected is described hereinabove with reference to Figs. 2-8.

[3973] GAM256 gene, herein designated GAM GENE, and GAM256 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3974] GAM256 gene, herein designated GAM GENE, encodes a GAM256 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM256 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM256 precursor RNA is designated SEQ ID:228, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:228 is located at position 780404 relative to contig NT_031915.4, on chromosome 19.

[3975] GAM256 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3976] An enzyme complex designated DICER COMPLEX, dices the GAM256 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM256 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM256 RNA is designated SEQ ID:1904, and is provided hereinbelow with reference to the sequence listing part.

[3977] GAM256 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM256 target RNA, herein designated GAM TARGET RNA. GAM256 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3978] GAM256 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM256 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM256 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM256 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM256 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[3979] The complementary binding of GAM256 RNA, herein designated GAM RNA, to target binding sites on GAM256 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM256 target RNA, herein designated GAM TARGET RNA, into GAM256 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3980] It is appreciated that GAM256 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM256 target genes. The mRNA of each one of this plurality of GAM256 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM256 RNA, herein designated GAM RNA, and which when bound by GAM256 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM256 target proteins.

[3981] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM256 gene, herein designated GAM GENE, on one or more GAM256 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3982] It is yet further appreciated that specific functions, and accordingly utilities, of GAM256 correlate with, and may be deduced from, the identity of the target genes which GAM256 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3983] Nucleotide sequences of the GAM256 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM256 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM256 are further described hereinbelow with reference to Table Table1.

[3984] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM256 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3985] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

257 (GAM257) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[3986] GAM257 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM257 was detected is described hereinabove with reference to Figs. 2-8.

[3987] GAM257 gene, herein designated GAM GENE, and GAM257 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[3988] GAM257 gene, herein designated GAM GENE, encodes a GAM257 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM257 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM257 precursor RNA is designated SEQ ID:229, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:229 is located at position 1698742 relative to contig NT_028309.8, on chromosome 11.

[3989] GAM257 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM257 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[3990] An enzyme complex designated DICER COMPLEX, dices the GAM257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM257 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM257 RNA is designated SEQ ID:1905, and is provided hereinbelow with reference to the sequence listing part.

[3991] GAM257 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM257 target RNA, herein designated GAM TARGET RNA. GAM257 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[3992] GAM257 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM257 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM257 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM257 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM257 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[3993] The complementary binding of GAM257 RNA, herein designated GAM RNA, to target binding sites on GAM257 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM257 target RNA, herein designated GAM TARGET RNA, into GAM257 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[3994] It is appreciated that GAM257 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM257 target genes. The mRNA of each one of this plurality of GAM257 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM257 RNA, herein designated GAM RNA, and which when bound by GAM257 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM257 target proteins.

[3995] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM257 gene, herein designated GAM GENE, on one or

more GAM257 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[3996] It is yet further appreciated that specific functions, and accordingly utilities, of GAM257 correlate with, and may be deduced from, the identity of the target genes which GAM257 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[3997] Nucleotide sequences of the GAM257 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM257 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM257 are further de-

scribed hereinbelow with reference to Table Table1.

[3998] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM257 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[3999] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 258 (GAM258) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4000] GAM258 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM258 was detected is described hereinabove with reference to Figs. 2-8.

[4001] GAM258 gene, herein designated GAM GENE, and GAM258 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4002] GAM258 gene, herein designated GAM GENE, encodes a GAM258 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM258 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM258 precursor RNA is designated SEQ ID:230, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:230 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[4003] GAM258 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4004] An enzyme complex designated DICER COMPLEX, dices the GAM258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM258 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM258 RNA is designated SEQ ID:1906, and is provided hereinbelow with reference to the sequence listing part.

[4005] GAM258 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM258 target RNA, herein designated GAM TARGET RNA. GAM258 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4006] GAM258 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM258 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM258 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM258 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM258 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4007] The complementary binding of GAM258 RNA, herein designated GAM RNA, to target binding sites on GAM258 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM258 target RNA, herein designated GAM TARGET RNA, into GAM258 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4008] It is appreciated that GAM258 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM258 target genes. The mRNA of each one of this plurality of GAM258 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM258 RNA, herein designated GAM RNA, and which when bound by GAM258 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM258 target proteins.

[4009] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM258 gene, herein designated GAM GENE, on one or more GAM258 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4010] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM258 correlate with, and may be deduced from, the identity of the target genes which GAM258 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4011] Nucleotide sequences of the GAM258 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM258 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM258 are further described hereinbelow with reference to Table Table1.

[4012] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM258 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4013] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 259 (GAM259) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4014] GAM259 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM259 was detected is described hereinabove with reference to Figs. 2-8.

[4015] GAM259 gene, herein designated GAM GENE, and GAM259 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4016] GAM259 gene, herein designated GAM GENE, encodes a GAM259 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM259 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM259 precursor RNA is designated SEQ ID:231, and is provided hereinbelow with reference to the sequence listing part.

[4017] GAM259 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4018] An enzyme complex designated DICER COMPLEX, dices the GAM259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM259 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM259 RNA is designated SEQ ID:1907, and is provided hereinbelow with reference to the sequence listing part.

[4019] GAM259 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM259 target RNA, herein designated GAM TARGET RNA. GAM259 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4020] GAM259 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM259 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM259 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM259 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM259 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4021] The complementary binding of GAM259 RNA, herein designated GAM RNA, to target binding sites on GAM259 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM259 target RNA, herein designated GAM TARGET RNA, into GAM259 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4022] It is appreciated that GAM259 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM259 target genes. The mRNA of each one of this plurality of GAM259 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM259 RNA, herein designated GAM RNA, and which when bound by GAM259 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM259 target proteins.

[4023] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM259 gene, herein designated GAM GENE, on one or more GAM259 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4024] It is yet further appreciated that specific functions, and accordingly utilities, of GAM259 correlate with, and may be deduced from, the identity of the target genes which GAM259 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4025] Nucleotide sequences of the GAM259 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM259 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM259 are further described hereinbelow with reference to Table Table1.

[4026] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM259 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4027] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 260 (GAM260) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4028] GAM260 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM260 was detected is described hereinabove with reference to Figs. 2-8.

[4029] GAM260 gene, herein designated GAM GENE, and GAM260 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4030] GAM260 gene, herein designated GAM GENE, encodes a GAM260 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM260 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM260 precursor RNA is designated SEQ ID:232, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:232 is located at position 15185847 relative to contig NT_008705.13, on chromosome 10.

[4031] GAM260 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4032] An enzyme complex designated DICER COMPLEX, dices the GAM260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM260 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM260 RNA is designated SEQ ID:1908, and is provided

hereinbelow with reference to the sequence listing part.

[4033] GAM260 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM260 target RNA, herein designated GAM TARGET RNA. GAM260 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4034] GAM260 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM260 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM260 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM260 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM260 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4035] The complementary binding of GAM260 RNA, herein designated GAM RNA, to target binding sites on GAM260 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM260 target RNA, herein designated GAM TARGET RNA, into GAM260 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4036] It is appreciated that GAM260 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM260 target genes. The mRNA of each one of this plurality of GAM260 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM260 RNA, herein designated GAM RNA, and which when bound by GAM260 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM260 tar-

get proteins.

[4037] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM260 gene, herein designated GAM GENE, on one or more GAM260 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4038] It is yet further appreciated that specific functions, and accordingly utilities, of GAM260 correlate with, and may be deduced from, the identity of the target genes which GAM260 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4039] Nucleotide sequences of the GAM260 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM260 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM260 are further described hereinbelow with reference to Table Table1.

[4040] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM260 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4041] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 261 (GAM261) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4042] GAM261 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM261 was detected is described hereinabove with reference to Figs. 2-8.

[4043] GAM261 gene, herein designated GAM GENE, and

GAM261 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4044] GAM261 gene, herein designated GAM GENE, encodes a GAM261 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM261 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM261 precursor RNA is designated SEQ ID:233, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:233 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[4045] GAM261 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4046] An enzyme complex designated DICER COMPLEX, dices the GAM261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM261 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM261 RNA is designated SEQ ID:1909, and is provided hereinbelow with reference to the sequence listing part.

[4047] GAM261 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM261 target RNA, herein designated GAM TARGET RNA. GAM261 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4048] GAM261 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM261 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM261 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM261 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM261 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4049] The complementary binding of GAM261 RNA, herein designated GAM RNA, to target binding sites on GAM261 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM261 target RNA, herein designated GAM TARGET RNA, into GAM261 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[4050] It is appreciated that GAM261 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM261 target genes. The mRNA of each one of this plurality of GAM261 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM261 RNA, herein designated GAM RNA, and which when bound by GAM261 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM261 target proteins.

[4051] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM261 gene, herein designated GAM GENE, on one or more GAM261 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4052] It is yet further appreciated that specific functions, and accordingly utilities, of GAM261 correlate with, and may be deduced from, the identity of the target genes which GAM261 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4053] Nucleotide sequences of the GAM261 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM261 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM261 are further described hereinbelow with reference to Table Table1.

[4054] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM261 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4055] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 262 (GAM262) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4056] GAM262 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM262 was detected is described hereinabove with reference to Figs. 2-8.

[4057] GAM262 gene, herein designated GAM GENE, and GAM262 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4058] GAM262 gene, herein designated GAM GENE, encodes a GAM262 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM262 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM262 precursor RNA is designated SEQ ID:234, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:234 is located at position 23535227 relative to contig NT_033899.3, on chromosome 11.

[4059] GAM262 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[4060] SEQ ID:98410 detected in mouse EST Accession BI714485.1.

[4061] SEQ ID:98411 detected in mouse EST Accession BE368829.1.

[4062] GAM262 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4063] An enzyme complex designated DICER COMPLEX, dices the GAM262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM262 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM262 RNA is designated SEQ ID:1910, and is provided hereinbelow with reference to the sequence listing part.

[4064] GAM262 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM262 target RNA, herein designated GAM TARGET RNA. GAM262 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4065] GAM262 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM262 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM262 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM262 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM262 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4066] The complementary binding of GAM262 RNA, herein designated GAM RNA, to target binding sites on GAM262 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM262 target RNA, herein designated GAM TARGET RNA, into GAM262 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4067] It is appreciated that GAM262 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM262 target genes. The mRNA of each one of this plu-

rality of GAM262 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM262 RNA, herein designated GAM RNA, and which when bound by GAM262 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM262 target proteins.

[4068] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM262 gene, herein designated GAM GENE, on one or more GAM262 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4069] It is yet further appreciated that specific functions, and accordingly utilities, of GAM262 correlate with, and may be deduced from, the identity of the target genes which GAM262 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4070] Nucleotide sequences of the GAM262 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM262 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM262 are further described hereinbelow with reference to Table Table1.

[4071] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM262 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4072] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 263 (GAM263) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[4073] GAM263 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM263 was detected is described hereinabove with reference to Figs. 2-8.

[4074] GAM263 gene, herein designated GAM GENE, and GAM263 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4075] GAM263 gene, herein designated GAM GENE, encodes a GAM263 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM263 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM263 precursor RNA is designated SEQ ID:235, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:235 is located at position 58159307 relative to contig NT_026437.9, on chromosome 14.

[4076] GAM263 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4077] An enzyme complex designated DICER COMPLEX, dices the GAM263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM263 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM263 RNA is designated SEQ ID:1911, and is provided hereinbelow with reference to the sequence listing part.

[4078] GAM263 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM263 target RNA, herein designated GAM TARGET RNA. GAM263 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4079] GAM263 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM263 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM263 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM263 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM263 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4080] The complementary binding of GAM263 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM263 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM263 target RNA, herein designated GAM TARGET RNA, into GAM263 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4081] It is appreciated that GAM263 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM263 target genes. The mRNA of each one of this plurality of GAM263 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM263 RNA, herein designated GAM RNA, and which when bound by GAM263 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM263 target proteins.

[4082] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM263 gene, herein designated GAM GENE, on one or more GAM263 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4083] It is yet further appreciated that specific functions, and accordingly utilities, of GAM263 correlate with, and may be deduced from, the identity of the target genes which GAM263 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4084] Nucleotide sequences of the GAM263 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM263 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM263 are further described hereinbelow with reference to Table Table1.

[4085] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM263 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4086] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 264 (GAM264) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4087] GAM264 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM264 was detected is described hereinabove with reference to Figs. 2-8.

[4088] GAM264 gene, herein designated GAM GENE, and GAM264 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4089] GAM264 gene, herein designated GAM GENE, encodes a GAM264 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM264 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM264 precursor RNA is designated SEQ ID:236, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:236 is located at position 1036024 relative to contig NT_024115.13, on chromosome 10.

[4090] GAM264 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4091] An enzyme complex designated DICER COMPLEX, dices the GAM264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM264 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM264 RNA is designated SEQ ID:1912, and is provided hereinbelow with reference to the sequence listing part.

[4092] GAM264 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM264 target RNA, herein designated GAM TARGET RNA. GAM264 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4093] GAM264 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM264 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM264 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM264 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM264 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4094] The complementary binding of GAM264 RNA, herein designated GAM RNA, to target binding sites on GAM264 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM264 target RNA, herein designated GAM TARGET RNA, into GAM264 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4095] It is appreciated that GAM264 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM264 target genes. The mRNA of each one of this plurality of GAM264 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM264 RNA,

herein designated GAM RNA, and which when bound by GAM264 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM264 target proteins.

[4096] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM264 gene, herein designated GAM GENE, on one or more GAM264 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4097] It is yet further appreciated that specific functions, and accordingly utilities, of GAM264 correlate with, and may be deduced from, the identity of the target genes which

GAM264 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4098] Nucleotide sequences of the GAM264 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM264 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM264 are further described hereinbelow with reference to Table Table1.

[4099] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM264 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4100] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 265 (GAM265) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4101] GAM265 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM265 was detected is described hereinabove with reference to Figs. 2-8.

[4102] GAM265 gene, herein designated GAM GENE, and GAM265 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4103] GAM265 gene, herein designated GAM GENE, encodes a GAM265 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM265 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM265 precursor RNA is designated SEQ ID:237, and is provided hereinbelow with reference to the sequence listing part.

[4104] GAM265 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4105] An enzyme complex designated DICER COMPLEX, dices the GAM265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM265 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM265 RNA is designated SEQ ID:1913, and is provided hereinbelow with reference to the sequence listing part.

[4106] GAM265 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM265 target RNA, herein designated GAM TARGET RNA. GAM265 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4107] GAM265 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM265 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM265 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM265 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM265 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4108] The complementary binding of GAM265 RNA, herein designated GAM RNA, to target binding sites on GAM265 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM265 target RNA, herein designated GAM TARGET RNA, into GAM265 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4109] It is appreciated that GAM265 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM265 target genes. The mRNA of each one of this plu-

rality of GAM265 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM265 RNA, herein designated GAM RNA, and which when bound by GAM265 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM265 target proteins.

[4110] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM265 gene, herein designated GAM GENE, on one or more GAM265 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4111] It is yet further appreciated that specific functions, and accordingly utilities, of GAM265 correlate with, and may be deduced from, the identity of the target genes which GAM265 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4112] Nucleotide sequences of the GAM265 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM265 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM265 are further described hereinbelow with reference to Table Table1.

[4113] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM265 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4114] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 266 (GAM266) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[4115] GAM266 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM266 was detected is described hereinabove with reference to Figs. 2-8.

[4116] GAM266 gene, herein designated GAM GENE, and GAM266 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4117] GAM266 gene, herein designated GAM GENE, encodes a GAM266 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM266 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM266 precursor RNA is designated SEQ ID:238, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:238 is located at position 387404 relative to contig NT_022508.11, on chromosome 3.

[4118] GAM266 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4119] An enzyme complex designated DICER COMPLEX, dices the GAM266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM266 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM266 RNA is designated SEQ ID:1914, and is provided hereinbelow with reference to the sequence listing part.

[4120] GAM266 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM266 target RNA, herein designated GAM TARGET RNA. GAM266 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4121] GAM266 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM266 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM266 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM266 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM266 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4122] The complementary binding of GAM266 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM266 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM266 target RNA, herein designated GAM TARGET RNA, into GAM266 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4123] It is appreciated that GAM266 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM266 target genes. The mRNA of each one of this plurality of GAM266 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM266 RNA, herein designated GAM RNA, and which when bound by GAM266 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM266 target proteins.

[4124] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM266 gene, herein designated GAM GENE, on one or more GAM266 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4125] It is yet further appreciated that specific functions, and accordingly utilities, of GAM266 correlate with, and may be deduced from, the identity of the target genes which GAM266 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4126] Nucleotide sequences of the GAM266 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM266 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM266 are further described hereinbelow with reference to Table Table1.

[4127] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM266 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4128] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 267 (GAM267) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4129] GAM267 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM267 was detected is described hereinabove with reference to Figs. 2-8.

[4130] GAM267 gene, herein designated GAM GENE, and GAM267 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4131] GAM267 gene, herein designated GAM GENE, encodes a GAM267 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM267 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM267 precursor RNA is designated SEQ ID:239, and is provided hereinbelow with reference to the sequence listing part.

[4132] GAM267 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4133] An enzyme complex designated DICER COMPLEX, dices the GAM267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM267 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM267 RNA is designated SEQ ID:1915, and is provided hereinbelow with reference to the sequence listing part.

[4134] GAM267 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM267 target RNA, herein designated GAM TARGET RNA. GAM267 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4135] GAM267 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM267 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM267 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM267 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM267 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4136] The complementary binding of GAM267 RNA, herein designated GAM RNA, to target binding sites on GAM267 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM267 target RNA, herein designated GAM TARGET RNA, into GAM267 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4137] It is appreciated that GAM267 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM267 target genes. The mRNA of each one of this plurality of GAM267 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM267 RNA, herein designated GAM RNA, and which when bound by GAM267 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM267 target proteins.

[4138] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM267 gene, herein designated GAM GENE, on one or more GAM267 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4139] It is yet further appreciated that specific functions, and accordingly utilities, of GAM267 correlate with, and may be deduced from, the identity of the target genes which GAM267 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4140] Nucleotide sequences of the GAM267 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM267 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM267 are further described hereinbelow with reference to Table Table1.

[4141] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM267 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4142] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 268 (GAM268) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4143] GAM268 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM268 was detected is described hereinabove with reference to Figs. 2-8.

[4144] GAM268 gene, herein designated GAM GENE, and GAM268 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4145] GAM268 gene, herein designated GAM GENE, encodes a GAM268 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM268 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM268 precursor RNA is designated SEQ ID:240, and is provided hereinbelow with reference to the sequence listing part.

[4146] GAM268 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4147] An enzyme complex designated DICER COMPLEX, dices

the GAM268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM268 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM268 RNA is designated SEQ ID:1916, and is provided hereinbelow with reference to the sequence listing part.

[4148] GAM268 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM268 target RNA, herein designated GAM TARGET RNA. GAM268 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4149] GAM268 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM268 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM268

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM268 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM268 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4150] The complementary binding of GAM268 RNA, herein designated GAM RNA, to target binding sites on GAM268 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM268 target RNA, herein designated GAM TARGET RNA, into GAM268 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4151] It is appreciated that GAM268 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM268 target genes. The mRNA of each one of this plurality of GAM268 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM268 RNA, herein designated GAM RNA, and which when bound by GAM268 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM268 target proteins.

[4152] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM268 gene, herein designated GAM GENE, on one or more GAM268 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4153] It is yet further appreciated that specific functions, and accordingly utilities, of GAM268 correlate with, and may be deduced from, the identity of the target genes which GAM268 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4154] Nucleotide sequences of the GAM268 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM268 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM268 are further described hereinbelow with reference to Table Table1.

[4155] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM268 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4156] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 269 (GAM269) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4157] GAM269 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM269 was detected is described hereinabove with reference to Figs. 2-8.

[4158] GAM269 gene, herein designated GAM GENE, and GAM269 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4159] GAM269 gene, herein designated GAM GENE, encodes a GAM269 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM269 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM269 precursor RNA is designated SEQ ID:241, and is provided hereinbelow with reference to the sequence listing part.

[4160] GAM269 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4161] An enzyme complex designated DICER COMPLEX, dices the GAM269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM269 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM269 RNA is designated SEQ ID:1917, and is provided hereinbelow with reference to the sequence listing part.

[4162] GAM269 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM269 target RNA, herein designated GAM TARGET RNA. GAM269 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4163] GAM269 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM269 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM269 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM269 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM269 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4164] The complementary binding of GAM269 RNA, herein designated GAM RNA, to target binding sites on GAM269 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM269 target RNA, herein designated GAM TARGET RNA, into GAM269 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4165] It is appreciated that GAM269 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM269 target genes. The mRNA of each one of this plurality of GAM269 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM269 RNA, herein designated GAM RNA, and which when bound by GAM269 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM269 target proteins.

[4166] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM269 gene, herein designated GAM GENE, on one or more GAM269 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4167] It is yet further appreciated that specific functions, and accordingly utilities, of GAM269 correlate with, and may be deduced from, the identity of the target genes which GAM269 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4168] Nucleotide sequences of the GAM269 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM269 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM269 are further described hereinbelow with reference to Table Table1.

[4169] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM269 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4170] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 270 (GAM270) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4171] GAM270 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM270 was detected is described hereinabove with reference to Figs. 2-8.

[4172] GAM270 gene, herein designated GAM GENE, and GAM270 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4173] GAM270 gene, herein designated GAM GENE, encodes a GAM270 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM270 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM270 precursor RNA is designated SEQ ID:242, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:242 is located at position 2554141 relative to contig NT_004852.13, on chromosome 1.

[4174] GAM270 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4175] An enzyme complex designated DICER COMPLEX, dices the GAM270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM270 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM270 RNA is designated SEQ ID:1918, and is provided hereinbelow with reference to the sequence listing part.

[4176] GAM270 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM270 target RNA, herein designated GAM TARGET RNA. GAM270 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4177] GAM270 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM270 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM270 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM270 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM270 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4178] The complementary binding of GAM270 RNA, herein designated GAM RNA, to target binding sites on GAM270 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM270 target RNA, herein designated GAM TARGET RNA, into GAM270 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4179] It is appreciated that GAM270 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM270 target genes. The mRNA of each one of this plurality of GAM270 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM270 RNA, herein designated GAM RNA, and which when bound by GAM270 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM270 target proteins.

[4180] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM270 gene, herein designated GAM GENE, on one or more GAM270 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4181] It is yet further appreciated that specific functions, and accordingly utilities, of GAM270 correlate with, and may

be deduced from, the identity of the target genes which GAM270 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4182] Nucleotide sequences of the GAM270 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM270 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM270 are further described hereinbelow with reference to Table Table1.

[4183] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM270 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4184] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 271 (GAM271) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4185] GAM271 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM271 was detected is described hereinabove with reference to Figs. 2-8.

[4186] GAM271 gene, herein designated GAM GENE, and GAM271 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4187] GAM271 gene, herein designated GAM GENE, encodes a GAM271 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM271 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM271 precursor RNA is designated SEQ ID:243, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:243 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[4188] GAM271 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4189] An enzyme complex designated DICER COMPLEX, dices the GAM271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM271 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM271 RNA is designated SEQ ID:1919, and is provided hereinbelow with reference to the sequence listing part.

[4190] GAM271 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM271 target RNA, herein designated GAM TARGET RNA. GAM271 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4191] GAM271 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM271 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM271 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM271 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM271 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4192] The complementary binding of GAM271 RNA, herein designated GAM RNA, to target binding sites on GAM271 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM271 target RNA, herein designated GAM TARGET RNA, into GAM271 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4193] It is appreciated that GAM271 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM271 target genes. The mRNA of each one of this plurality of GAM271 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM271 RNA, herein designated GAM RNA, and which when bound by GAM271 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM271 target proteins.

[4194] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM271 gene, herein designated GAM GENE, on one or more GAM271 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4195] It is yet further appreciated that specific functions, and accordingly utilities, of GAM271 correlate with, and may be deduced from, the identity of the target genes which GAM271 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4196] Nucleotide sequences of the GAM271 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM271 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM271 are further described hereinbelow with reference to Table Table1.

[4197] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM271 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4198] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 272 (GAM272) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4199] GAM272 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM272 was detected is described hereinabove with reference to Figs. 2-8.

[4200] GAM272 gene, herein designated GAM GENE, and GAM272 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4201] GAM272 gene, herein designated GAM GENE, encodes a GAM272 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM272 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM272 precursor RNA is desig-

nated SEQ ID:244, and is provided hereinbelow with reference to the sequence listing part.

[4202] GAM272 has 10 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[4203] SEQ ID:98458 detected in mouse EST Accession BE134795.1.

[4204] SEQ ID:98459 detected in mouse EST Accession BF319810.1.

[4205] SEQ ID:98460 detected in mouse EST Accession BE993658.1.

[4206] SEQ ID:98461 detected in mouse EST Accession BI789800.1.

[4207] SEQ ID:98462 detected in mouse EST Accession BG802973.1.

[4208] SEQ ID:98463 detected in mouse EST Accession BI102547.1.

[4209] SEQ ID:98464 detected in mouse EST Accession AA245147.1.

[4210] SEQ ID:98465 detected in mouse EST Accession AI428210.1.

[4211] SEQ ID:98069 detected in mouse EST Accession AW913506.1.

[4212] SEQ ID:98070 detected in mouse EST Accession BI715710.1.

[4213] GAM272 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4214] An enzyme complex designated DICER COMPLEX, dices the GAM272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM272 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM272 RNA is designated SEQ ID:1920, and is provided hereinbelow with reference to the sequence listing part.

[4215] GAM272 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM272 target RNA, herein designated GAM TARGET RNA. GAM272 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4216] GAM272 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM272 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM272 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM272 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM272 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4217] The complementary binding of GAM272 RNA, herein designated GAM RNA, to target binding sites on GAM272 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM272 target RNA, herein designated GAM TARGET RNA, into GAM272 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4218] It is appreciated that GAM272 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM272 target genes. The mRNA of each one of this plurality of GAM272 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM272 RNA, herein designated GAM RNA, and which when bound by GAM272 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM272 target proteins.

[4219] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM272 gene, herein designated GAM GENE, on one or more GAM272 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4220] It is yet further appreciated that specific functions, and accordingly utilities, of GAM272 correlate with, and may be deduced from, the identity of the target genes which GAM272 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4221] Nucleotide sequences of the GAM272 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM272 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM272 are further described hereinbelow with reference to Table Table1.

[4222] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM272 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4223] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 273 (GAM273) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4224] GAM273 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM273 was detected is described hereinabove with reference to Figs. 2-8.

[4225] GAM273 gene, herein designated GAM GENE, and GAM273 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4226] GAM273 gene, herein designated GAM GENE, encodes a GAM273 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM273 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM273 precursor RNA is designated SEQ ID:245, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:245 is located at position 6185718 relative to contig NT_005332.11, on chromosome 2.

[4227] GAM273 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[4228] An enzyme complex designated DICER COMPLEX, dices the GAM273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM273 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM273 RNA is designated SEQ ID:1921, and is provided hereinbelow with reference to the sequence listing part.

[4229] GAM273 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM273 target RNA, herein designated GAM TARGET RNA. GAM273 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4230] GAM273 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM273 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM273 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM273 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM273 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4231] The complementary binding of GAM273 RNA, herein designated GAM RNA, to target binding sites on GAM273 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM273 target RNA, herein designated GAM TARGET RNA, into GAM273 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4232] It is appreciated that GAM273 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM273 target genes. The mRNA of each one of this plurality of GAM273 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM273 RNA, herein designated GAM RNA, and which when bound by GAM273 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM273 target proteins.

[4233] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM273 gene, herein designated GAM GENE, on one or more GAM273 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4234] It is yet further appreciated that specific functions, and accordingly utilities, of GAM273 correlate with, and may be deduced from, the identity of the target genes which GAM273 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4235] Nucleotide sequences of the GAM273 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM273 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM273 are further described hereinbelow with reference to Table Table1.

[4236] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM273 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4237] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 274 (GAM274) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4238] GAM274 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM274 was detected is described hereinabove with reference to Figs. 2-8.

[4239] GAM274 gene, herein designated GAM GENE, and GAM274 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4240] GAM274 gene, herein designated GAM GENE, encodes a GAM274 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM274 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM274 precursor RNA is designated SEQ ID:246, and is provided hereinbelow with reference to the sequence listing part.

[4241] GAM274 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4242] An enzyme complex designated DICER COMPLEX, dices the GAM274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM274 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM274 RNA is designated SEQ ID:1922, and is provided hereinbelow with reference to the sequence listing part.

[4243] GAM274 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM274 target RNA, herein designated GAM TARGET RNA.

GAM274 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4244] GAM274 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM274 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM274 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM274 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM274 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4245] The complementary binding of GAM274 RNA, herein designated GAM RNA, to target binding sites on GAM274 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM274 target RNA, herein designated GAM TARGET RNA, into GAM274 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4246] It is appreciated that GAM274 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM274 target genes. The mRNA of each one of this plurality of GAM274 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM274 RNA, herein designated GAM RNA, and which when bound by GAM274 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM274 target proteins.

[4247] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM274 gene, herein designated GAM GENE, on one or more GAM274 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4248] It is yet further appreciated that specific functions, and accordingly utilities, of GAM274 correlate with, and may be deduced from, the identity of the target genes which GAM274 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4249] Nucleotide sequences of the GAM274 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM274 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM274 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM274 are further described hereinbelow with reference to Table Table1.

[4250] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM274 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4251] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 275 (GAM275) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4252] GAM275 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM275 was detected is described hereinabove with reference to Figs. 2-8.

[4253] GAM275 gene, herein designated GAM GENE, and GAM275 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4254] GAM275 gene, herein designated GAM GENE, encodes a GAM275 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM275 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM275 precursor RNA is designated SEQ ID:247, and is provided hereinbelow with reference to the sequence listing part.

[4255] GAM275 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4256] An enzyme complex designated DICER COMPLEX, dices the GAM275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM275 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM275 RNA is designated SEQ ID:1923, and is provided hereinbelow with reference to the sequence listing part.

[4257] GAM275 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM275 target RNA, herein designated GAM TARGET RNA. GAM275 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4258] GAM275 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM275 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM275 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM275 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM275 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4259] The complementary binding of GAM275 RNA, herein designated GAM RNA, to target binding sites on GAM275 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM275 target RNA, herein designated GAM TARGET RNA, into GAM275 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4260] It is appreciated that GAM275 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM275 target genes. The mRNA of each one of this plurality of GAM275 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM275 RNA, herein designated GAM RNA, and which when bound by GAM275 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM275 target proteins.

[4261] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM275 gene, herein designated GAM GENE, on one or more GAM275 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4262] It is yet further appreciated that specific functions, and accordingly utilities, of GAM275 correlate with, and may

be deduced from, the identity of the target genes which GAM275 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4263] Nucleotide sequences of the GAM275 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM275 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM275 are further described hereinbelow with reference to Table Table1.

[4264] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM275 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4265] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 276 (GAM276) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4266] GAM276 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM276 was detected is described hereinabove with reference to Figs. 2-8.

[4267] GAM276 gene, herein designated GAM GENE, and GAM276 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4268] GAM276 gene, herein designated GAM GENE, encodes a GAM276 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM276 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM276 precursor RNA is designated SEQ ID:248, and is provided hereinbelow with reference to the sequence listing part.

[4269] GAM276 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[4270] An enzyme complex designated DICER COMPLEX, dices the GAM276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM276 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM276 RNA is designated SEQ ID:1924, and is provided hereinbelow with reference to the sequence listing part.

[4271] GAM276 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM276 target RNA, herein designated GAM TARGET RNA.
GAM276 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4272] GAM276 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM276 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM276 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM276 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM276 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4273] The complementary binding of GAM276 RNA, herein designated GAM RNA, to target binding sites on GAM276 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM276 target RNA, herein desig-

nated GAM TARGET RNA, into GAM276 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4274] It is appreciated that GAM276 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM276 target genes. The mRNA of each one of this plurality of GAM276 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM276 RNA, herein designated GAM RNA, and which when bound by GAM276 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM276 target proteins.

[4275] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM276 gene, herein designated GAM GENE, on one or more GAM276 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4276] It is yet further appreciated that specific functions, and accordingly utilities, of GAM276 correlate with, and may be deduced from, the identity of the target genes which GAM276 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4277] Nucleotide sequences of the GAM276 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM276 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM276 are further described hereinbelow with reference to Table Table1.

[4278] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM276 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[4279] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 277 (GAM277) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4280] GAM277 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM277 was detected is described hereinabove with reference to Figs. 2-8.

[4281] GAM277 gene, herein designated GAM GENE, and GAM277 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4282] GAM277 gene, herein designated GAM GENE, encodes a GAM277 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM277 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM277 precursor RNA is designated SEQ ID:249, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:249 is located at position 1184411 relative to contig NT_033241.3, on chromosome 11.

[4283] GAM277 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4284] An enzyme complex designated DICER COMPLEX, dices the GAM277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM277 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM277 RNA is designated SEQ ID:1925, and is provided hereinbelow with reference to the sequence listing part.

[4285] GAM277 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM277 target RNA, herein designated GAM TARGET RNA. GAM277 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4286] GAM277 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM277 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM277 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM277 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM277

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4287] The complementary binding of GAM277 RNA, herein designated GAM RNA, to target binding sites on GAM277 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM277 target RNA, herein designated GAM TARGET RNA, into GAM277 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4288] It is appreciated that GAM277 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM277 target genes. The mRNA of each one of this plurality of GAM277 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM277 RNA, herein designated GAM RNA, and which when bound by GAM277 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM277 target proteins.

[4289] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM277 gene, herein designated GAM GENE, on one or more GAM277 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4290] It is yet further appreciated that specific functions, and accordingly utilities, of GAM277 correlate with, and may be deduced from, the identity of the target genes which GAM277 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4291] Nucleotide sequences of the GAM277 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM277 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM277 are further described hereinbelow with reference to Table Table1.

[4292] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM277 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4293] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 278 (GAM278) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4294] GAM278 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM278 was detected is described hereinabove with reference to Figs. 2-8.

[4295] GAM278 gene, herein designated GAM GENE, and GAM278 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[4296] GAM278 gene, herein designated GAM GENE, encodes a GAM278 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM278 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM278 precursor RNA is designated SEQ ID:250, and is provided hereinbelow with reference to the sequence listing part.

[4297] GAM278 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4298] An enzyme complex designated DICER COMPLEX, dices the GAM278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM278 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM278 RNA is designated SEQ ID:1926, and is provided hereinbelow with reference to the sequence listing part.

[4299] GAM278 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM278 target RNA, herein designated GAM TARGET RNA. GAM278 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4300] GAM278 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM278 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM278 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM278 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM278 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4301] The complementary binding of GAM278 RNA, herein designated GAM RNA, to target binding sites on GAM278 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM278 target RNA, herein designated GAM TARGET RNA, into GAM278 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4302] It is appreciated that GAM278 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM278 target genes. The mRNA of each one of this plurality of GAM278 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM278 RNA, herein designated GAM RNA, and which when bound by GAM278 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM278 target proteins.

[4303] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM278 gene, herein designated GAM GENE, on one or more GAM278 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[4304] It is yet further appreciated that specific functions, and accordingly utilities, of GAM278 correlate with, and may be deduced from, the identity of the target genes which GAM278 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4305] Nucleotide sequences of the GAM278 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM278 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM278 are further described hereinbelow with reference to Table Table1.

[4306] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM278 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4307] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 279 (GAM279) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[4308] GAM279 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM279 was detected is described hereinabove with reference to Figs. 2-8.

[4309] GAM279 gene, herein designated GAM GENE, and GAM279 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4310] GAM279 gene, herein designated GAM GENE, encodes a GAM279 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM279 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM279 precursor RNA is designated SEQ ID:251, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:251 is located at position 1184411 relative to contig NT_033241.3, on chromosome 11.

[4311] GAM279 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4312] An enzyme complex designated DICER COMPLEX, dices the GAM279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM279 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM279 RNA is designated SEQ ID:1927, and is provided hereinbelow with reference to the sequence listing part.

[4313] GAM279 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM279 target RNA, herein designated GAM TARGET RNA. GAM279 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4314] GAM279 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM279 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM279 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM279 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM279 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4315] The complementary binding of GAM279 RNA, herein designated GAM RNA, to target binding sites on GAM279 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM279 target RNA, herein designated GAM TARGET RNA, into GAM279 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4316] It is appreciated that GAM279 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM279 target genes. The mRNA of each one of this plurality of GAM279 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM279 RNA, herein designated GAM RNA, and which when bound by GAM279 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM279 target proteins.

[4317] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM279 gene, herein designated GAM GENE, on one or more GAM279 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4318] It is yet further appreciated that specific functions, and accordingly utilities, of GAM279 correlate with, and may be deduced from, the identity of the target genes which GAM279 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4319] Nucleotide sequences of the GAM279 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM279 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM279 are further described hereinbelow with reference to Table Table1.

[4320] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM279 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4321] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 280 (GAM280) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4322] GAM280 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM280 was detected is described hereinabove with reference to Figs. 2-8.

[4323] GAM280 gene, herein designated GAM GENE, and GAM280 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4324] GAM280 gene, herein designated GAM GENE, encodes a GAM280 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM280 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM280 precursor RNA is designated SEQ ID:252, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:252 is located at position 1654434 relative to contig NT_005986.13, on chromosome 3.

[4325] GAM280 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4326] An enzyme complex designated DICER COMPLEX, dices the GAM280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM280 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM280 RNA is designated SEQ ID:1928, and is provided hereinbelow with reference to the sequence listing part.

[4327] GAM280 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM280 target RNA, herein designated GAM TARGET RNA. GAM280 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4328] GAM280 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM280 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM280 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM280 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM280 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4329] The complementary binding of GAM280 RNA, herein designated GAM RNA, to target binding sites on GAM280 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM280 target RNA, herein designated GAM TARGET RNA, into GAM280 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4330] It is appreciated that GAM280 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM280 target genes. The mRNA of each one of this plurality of GAM280 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM280 RNA, herein designated GAM RNA, and which when bound by GAM280 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM280 target proteins.

[4331] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM280 gene, herein designated GAM GENE, on one or more GAM280 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4332] It is yet further appreciated that specific functions, and accordingly utilities, of GAM280 correlate with, and may

be deduced from, the identity of the target genes which GAM280 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4333] Nucleotide sequences of the GAM280 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM280 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM280 are further described hereinbelow with reference to Table Table1.

[4334] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM280 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4335] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 281 (GAM281) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4336] GAM281 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM281 was detected is described hereinabove with reference to Figs. 2-8.

[4337] GAM281 gene, herein designated GAM GENE, and GAM281 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4338] GAM281 gene, herein designated GAM GENE, encodes a GAM281 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM281 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM281 precursor RNA is designated SEQ ID:253, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:253 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[4339] GAM281 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[4340] SEQ ID:100183 detected in mouse EST Accession

AA144533.1.

[4341] SEQ ID:100184 detected in mouse EST Accession BE943987.1.

[4342] SEQ ID:100185 detected in mouse EST Accession BE691413.1.

[4343] SEQ ID:100186 detected in mouse EST Accession BE691447.1.

[4344] SEQ ID:100187 detected in mouse EST Accession BG808025.1.

[4345] SEQ ID:100188 detected in mouse EST Accession BG808010.1.

[4346] SEQ ID:100189 detected in mouse EST Accession BG807850.1.

[4347] SEQ ID:100190 detected in mouse EST Accession BG805970.1.

[4348] SEQ ID:100191 detected in mouse EST Accession AW208601.1.

[4349] SEQ ID:100192 detected in mouse EST Accession AA671455.1.

[4350] SEQ ID:100193 detected in mouse EST Accession AW824753.1.

[4351] SEQ ID:100194 detected in mouse EST Accession BG145596.1.

[4352] SEQ ID:100195 detected in mouse EST Accession BE692802.1.

[4353] SEQ ID:100196 detected in mouse EST Accession BB609859.1.

[4354] SEQ ID:100197 detected in mouse EST Accession BB610842.1.

[4355] GAM281 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4356] An enzyme complex designated DICER COMPLEX, dices the GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM281 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM281 RNA is designated SEQ ID:1929, and is provided hereinbelow with reference to the sequence listing part.

[4357] GAM281 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM281 target RNA, herein designated GAM TARGET RNA. GAM281 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4358] GAM281 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM281 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM281 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM281 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM281 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4359] The complementary binding of GAM281 RNA, herein designated GAM RNA, to target binding sites on GAM281 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM281 target RNA, herein designated GAM TARGET RNA, into GAM281 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4360] It is appreciated that GAM281 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM281 target genes. The mRNA of each one of this plurality of GAM281 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM281 RNA,

herein designated GAM RNA, and which when bound by GAM281 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM281 target proteins.

[4361] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM281 gene, herein designated GAM GENE, on one or more GAM281 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4362] It is yet further appreciated that specific functions, and accordingly utilities, of GAM281 correlate with, and may be deduced from, the identity of the target genes which

GAM281 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4363] Nucleotide sequences of the GAM281 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM281 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM281 are further described hereinbelow with reference to Table Table1.

[4364] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM281 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4365] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 282 (GAM282) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4366] GAM282 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM282 was detected is described hereinabove with reference to Figs. 2-8.

[4367] GAM282 gene, herein designated GAM GENE, and GAM282 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4368] GAM282 gene, herein designated GAM GENE, encodes a GAM282 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM282 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM282 precursor RNA is designated SEQ ID:254, and is provided hereinbelow with reference to the sequence listing part.

[4369] GAM282 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[4370] An enzyme complex designated DICER COMPLEX, dices the GAM282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM282 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM282 RNA is designated SEQ ID:1930, and is provided hereinbelow with reference to the sequence listing part.

[4371] GAM282 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM282 target RNA, herein designated GAM TARGET RNA. GAM282 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4372] GAM282 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM282 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM282 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM282 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM282 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4373] The complementary binding of GAM282 RNA, herein designated GAM RNA, to target binding sites on GAM282 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM282 target RNA, herein designated GAM TARGET RNA, into GAM282 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4374] It is appreciated that GAM282 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM282 target genes. The mRNA of each one of this plurality of GAM282 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM282 RNA, herein designated GAM RNA, and which when bound by GAM282 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM282 target proteins.

[4375] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM282 gene, herein designated GAM GENE, on one or more GAM282 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4376] It is yet further appreciated that specific functions, and accordingly utilities, of GAM282 correlate with, and may be deduced from, the identity of the target genes which GAM282 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4377] Nucleotide sequences of the GAM282 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM282 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM282 are further described hereinbelow with reference to Table Table1.

[4378] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM282 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4379] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 283 (GAM283) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4380] GAM283 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM283 was detected is described hereinabove with reference to Figs. 2-8.

[4381] GAM283 gene, herein designated GAM GENE, and GAM283 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4382] GAM283 gene, herein designated GAM GENE, encodes a GAM283 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM283 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM283 precursor RNA is designated SEQ ID:255, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:255 is located at position 33703762 relative to

contig NT_007592.11, on chromosome 6.

[4383] GAM283 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4384] An enzyme complex designated DICER COMPLEX, dices the GAM283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM283 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM283 RNA is designated SEQ ID:1931, and is provided hereinbelow with reference to the sequence listing part.

[4385] GAM283 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM283 target RNA, herein designated GAM TARGET RNA.

GAM283 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4386] GAM283 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM283 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM283 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM283 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM283 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4387] The complementary binding of GAM283 RNA, herein designated GAM RNA, to target binding sites on GAM283 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM283 target RNA, herein designated GAM TARGET RNA, into GAM283 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4388] It is appreciated that GAM283 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM283 target genes. The mRNA of each one of this plurality of GAM283 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM283 RNA, herein designated GAM RNA, and which when bound by GAM283 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM283 target proteins.

[4389] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM283 gene, herein designated GAM GENE, on one or more GAM283 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4390] It is yet further appreciated that specific functions, and accordingly utilities, of GAM283 correlate with, and may be deduced from, the identity of the target genes which GAM283 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4391] Nucleotide sequences of the GAM283 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM283 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM283 are further described hereinbelow with reference to Table Table1.

[4392] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM283 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4393] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 284 (GAM284) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4394] GAM284 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM284 was detected is described hereinabove with reference to Figs. 2-8.

[4395] GAM284 gene, herein designated GAM GENE, and GAM284 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4396] GAM284 gene, herein designated GAM GENE, encodes a GAM284 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM284 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM284 precursor RNA is designated SEQ ID:256, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:256 is located at position 28263 relative to contig NT_009526.11, on chromosome 12.

[4397] GAM284 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[4398] SEQ ID:98456 detected in mouse EST Accession AI326210.1.

[4399] SEQ ID:98457 detected in mouse EST Accession BI965652.1.

[4400] SEQ ID:99542 detected in mouse EST Accession BI965972.1.

[4401] GAM284 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4402] An enzyme complex designated DICER COMPLEX, dices the GAM284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM284 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM284 RNA is designated SEQ ID:1932, and is provided hereinbelow with reference to the sequence listing part.

[4403] GAM284 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM284 target RNA, herein designated GAM TARGET RNA.

GAM284 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4404] GAM284 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM284 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM284 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM284 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM284 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4405] The complementary binding of GAM284 RNA, herein designated GAM RNA, to target binding sites on GAM284 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM284 target RNA, herein designated GAM TARGET RNA, into GAM284 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4406] It is appreciated that GAM284 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM284 target genes. The mRNA of each one of this plurality of GAM284 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM284 RNA, herein designated GAM RNA, and which when bound by GAM284 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM284 target proteins.

[4407] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM284 gene, herein designated GAM GENE, on one or more GAM284 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4408] It is yet further appreciated that specific functions, and accordingly utilities, of GAM284 correlate with, and may be deduced from, the identity of the target genes which GAM284 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4409] Nucleotide sequences of the GAM284 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM284 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM284 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM284 are further described hereinbelow with reference to Table Table1.

[4410] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM284 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4411] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 285 (GAM285) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4412] GAM285 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM285 was detected is described hereinabove with reference to Figs. 2-8.

[4413] GAM285 gene, herein designated GAM GENE, and GAM285 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4414] GAM285 gene, herein designated GAM GENE, encodes a GAM285 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM285 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM285 precursor RNA is designated SEQ ID:257, and is provided hereinbelow with reference to the sequence listing part.

[4415] GAM285 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4416] An enzyme complex designated DICER COMPLEX, dices the GAM285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM285 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM285 RNA is designated SEQ ID:1933, and is provided hereinbelow with reference to the sequence listing part.

[4417] GAM285 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM285 target RNA, herein designated GAM TARGET RNA. GAM285 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4418] GAM285 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM285 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM285 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM285 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM285 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4419] The complementary binding of GAM285 RNA, herein designated GAM RNA, to target binding sites on GAM285 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM285 target RNA, herein designated GAM TARGET RNA, into GAM285 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4420] It is appreciated that GAM285 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM285 target genes. The mRNA of each one of this plurality of GAM285 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM285 RNA, herein designated GAM RNA, and which when bound by GAM285 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM285 target proteins.

[4421] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM285 gene, herein designated GAM GENE, on one or more GAM285 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4422] It is yet further appreciated that specific functions, and accordingly utilities, of GAM285 correlate with, and may

be deduced from, the identity of the target genes which GAM285 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4423] Nucleotide sequences of the GAM285 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM285 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM285 are further described hereinbelow with reference to Table Table1.

[4424] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM285 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4425] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 286 (GAM286) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4426] GAM286 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM286 was detected is described hereinabove with reference to Figs. 2-8.

[4427] GAM286 gene, herein designated GAM GENE, and GAM286 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4428] GAM286 gene, herein designated GAM GENE, encodes a GAM286 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM286 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM286 precursor RNA is designated SEQ ID:258, and is provided hereinbelow with reference to the sequence listing part.

[4429] GAM286 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[4430] An enzyme complex designated DICER COMPLEX, dices the GAM286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM286 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM286 RNA is designated SEQ ID:1934, and is provided hereinbelow with reference to the sequence listing part.

[4431] GAM286 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM286 target RNA, herein designated GAM TARGET RNA.
GAM286 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4432] GAM286 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM286 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM286 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM286 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM286 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4433] The complementary binding of GAM286 RNA, herein designated GAM RNA, to target binding sites on GAM286 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM286 target RNA, herein desig-

nated GAM TARGET RNA, into GAM286 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4434] It is appreciated that GAM286 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM286 target genes. The mRNA of each one of this plurality of GAM286 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM286 RNA, herein designated GAM RNA, and which when bound by GAM286 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM286 target proteins.

[4435] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM286 gene, herein designated GAM GENE, on one or more GAM286 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4436] It is yet further appreciated that specific functions, and accordingly utilities, of GAM286 correlate with, and may be deduced from, the identity of the target genes which GAM286 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4437] Nucleotide sequences of the GAM286 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM286 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM286 are further described hereinbelow with reference to Table Table1.

[4438] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM286 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[4439] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 287 (GAM287) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4440] GAM287 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM287 was detected is described hereinabove with reference to Figs. 2-8.

[4441] GAM287 gene, herein designated GAM GENE, and GAM287 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4442] GAM287 gene, herein designated GAM GENE, encodes a GAM287 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM287 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM287 precursor RNA is designated SEQ ID:259, and is provided hereinbelow with reference to the sequence listing part.

[4443] GAM287 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4444] An enzyme complex designated DICER COMPLEX, dices the GAM287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM287 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM287 RNA is designated SEQ ID:1935, and is provided hereinbelow with reference to the sequence listing part.

[4445] GAM287 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM287

target RNA, herein designated GAM TARGET RNA.

GAM287 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4446] GAM287 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM287 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM287 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM287 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM287 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4447] The complementary binding of GAM287 RNA, herein designated GAM RNA, to target binding sites on GAM287 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM287 target RNA, herein designated GAM TARGET RNA, into GAM287 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4448] It is appreciated that GAM287 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM287 target genes. The mRNA of each one of this plurality of GAM287 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM287 RNA, herein designated GAM RNA, and which when bound by GAM287 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM287 target proteins.

[4449] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM287 gene, herein designated GAM GENE, on one or more GAM287 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4450] It is yet further appreciated that specific functions, and accordingly utilities, of GAM287 correlate with, and may be deduced from, the identity of the target genes which GAM287 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4451] Nucleotide sequences of the GAM287 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM287 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM287 are further described hereinbelow with reference to Table Table1.

[4452] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM287 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4453] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 288 (GAM288) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4454] GAM288 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM288 was detected is described hereinabove with reference to Figs. 2-8.

[4455] GAM288 gene, herein designated GAM GENE, and GAM288 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4456] GAM288 gene, herein designated GAM GENE, encodes a

GAM288 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM288 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM288 precursor RNA is designated SEQ ID:260, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:260 is located at position 3263798 relative to contig NT_028392.4, on chromosome 20.

[4457] GAM288 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4458] An enzyme complex designated DICER COMPLEX, dices the GAM288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM288 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM288 RNA is designated SEQ ID:1936, and is provided hereinbelow with reference to the sequence listing part.

[4459] GAM288 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM288 target RNA, herein designated GAM TARGET RNA. GAM288 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4460] GAM288 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM288 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM288 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM288 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM288 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4461] The complementary binding of GAM288 RNA, herein designated GAM RNA, to target binding sites on GAM288 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM288 target RNA, herein designated GAM TARGET RNA, into GAM288 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4462] It is appreciated that GAM288 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM288 target genes. The mRNA of each one of this plurality of GAM288 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM288 RNA, herein designated GAM RNA, and which when bound by GAM288 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM288 target proteins.

[4463] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM288 gene, herein designated GAM GENE, on one or more GAM288 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[4464] It is yet further appreciated that specific functions, and accordingly utilities, of GAM288 correlate with, and may be deduced from, the identity of the target genes which GAM288 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4465] Nucleotide sequences of the GAM288 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM288 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM288 are further described hereinbelow with reference to Table Table1.

[4466] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM288 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4467] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 289 (GAM289) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[4468] GAM289 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM289 was detected is described hereinabove with reference to Figs. 2-8.

[4469] GAM289 gene, herein designated GAM GENE, and GAM289 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4470] GAM289 gene, herein designated GAM GENE, encodes a GAM289 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM289 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM289 precursor RNA is designated SEQ ID:261, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:261 is located at position 479222 relative to contig NT_011726.8, on chromosome X.

[4471] GAM289 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4472] An enzyme complex designated DICER COMPLEX, dices the GAM289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM289 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM289 RNA is designated SEQ ID:1937, and is provided hereinbelow with reference to the sequence listing part.

[4473] GAM289 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM289 target RNA, herein designated GAM TARGET RNA. GAM289 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4474] GAM289 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM289 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM289 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM289 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM289 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4475] The complementary binding of GAM289 RNA, herein designated GAM RNA, to target binding sites on GAM289 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM289 target RNA, herein designated GAM TARGET RNA, into GAM289 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4476] It is appreciated that GAM289 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM289 target genes. The mRNA of each one of this plurality of GAM289 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM289 RNA, herein designated GAM RNA, and which when bound by GAM289 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM289 target proteins.

[4477] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM289 gene, herein designated GAM GENE, on one or more GAM289 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4478] It is yet further appreciated that specific functions, and accordingly utilities, of GAM289 correlate with, and may be deduced from, the identity of the target genes which GAM289 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4479] Nucleotide sequences of the GAM289 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM289 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM289 are further described hereinbelow with reference to Table Table1.

[4480] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM289 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4481] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 290 (GAM290) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4482] GAM290 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM290 was detected is described hereinabove with reference to Figs. 2-8.

[4483] GAM290 gene, herein designated GAM GENE, and GAM290 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4484] GAM290 gene, herein designated GAM GENE, encodes a GAM290 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM290 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM290 precursor RNA is designated SEQ ID:262, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:262 is located at position 14626756 relative to contig NT_011109.13, on chromosome 19.

[4485] GAM290 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4486] An enzyme complex designated DICER COMPLEX, dices the GAM290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM290 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM290 RNA is designated SEQ ID:1938, and is provided hereinbelow with reference to the sequence listing part.

[4487] GAM290 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM290 target RNA, herein designated GAM TARGET RNA. GAM290 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4488] GAM290 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM290 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM290 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM290 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM290 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4489] The complementary binding of GAM290 RNA, herein designated GAM RNA, to target binding sites on GAM290 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM290 target RNA, herein designated GAM TARGET RNA, into GAM290 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4490] It is appreciated that GAM290 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM290 target genes. The mRNA of each one of this plurality of GAM290 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM290 RNA, herein designated GAM RNA, and which when bound by GAM290 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM290 target proteins.

[4491] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM290 gene, herein designated GAM GENE, on one or more GAM290 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4492] It is yet further appreciated that specific functions, and accordingly utilities, of GAM290 correlate with, and may

be deduced from, the identity of the target genes which GAM290 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4493] Nucleotide sequences of the GAM290 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM290 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM290 are further described hereinbelow with reference to Table Table1.

[4494] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM290 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4495] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 291 (GAM291) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4496] GAM291 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM291 was detected is described hereinabove with reference to Figs. 2-8.

[4497] GAM291 gene, herein designated GAM GENE, and GAM291 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4498] GAM291 gene, herein designated GAM GENE, encodes a GAM291 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM291 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM291 precursor RNA is designated SEQ ID:263, and is provided hereinbelow with reference to the sequence listing part.

[4499] GAM291 has 52 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[4500] SEQ ID:98092 detected in mouse EST Accession W16182.1.

[4501] SEQ ID:98093 detected in mouse EST Accession

AW110985.1.

[4502] SEQ ID:98094 detected in mouse EST Accession AA237404.1.

[4503] SEQ ID:98095 detected in mouse EST Accession BE692663.1.

[4504] SEQ ID:98096 detected in mouse EST Accession AA237479.1.

[4505] SEQ ID:98097 detected in mouse EST Accession BE689976.1.

[4506] SEQ ID:98098 detected in mouse EST Accession BF020203.1.

[4507] SEQ ID:98099 detected in mouse EST Accession AI152470.1.

[4508] SEQ ID:98100 detected in mouse EST Accession AW241043.1.

[4509] SEQ ID:98101 detected in mouse EST Accession BE335469.1.

[4510] SEQ ID:98102 detected in mouse EST Accession BF116785.1.

[4511] SEQ ID:98103 detected in mouse EST Accession BE199228.1.

[4512] SEQ ID:98104 detected in mouse EST Accession AA230354.1.

[4513] SEQ ID:98105 detected in mouse EST Accession AW909366.1.

[4514] SEQ ID:98106 detected in mouse EST Accession AI255679.1.

[4515] SEQ ID:98107 detected in mouse EST Accession BE199152.1.

[4516] SEQ ID:98108 detected in mouse EST Accession BF227614.1.

[4517] SEQ ID:98109 detected in mouse EST Accession AI785459.1.

[4518] SEQ ID:98110 detected in mouse EST Accession AI323769.1.

[4519] SEQ ID:98111 detected in mouse EST Accession BF179498.1.

[4520] SEQ ID:98112 detected in mouse EST Accession AW209037.1.

[4521] SEQ ID:98113 detected in mouse EST Accession AW701118.1.

[4522] SEQ ID:98114 detected in mouse EST Accession AI646857.1.

[4523] SEQ ID:98115 detected in mouse EST Accession AW212849.1.

[4524] SEQ ID:98116 detected in mouse EST Accession

AI195467.1.

[4525] SEQ ID:98117 detected in mouse EST Accession AI747413.1.

[4526] SEQ ID:98118 detected in mouse EST Accession BI246484.1.

[4527] SEQ ID:98119 detected in mouse EST Accession AI114892.1.

[4528] SEQ ID:98120 detected in mouse EST Accession AI194959.1.

[4529] SEQ ID:98121 detected in mouse EST Accession BI250124.1.

[4530] SEQ ID:98122 detected in mouse EST Accession BF450285.1.

[4531] SEQ ID:98123 detected in mouse EST Accession BE690148.1.

[4532] SEQ ID:98124 detected in mouse EST Accession AW908422.1.

[4533] SEQ ID:98125 detected in mouse EST Accession AW989706.1.

[4534] SEQ ID:98126 detected in mouse EST Accession BI110254.1.

[4535] SEQ ID:98127 detected in mouse EST Accession AW322040.1.

[4536] SEQ ID:98128 detected in mouse EST Accession AW987156.1.

[4537] SEQ ID:98129 detected in mouse EST Accession AA270973.1.

[4538] SEQ ID:98130 detected in mouse EST Accession BE690578.1.

[4539] SEQ ID:98131 detected in mouse EST Accession BE624221.1.

[4540] SEQ ID:98132 detected in mouse EST Accession BE650065.1.

[4541] SEQ ID:98133 detected in mouse EST Accession AW018407.1.

[4542] SEQ ID:98134 detected in mouse EST Accession BF227510.1.

[4543] SEQ ID:98135 detected in mouse EST Accession AW018398.1.

[4544] SEQ ID:98136 detected in mouse EST Accession AA239428.1.

[4545] SEQ ID:98137 detected in mouse EST Accession AW113760.1.

[4546] SEQ ID:98138 detected in mouse EST Accession AA238246.1.

[4547] SEQ ID:98139 detected in mouse EST Accession

BF226299.1.

[4548] SEQ ID:98140 detected in mouse EST Accession AW110984.1.

[4549] SEQ ID:98141 detected in mouse EST Accession BI248794.1.

[4550] SEQ ID:98142 detected in mouse EST Accession AA764472.1.

[4551] SEQ ID:98143 detected in mouse EST Accession BI111409.1.

[4552] GAM291 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4553] An enzyme complex designated DICER COMPLEX, dices the GAM291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM291 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM291 RNA is designated SEQ ID:1939, and is provided hereinbelow with reference to the sequence listing part.

[4554] GAM291 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM291 target RNA, herein designated GAM TARGET RNA. GAM291 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4555] GAM291 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM291 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM291 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM291 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM291 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4556] The complementary binding of GAM291 RNA, herein designated GAM RNA, to target binding sites on GAM291 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM291 target RNA, herein designated GAM TARGET RNA, into GAM291 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4557] It is appreciated that GAM291 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM291 target genes. The mRNA of each one of this plu-

rality of GAM291 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM291 RNA, herein designated GAM RNA, and which when bound by GAM291 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM291 target proteins.

[4558] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM291 gene, herein designated GAM GENE, on one or more GAM291 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4559] It is yet further appreciated that specific functions, and accordingly utilities, of GAM291 correlate with, and may be deduced from, the identity of the target genes which GAM291 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4560] Nucleotide sequences of the GAM291 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM291 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM291 are further described hereinbelow with reference to Table Table1.

[4561] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM291 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4562] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 292 (GAM292) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[4563] GAM292 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM292 was detected is described hereinabove with reference to Figs. 2-8.

[4564] GAM292 gene, herein designated GAM GENE, and GAM292 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4565] GAM292 gene, herein designated GAM GENE, encodes a GAM292 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM292 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM292 precursor RNA is designated SEQ ID:264, and is provided hereinbelow with reference to the sequence listing part.

[4566] GAM292 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4567] An enzyme complex designated DICER COMPLEX, dices the GAM292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM292 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM292 RNA is designated SEQ ID:1940, and is provided hereinbelow with reference to the sequence listing part.

[4568] GAM292 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM292 target RNA, herein designated GAM TARGET RNA.
GAM292 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4569] GAM292 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM292 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM292 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM292 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM292 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4570] The complementary binding of GAM292 RNA, herein designated GAM RNA, to target binding sites on GAM292 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM292 target RNA, herein designated GAM TARGET RNA, into GAM292 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4571] It is appreciated that GAM292 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM292 target genes. The mRNA of each one of this plurality of GAM292 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM292 RNA, herein designated GAM RNA, and which when bound by GAM292 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM292 target proteins.

[4572] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM292 gene, herein designated GAM GENE, on one or more GAM292 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4573] It is yet further appreciated that specific functions, and accordingly utilities, of GAM292 correlate with, and may be deduced from, the identity of the target genes which GAM292 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4574] Nucleotide sequences of the GAM292 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM292 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM292 are further described hereinbelow with reference to Table Table1.

[4575] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM292 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4576] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 293 (GAM293) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4577] GAM293 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM293 was detected is described hereinabove with reference to Figs. 2-8.

[4578] GAM293 gene, herein designated GAM GENE, and GAM293 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4579] GAM293 gene, herein designated GAM GENE, encodes a GAM293 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM293 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM293 precursor RNA is desig-

nated SEQ ID:265, and is provided hereinbelow with reference to the sequence listing part.

[4580] GAM293 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4581] An enzyme complex designated DICER COMPLEX, dices the GAM293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM293 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM293 RNA is designated SEQ ID:1941, and is provided hereinbelow with reference to the sequence listing part.

[4582] GAM293 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM293 target RNA, herein designated GAM TARGET RNA. GAM293 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4583] GAM293 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM293 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM293 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM293 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM293

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4584] The complementary binding of GAM293 RNA, herein designated GAM RNA, to target binding sites on GAM293 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM293 target RNA, herein designated GAM TARGET RNA, into GAM293 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4585] It is appreciated that GAM293 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM293 target genes. The mRNA of each one of this plurality of GAM293 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM293 RNA, herein designated GAM RNA, and which when bound by GAM293 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM293 target proteins.

[4586] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM293 gene, herein designated GAM GENE, on one or more GAM293 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4587] It is yet further appreciated that specific functions, and accordingly utilities, of GAM293 correlate with, and may be deduced from, the identity of the target genes which GAM293 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4588] Nucleotide sequences of the GAM293 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM293 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM293 are further described hereinbelow with reference to Table Table1.

[4589] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM293 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4590] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 294 (GAM294) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4591] GAM294 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM294 was detected is described hereinabove with reference to Figs. 2-8.

[4592] GAM294 gene, herein designated GAM GENE, and GAM294 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[4593] GAM294 gene, herein designated GAM GENE, encodes a GAM294 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM294 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM294 precursor RNA is designated SEQ ID:266, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:266 is located at position 58159307 relative to contig NT_026437.9, on chromosome 14.

[4594] GAM294 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4595] An enzyme complex designated DICER COMPLEX, dices

the GAM294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM294 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM294 RNA is designated SEQ ID:1942, and is provided hereinbelow with reference to the sequence listing part.

[4596] GAM294 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM294 target RNA, herein designated GAM TARGET RNA. GAM294 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4597] GAM294 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM294 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM294

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM294 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM294 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4598] The complementary binding of GAM294 RNA, herein designated GAM RNA, to target binding sites on GAM294 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM294 target RNA, herein designated GAM TARGET RNA, into GAM294 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4599] It is appreciated that GAM294 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM294 target genes. The mRNA of each one of this plurality of GAM294 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM294 RNA, herein designated GAM RNA, and which when bound by GAM294 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM294 target proteins.

[4600] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM294 gene, herein designated GAM GENE, on one or more GAM294 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4601] It is yet further appreciated that specific functions, and accordingly utilities, of GAM294 correlate with, and may be deduced from, the identity of the target genes which GAM294 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4602] Nucleotide sequences of the GAM294 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM294 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM294 are further described hereinbelow with reference to Table Table1.

[4603] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM294 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4604] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 295 (GAM295) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4605] GAM295 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM295 was detected is described hereinabove with reference to Figs. 2-8.

[4606] GAM295 gene, herein designated GAM GENE, and GAM295 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4607] GAM295 gene, herein designated GAM GENE, encodes a GAM295 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM295 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM295 precursor RNA is designated SEQ ID:267, and is provided hereinbelow with reference to the sequence listing part.

[4608] GAM295 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4609] An enzyme complex designated DICER COMPLEX, dices the GAM295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM295 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM295 RNA is designated SEQ ID:1943, and is provided hereinbelow with reference to the sequence listing part.

[4610] GAM295 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM295 target RNA, herein designated GAM TARGET RNA. GAM295 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4611] GAM295 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM295 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM295 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM295 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM295 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4612] The complementary binding of GAM295 RNA, herein designated GAM RNA, to target binding sites on GAM295 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM295 target RNA, herein designated GAM TARGET RNA, into GAM295 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4613] It is appreciated that GAM295 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM295 target genes. The mRNA of each one of this plurality of GAM295 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM295 RNA, herein designated GAM RNA, and which when bound by GAM295 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM295 target proteins.

[4614] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM295 gene, herein designated GAM GENE, on one or more GAM295 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4615] It is yet further appreciated that specific functions, and accordingly utilities, of GAM295 correlate with, and may be deduced from, the identity of the target genes which GAM295 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4616] Nucleotide sequences of the GAM295 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM295 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM295 are further described hereinbelow with reference to Table Table1.

[4617] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM295 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4618] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 296 (GAM296) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4619] GAM296 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM296 was detected is described hereinabove with reference to Figs. 2-8.

[4620] GAM296 gene, herein designated GAM GENE, and GAM296 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4621] GAM296 gene, herein designated GAM GENE, encodes a GAM296 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM296 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM296 precursor RNA is designated SEQ ID:268, and is provided hereinbelow with reference to the sequence listing part.

[4622] GAM296 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4623] An enzyme complex designated DICER COMPLEX, dices the GAM296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM296 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM296 RNA is designated SEQ ID:1944, and is provided hereinbelow with reference to the sequence listing part.

[4624] GAM296 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM296 target RNA, herein designated GAM TARGET RNA. GAM296 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4625] GAM296 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM296 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM296 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM296 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM296 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4626] The complementary binding of GAM296 RNA, herein designated GAM RNA, to target binding sites on GAM296 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM296 target RNA, herein designated GAM TARGET RNA, into GAM296 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4627] It is appreciated that GAM296 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM296 target genes. The mRNA of each one of this plurality of GAM296 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM296 RNA, herein designated GAM RNA, and which when bound by

GAM296 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM296 target proteins.

[4628] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM296 gene, herein designated GAM GENE, on one or more GAM296 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4629] It is yet further appreciated that specific functions, and accordingly utilities, of GAM296 correlate with, and may be deduced from, the identity of the target genes which GAM296 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[4630] Nucleotide sequences of the GAM296 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM296 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM296 are further described hereinbelow with reference to Table Table1.

[4631] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM296 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4632] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 297 (GAM297) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4633] GAM297 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM297 was detected is described hereinabove

with reference to Figs. 2-8.

[4634] GAM297 gene, herein designated GAM GENE, and GAM297 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4635] GAM297 gene, herein designated GAM GENE, encodes a GAM297 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM297 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM297 precursor RNA is designated SEQ ID:269, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:269 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[4636] GAM297 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[4637] An enzyme complex designated DICER COMPLEX, dices the GAM297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM297 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM297 RNA is designated SEQ ID:1945, and is provided hereinbelow with reference to the sequence listing part.

[4638] GAM297 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM297 target RNA, herein designated GAM TARGET RNA.
GAM297 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4639] GAM297 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM297 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM297 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM297 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM297 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4640] The complementary binding of GAM297 RNA, herein designated GAM RNA, to target binding sites on GAM297 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM297 target RNA, herein desig-

nated GAM TARGET RNA, into GAM297 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4641] It is appreciated that GAM297 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM297 target genes. The mRNA of each one of this plurality of GAM297 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM297 RNA, herein designated GAM RNA, and which when bound by GAM297 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM297 target proteins.

[4642] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM297 gene, herein designated GAM GENE, on one or more GAM297 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4643] It is yet further appreciated that specific functions, and accordingly utilities, of GAM297 correlate with, and may be deduced from, the identity of the target genes which GAM297 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4644] Nucleotide sequences of the GAM297 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM297 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM297 are further described hereinbelow with reference to Table Table1.

[4645] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM297 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[4646] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 298 (GAM298) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4647] GAM298 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM298 was detected is described hereinabove with reference to Figs. 2-8.

[4648] GAM298 gene, herein designated GAM GENE, and GAM298 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4649] GAM298 gene, herein designated GAM GENE, encodes a GAM298 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM298 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM298 precursor RNA is designated SEQ ID:270, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:270 is located at position 58159291 relative to contig NT_026437.9, on chromosome 14.

[4650] GAM298 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4651] An enzyme complex designated DICER COMPLEX, dices the GAM298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM298 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM298 RNA is designated SEQ ID:1946, and is provided hereinbelow with reference to the sequence listing part.

[4652] GAM298 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM298 target RNA, herein designated GAM TARGET RNA. GAM298 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4653] GAM298 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM298 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM298 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM298 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM298

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4654] The complementary binding of GAM298 RNA, herein designated GAM RNA, to target binding sites on GAM298 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM298 target RNA, herein designated GAM TARGET RNA, into GAM298 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4655] It is appreciated that GAM298 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM298 target genes. The mRNA of each one of this plurality of GAM298 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM298 RNA, herein designated GAM RNA, and which when bound by GAM298 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM298 target proteins.

[4656] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM298 gene, herein designated GAM GENE, on one or more GAM298 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4657] It is yet further appreciated that specific functions, and accordingly utilities, of GAM298 correlate with, and may be deduced from, the identity of the target genes which GAM298 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4658] Nucleotide sequences of the GAM298 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM298 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM298 are further described hereinbelow with reference to Table Table1.

[4659] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM298 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4660] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 299 (GAM299) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4661] GAM299 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM299 was detected is described hereinabove with reference to Figs. 2-8.

[4662] GAM299 gene, herein designated GAM GENE, and GAM299 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[4663] GAM299 gene, herein designated GAM GENE, encodes a GAM299 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM299 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM299 precursor RNA is designated SEQ ID:271, and is provided hereinbelow with reference to the sequence listing part.

[4664] GAM299 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4665] An enzyme complex designated DICER COMPLEX, dices the GAM299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM299 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM299 RNA is designated SEQ ID:1947, and is provided hereinbelow with reference to the sequence listing part.

[4666] GAM299 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM299 target RNA, herein designated GAM TARGET RNA. GAM299 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4667] GAM299 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM299 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM299 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM299 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM299 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4668] The complementary binding of GAM299 RNA, herein designated GAM RNA, to target binding sites on GAM299 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM299 target RNA, herein designated GAM TARGET RNA, into GAM299 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4669] It is appreciated that GAM299 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM299 target genes. The mRNA of each one of this plurality of GAM299 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM299 RNA, herein designated GAM RNA, and which when bound by GAM299 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM299 target proteins.

[4670] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM299 gene, herein designated GAM GENE, on one or more GAM299 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[4671] It is yet further appreciated that specific functions, and accordingly utilities, of GAM299 correlate with, and may be deduced from, the identity of the target genes which GAM299 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4672] Nucleotide sequences of the GAM299 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM299 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM299 are further described hereinbelow with reference to Table Table1.

[4673] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM299 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4674] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 300 (GAM300) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[4675] GAM300 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM300 was detected is described hereinabove with reference to Figs. 2-8.

[4676] GAM300 gene, herein designated GAM GENE, and GAM300 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4677] GAM300 gene, herein designated GAM GENE, encodes a GAM300 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM300 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM300 precursor RNA is designated SEQ ID:272, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:272 is located at position 3428384 relative to contig NT_023666.13, on chromosome 8.

[4678] GAM300 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4679] An enzyme complex designated DICER COMPLEX, dices the GAM300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM300 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM300 RNA is designated SEQ ID:1948, and is provided hereinbelow with reference to the sequence listing part.

[4680] GAM300 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM300 target RNA, herein designated GAM TARGET RNA. GAM300 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4681] GAM300 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM300 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM300 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM300 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM300 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4682] The complementary binding of GAM300 RNA, herein designated GAM RNA, to target binding sites on GAM300 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM300 target RNA, herein designated GAM TARGET RNA, into GAM300 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4683] It is appreciated that GAM300 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM300 target genes. The mRNA of each one of this plurality of GAM300 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM300 RNA, herein designated GAM RNA, and which when bound by GAM300 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM300 target proteins.

[4684] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM300 gene, herein designated GAM GENE, on one or more GAM300 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4685] It is yet further appreciated that specific functions, and accordingly utilities, of GAM300 correlate with, and may be deduced from, the identity of the target genes which GAM300 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4686] Nucleotide sequences of the GAM300 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM300 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM300 are further described hereinbelow with reference to Table Table1.

[4687] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM300 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4688] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 301 (GAM301) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4689] GAM301 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM301 was detected is described hereinabove with reference to Figs. 2-8.

[4690] GAM301 gene, herein designated GAM GENE, and GAM301 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4691] GAM301 gene, herein designated GAM GENE, encodes a GAM301 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM301 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM301 precursor RNA is designated SEQ ID:273, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:273 is located at position 230243 relative to contig NT_033277.3, on chromosome 15.

[4692] GAM301 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4693] An enzyme complex designated DICER COMPLEX, dices the GAM301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM301 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM301 RNA is designated SEQ ID:1949, and is provided hereinbelow with reference to the sequence listing part.

[4694] GAM301 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM301 target RNA, herein designated GAM TARGET RNA. GAM301 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4695] GAM301 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM301 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM301 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM301 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM301 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4696] The complementary binding of GAM301 RNA, herein designated GAM RNA, to target binding sites on GAM301 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM301 target RNA, herein designated GAM TARGET RNA, into GAM301 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4697] It is appreciated that GAM301 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM301 target genes. The mRNA of each one of this plurality of GAM301 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM301 RNA, herein designated GAM RNA, and which when bound by GAM301 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM301 target proteins.

[4698] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM301 gene, herein designated GAM GENE, on one or more GAM301 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4699] It is yet further appreciated that specific functions, and accordingly utilities, of GAM301 correlate with, and may

be deduced from, the identity of the target genes which GAM301 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4700] Nucleotide sequences of the GAM301 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM301 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM301 are further described hereinbelow with reference to Table Table1.

[4701] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM301 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4702] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 302 (GAM302) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4703] GAM302 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM302 was detected is described hereinabove with reference to Figs. 2-8.

[4704] GAM302 gene, herein designated GAM GENE, and GAM302 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4705] GAM302 gene, herein designated GAM GENE, encodes a GAM302 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM302 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM302 precursor RNA is designated SEQ ID:274, and is provided hereinbelow with reference to the sequence listing part.

[4706] GAM302 has 9 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[4707] SEQ ID:98385 detected in mouse EST Accession BF178922.1.

[4708] SEQ ID:98386 detected in mouse EST Accession

BF472526.1.

[4709] SEQ ID:98414 detected in mouse EST Accession AW227328.1.

[4710] SEQ ID:98415 detected in mouse EST Accession BF151056.1.

[4711] SEQ ID:98416 detected in mouse EST Accession BB635316.1.

[4712] SEQ ID:98417 detected in mouse EST Accession BB627306.1.

[4713] SEQ ID:98418 detected in mouse EST Accession BE375279.1.

[4714] SEQ ID:98419 detected in mouse EST Accession BF232633.1.

[4715] SEQ ID:98420 detected in mouse EST Accession BI731628.1.

[4716] GAM302 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[4717] An enzyme complex designated DICER COMPLEX, dices the GAM302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM302 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM302 RNA is designated SEQ ID:1950, and is provided hereinbelow with reference to the sequence listing part.

[4718] GAM302 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM302 target RNA, herein designated GAM TARGET RNA.
GAM302 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4719] GAM302 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM302 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM302 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM302 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM302 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4720] The complementary binding of GAM302 RNA, herein designated GAM RNA, to target binding sites on GAM302 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM302 target RNA, herein desig-

nated GAM TARGET RNA, into GAM302 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4721] It is appreciated that GAM302 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM302 target genes. The mRNA of each one of this plurality of GAM302 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM302 RNA, herein designated GAM RNA, and which when bound by GAM302 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM302 target proteins.

[4722] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM302 gene, herein designated GAM GENE, on one or more GAM302 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4723] It is yet further appreciated that specific functions, and accordingly utilities, of GAM302 correlate with, and may be deduced from, the identity of the target genes which GAM302 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4724] Nucleotide sequences of the GAM302 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM302 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM302 are further described hereinbelow with reference to Table Table1.

[4725] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM302 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[4726] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 303 (GAM303) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4727] GAM303 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM303 was detected is described hereinabove with reference to Figs. 2-8.

[4728] GAM303 gene, herein designated GAM GENE, and GAM303 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4729] GAM303 gene, herein designated GAM GENE, encodes a GAM303 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM303 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM303 precursor RNA is designated SEQ ID:275, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:275 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[4730] GAM303 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4731] An enzyme complex designated DICER COMPLEX, dices the GAM303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM303 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM303 RNA is designated SEQ ID:1951, and is provided hereinbelow with reference to the sequence listing part.

[4732] GAM303 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM303 target RNA, herein designated GAM TARGET RNA. GAM303 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4733] GAM303 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM303 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM303 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM303 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM303

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4734] The complementary binding of GAM303 RNA, herein designated GAM RNA, to target binding sites on GAM303 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM303 target RNA, herein designated GAM TARGET RNA, into GAM303 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4735] It is appreciated that GAM303 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM303 target genes. The mRNA of each one of this plurality of GAM303 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM303 RNA, herein designated GAM RNA, and which when bound by GAM303 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM303 target proteins.

[4736] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM303 gene, herein designated GAM GENE, on one or more GAM303 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4737] It is yet further appreciated that specific functions, and accordingly utilities, of GAM303 correlate with, and may be deduced from, the identity of the target genes which GAM303 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4738] Nucleotide sequences of the GAM303 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM303 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM303 are further described hereinbelow with reference to Table Table1.

[4739] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM303 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4740] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 304 (GAM304) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4741] GAM304 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM304 was detected is described hereinabove with reference to Figs. 2-8.

[4742] GAM304 gene, herein designated GAM GENE, and GAM304 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[4743] GAM304 gene, herein designated GAM GENE, encodes a GAM304 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM304 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM304 precursor RNA is designated SEQ ID:276, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:276 is located at position 1252857 relative to contig NT_029865.8, on chromosome 1.

[4744] GAM304 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4745] An enzyme complex designated DICER COMPLEX, dices

the GAM304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM304 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM304 RNA is designated SEQ ID:1952, and is provided hereinbelow with reference to the sequence listing part.

[4746] GAM304 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM304 target RNA, herein designated GAM TARGET RNA. GAM304 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4747] GAM304 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM304 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM304

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM304 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM304 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4748] The complementary binding of GAM304 RNA, herein designated GAM RNA, to target binding sites on GAM304 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM304 target RNA, herein designated GAM TARGET RNA, into GAM304 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4749] It is appreciated that GAM304 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM304 target genes. The mRNA of each one of this plurality of GAM304 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM304 RNA, herein designated GAM RNA, and which when bound by GAM304 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM304 target proteins.

[4750] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM304 gene, herein designated GAM GENE, on one or more GAM304 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4751] It is yet further appreciated that specific functions, and accordingly utilities, of GAM304 correlate with, and may be deduced from, the identity of the target genes which GAM304 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4752] Nucleotide sequences of the GAM304 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM304 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM304 are further described hereinbelow with reference to Table Table1.

[4753] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM304 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4754] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 305 (GAM305) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4755] GAM305 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM305 was detected is described hereinabove with reference to Figs. 2-8.

[4756] GAM305 gene, herein designated GAM GENE, and GAM305 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4757] GAM305 gene, herein designated GAM GENE, encodes a GAM305 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM305 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM305 precursor RNA is designated SEQ ID:277, and is provided hereinbelow with reference to the sequence listing part.

[4758] GAM305 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4759] An enzyme complex designated DICER COMPLEX, dices the GAM305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM305 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM305 RNA is designated SEQ ID:1953, and is provided hereinbelow with reference to the sequence listing part.

[4760] GAM305 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM305 target RNA, herein designated GAM TARGET RNA. GAM305 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4761] GAM305 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM305 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM305 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM305 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM305 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4762] The complementary binding of GAM305 RNA, herein designated GAM RNA, to target binding sites on GAM305 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM305 target RNA, herein designated GAM TARGET RNA, into GAM305 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4763] It is appreciated that GAM305 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM305 target genes. The mRNA of each one of this plurality of GAM305 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM305 RNA, herein designated GAM RNA, and which when bound by GAM305 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM305 target proteins.

[4764] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM305 gene, herein designated GAM GENE, on one or more GAM305 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4765] It is yet further appreciated that specific functions, and accordingly utilities, of GAM305 correlate with, and may be deduced from, the identity of the target genes which GAM305 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4766] Nucleotide sequences of the GAM305 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM305 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM305 are further described hereinbelow with reference to Table Table1.

[4767] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM305 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4768] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 306 (GAM306) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4769] GAM306 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM306 was detected is described hereinabove with reference to Figs. 2-8.

[4770] GAM306 gene, herein designated GAM GENE, and GAM306 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4771] GAM306 gene, herein designated GAM GENE, encodes a GAM306 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM306 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM306 precursor RNA is designated SEQ ID:278, and is provided hereinbelow with reference to the sequence listing part.

[4772] GAM306 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4773] An enzyme complex designated DICER COMPLEX, dices the GAM306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM306 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM306 RNA is designated SEQ ID:1954, and is provided hereinbelow with reference to the sequence listing part.

[4774] GAM306 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM306 target RNA, herein designated GAM TARGET RNA. GAM306 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4775] GAM306 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM306 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM306 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM306 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM306 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4776] The complementary binding of GAM306 RNA, herein designated GAM RNA, to target binding sites on GAM306 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM306 target RNA, herein designated GAM TARGET RNA, into GAM306 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4777] It is appreciated that GAM306 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM306 target genes. The mRNA of each one of this plurality of GAM306 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM306 RNA, herein designated GAM RNA, and which when bound by

GAM306 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM306 target proteins.

[4778] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM306 gene, herein designated GAM GENE, on one or more GAM306 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4779] It is yet further appreciated that specific functions, and accordingly utilities, of GAM306 correlate with, and may be deduced from, the identity of the target genes which GAM306 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[4780] Nucleotide sequences of the GAM306 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM306 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM306 are further described hereinbelow with reference to Table Table1.

[4781] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM306 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4782] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 307 (GAM307) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4783] GAM307 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM307 was detected is described hereinabove

with reference to Figs. 2-8.

[4784] GAM307 gene, herein designated GAM GENE, and GAM307 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4785] GAM307 gene, herein designated GAM GENE, encodes a GAM307 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM307 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM307 precursor RNA is designated SEQ ID:279, and is provided hereinbelow with reference to the sequence listing part.

[4786] GAM307 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4787] An enzyme complex designated DICER COMPLEX, dices the GAM307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM307 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM307 RNA is designated SEQ ID:1955, and is provided hereinbelow with reference to the sequence listing part.

[4788] GAM307 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM307 target RNA, herein designated GAM TARGET RNA. GAM307 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4789] GAM307 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM307 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM307 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM307 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM307 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4790] The complementary binding of GAM307 RNA, herein designated GAM RNA, to target binding sites on GAM307 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM307 target RNA, herein designated GAM TARGET RNA, into GAM307 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[4791] It is appreciated that GAM307 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM307 target genes. The mRNA of each one of this plurality of GAM307 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM307 RNA, herein designated GAM RNA, and which when bound by GAM307 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM307 target proteins.

[4792] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM307 gene, herein designated GAM GENE, on one or more GAM307 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4793] It is yet further appreciated that specific functions, and accordingly utilities, of GAM307 correlate with, and may be deduced from, the identity of the target genes which GAM307 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4794] Nucleotide sequences of the GAM307 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM307 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM307 are further described hereinbelow with reference to Table Table1.

[4795] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM307 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4796] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 308 (GAM308) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4797] GAM308 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM308 was detected is described hereinabove with reference to Figs. 2-8.

[4798] GAM308 gene, herein designated GAM GENE, and GAM308 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4799] GAM308 gene, herein designated GAM GENE, encodes a GAM308 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM308 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM308 precursor RNA is designated SEQ ID:280, and is provided hereinbelow with reference to the sequence listing part.

[4800] GAM308 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM308 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4801] An enzyme complex designated DICER COMPLEX, dices the GAM308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM308 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM308 RNA is designated SEQ ID:1956, and is provided hereinbelow with reference to the sequence listing part.

[4802] GAM308 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM308 target RNA, herein designated GAM TARGET RNA. GAM308 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4803] GAM308 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM308 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM308 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM308 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM308 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[4804] The complementary binding of GAM308 RNA, herein designated GAM RNA, to target binding sites on GAM308 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM308 target RNA, herein designated GAM TARGET RNA, into GAM308 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4805] It is appreciated that GAM308 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM308 target genes. The mRNA of each one of this plurality of GAM308 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM308 RNA, herein designated GAM RNA, and which when bound by GAM308 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM308 target proteins.

[4806] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM308 gene, herein designated GAM GENE, on one or

more GAM308 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4807] It is yet further appreciated that specific functions, and accordingly utilities, of GAM308 correlate with, and may be deduced from, the identity of the target genes which GAM308 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4808] Nucleotide sequences of the GAM308 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM308 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM308 are further de-

scribed hereinbelow with reference to Table Table1.

[4809] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM308 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4810] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 309 (GAM309) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4811] GAM309 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM309 was detected is described hereinabove with reference to Figs. 2-8.

[4812] GAM309 gene, herein designated GAM GENE, and GAM309 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4813] GAM309 gene, herein designated GAM GENE, encodes a GAM309 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM309 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM309 precursor RNA is designated SEQ ID:281, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:281 is located at position 615200 relative to contig NT_034706.2, on chromosome 4.

[4814] GAM309 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4815] An enzyme complex designated DICER COMPLEX, dices the GAM309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM309 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM309 RNA is designated SEQ ID:1957, and is provided hereinbelow with reference to the sequence listing part.

[4816] GAM309 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM309 target RNA, herein designated GAM TARGET RNA. GAM309 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4817] GAM309 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM309 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM309 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM309 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM309 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4818] The complementary binding of GAM309 RNA, herein designated GAM RNA, to target binding sites on GAM309 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM309 target RNA, herein designated GAM TARGET RNA, into GAM309 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4819] It is appreciated that GAM309 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM309 target genes. The mRNA of each one of this plurality of GAM309 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM309 RNA, herein designated GAM RNA, and which when bound by GAM309 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM309 target proteins.

[4820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM309 gene, herein designated GAM GENE, on one or more GAM309 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4821] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM309 correlate with, and may be deduced from, the identity of the target genes which GAM309 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4822] Nucleotide sequences of the GAM309 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM309 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM309 are further described hereinbelow with reference to Table Table1.

[4823] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM309 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4824] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 310 (GAM310) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4825] GAM310 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM310 was detected is described hereinabove with reference to Figs. 2-8.

[4826] GAM310 gene, herein designated GAM GENE, and GAM310 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4827] GAM310 gene, herein designated GAM GENE, encodes a GAM310 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM310 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM310 precursor RNA is designated SEQ ID:282, and is provided hereinbelow with reference to the sequence listing part.

[4828] GAM310 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4829] An enzyme complex designated DICER COMPLEX, dices the GAM310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM310 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM310 RNA is designated SEQ ID:1958, and is provided hereinbelow with reference to the sequence listing part.

[4830] GAM310 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM310 target RNA, herein designated GAM TARGET RNA. GAM310 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4831] GAM310 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM310 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM310 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM310 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM310 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4832] The complementary binding of GAM310 RNA, herein designated GAM RNA, to target binding sites on GAM310 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM310 target RNA, herein designated GAM TARGET RNA, into GAM310 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4833] It is appreciated that GAM310 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM310 target genes. The mRNA of each one of this plurality of GAM310 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM310 RNA, herein designated GAM RNA, and which when bound by GAM310 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM310 target proteins.

[4834] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM310 gene, herein designated GAM GENE, on one or more GAM310 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4835] It is yet further appreciated that specific functions, and accordingly utilities, of GAM310 correlate with, and may be deduced from, the identity of the target genes which GAM310 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4836] Nucleotide sequences of the GAM310 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM310 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM310 are further described hereinbelow with reference to Table Table1.

[4837] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM310 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4838] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 311 (GAM311) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4839] GAM311 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM311 was detected is described hereinabove with reference to Figs. 2-8.

[4840] GAM311 gene, herein designated GAM GENE, and GAM311 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4841] GAM311 gene, herein designated GAM GENE, encodes a GAM311 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM311 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM311 precursor RNA is designated SEQ ID:283, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:283 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[4842] GAM311 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4843] An enzyme complex designated DICER COMPLEX, dices the GAM311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM311 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM311 RNA is designated SEQ ID:1959, and is provided

hereinbelow with reference to the sequence listing part.

[4844] GAM311 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM311 target RNA, herein designated GAM TARGET RNA. GAM311 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4845] GAM311 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM311 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM311 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM311 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM311 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4846] The complementary binding of GAM311 RNA, herein designated GAM RNA, to target binding sites on GAM311 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM311 target RNA, herein designated GAM TARGET RNA, into GAM311 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4847] It is appreciated that GAM311 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM311 target genes. The mRNA of each one of this plurality of GAM311 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM311 RNA, herein designated GAM RNA, and which when bound by GAM311 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM311 tar-

get proteins.

[4848] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM311 gene, herein designated GAM GENE, on one or more GAM311 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4849] It is yet further appreciated that specific functions, and accordingly utilities, of GAM311 correlate with, and may be deduced from, the identity of the target genes which GAM311 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4850] Nucleotide sequences of the GAM311 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM311 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM311 are further described hereinbelow with reference to Table Table1.

[4851] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM311 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4852] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 312 (GAM312) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4853] GAM312 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM312 was detected is described hereinabove with reference to Figs. 2-8.

[4854] GAM312 gene, herein designated GAM GENE, and

GAM312 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4855] GAM312 gene, herein designated GAM GENE, encodes a GAM312 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM312 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM312 precursor RNA is designated SEQ ID:284, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:284 is located at position 33703788 relative to contig NT_007592.11, on chromosome 6.

[4856] GAM312 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4857] An enzyme complex designated DICER COMPLEX, dices the GAM312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM312 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM312 RNA is designated SEQ ID:1960, and is provided hereinbelow with reference to the sequence listing part.

[4858] GAM312 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM312 target RNA, herein designated GAM TARGET RNA. GAM312 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4859] GAM312 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM312 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM312 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM312 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM312 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4860] The complementary binding of GAM312 RNA, herein designated GAM RNA, to target binding sites on GAM312 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM312 target RNA, herein designated GAM TARGET RNA, into GAM312 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[4861] It is appreciated that GAM312 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM312 target genes. The mRNA of each one of this plurality of GAM312 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM312 RNA, herein designated GAM RNA, and which when bound by GAM312 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM312 target proteins.

[4862] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM312 gene, herein designated GAM GENE, on one or more GAM312 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4863] It is yet further appreciated that specific functions, and accordingly utilities, of GAM312 correlate with, and may be deduced from, the identity of the target genes which GAM312 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4864] Nucleotide sequences of the GAM312 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM312 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM312 are further described hereinbelow with reference to Table Table1.

[4865] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM312 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4866] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 313 (GAM313) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4867] GAM313 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM313 was detected is described hereinabove with reference to Figs. 2-8.

[4868] GAM313 gene, herein designated GAM GENE, and GAM313 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4869] GAM313 gene, herein designated GAM GENE, encodes a GAM313 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM313 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM313 precursor RNA is designated SEQ ID:285, and is provided hereinbelow with reference to the sequence listing part.

[4870] GAM313 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's.

Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[4871] SEQ ID:99376 detected in mouse EST Accession BI691637.1.

[4872] SEQ ID:99378 detected in mouse EST Accession AV301838.1.

[4873] SEQ ID:99379 detected in mouse EST Accession AV247863.1.

[4874] SEQ ID:99380 detected in mouse EST Accession AV342755.1.

[4875] SEQ ID:99381 detected in mouse EST Accession AV146001.1.

[4876] SEQ ID:99385 detected in mouse EST Accession AV146895.1.

[4877] SEQ ID:99395 detected in mouse EST Accession AV312556.1.

[4878] SEQ ID:99396 detected in mouse EST Accession BB050344.1.

[4879] GAM313 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4880] An enzyme complex designated DICER COMPLEX, dices the GAM313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM313 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM313 RNA is designated SEQ ID:1961, and is provided hereinbelow with reference to the sequence listing part.

[4881] GAM313 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM313 target RNA, herein designated GAM TARGET RNA. GAM313 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4882] GAM313 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM313 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM313 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM313 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM313 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4883] The complementary binding of GAM313 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM313 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM313 target RNA, herein designated GAM TARGET RNA, into GAM313 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4884] It is appreciated that GAM313 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM313 target genes. The mRNA of each one of this plurality of GAM313 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM313 RNA, herein designated GAM RNA, and which when bound by GAM313 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM313 target proteins.

[4885] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM313 gene, herein designated GAM GENE, on one or more GAM313 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4886] It is yet further appreciated that specific functions, and accordingly utilities, of GAM313 correlate with, and may be deduced from, the identity of the target genes which GAM313 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4887] Nucleotide sequences of the GAM313 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM313 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM313 are further described hereinbelow with reference to Table Table1.

[4888] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM313 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4889] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 314 (GAM314) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4890] GAM314 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM314 was detected is described hereinabove with reference to Figs. 2-8.

[4891] GAM314 gene, herein designated GAM GENE, and GAM314 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4892] GAM314 gene, herein designated GAM GENE, encodes a GAM314 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM314 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM314 precursor RNA is designated SEQ ID:286, and is provided hereinbelow with reference to the sequence listing part.

[4893] GAM314 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4894] An enzyme complex designated DICER COMPLEX, dices the GAM314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM314 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM314 RNA is designated SEQ ID:1962, and is provided hereinbelow with reference to the sequence listing part.

[4895] GAM314 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM314 target RNA, herein designated GAM TARGET RNA. GAM314 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4896] GAM314 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM314 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM314 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM314 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM314 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4897] The complementary binding of GAM314 RNA, herein designated GAM RNA, to target binding sites on GAM314 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM314 target RNA, herein designated GAM TARGET RNA, into GAM314 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4898] It is appreciated that GAM314 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM314 target genes. The mRNA of each one of this plurality of GAM314 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM314 RNA, herein designated GAM RNA, and which when bound by GAM314 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM314 target proteins.

[4899] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM314 gene, herein designated GAM GENE, on one or more GAM314 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4900] It is yet further appreciated that specific functions, and accordingly utilities, of GAM314 correlate with, and may be deduced from, the identity of the target genes which GAM314 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4901] Nucleotide sequences of the GAM314 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM314 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM314 are further described hereinbelow with reference to Table Table1.

[4902] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM314 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4903] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 315 (GAM315) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4904] GAM315 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM315 was detected is described hereinabove with reference to Figs. 2-8.

[4905] GAM315 gene, herein designated GAM GENE, and GAM315 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4906] GAM315 gene, herein designated GAM GENE, encodes a GAM315 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM315 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM315 precursor RNA is designated SEQ ID:287, and is provided hereinbelow with reference to the sequence listing part.

[4907] GAM315 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4908] An enzyme complex designated DICER COMPLEX, dices

the GAM315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM315 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM315 RNA is designated SEQ ID:1963, and is provided hereinbelow with reference to the sequence listing part.

[4909] GAM315 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM315 target RNA, herein designated GAM TARGET RNA. GAM315 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4910] GAM315 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM315 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM315

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM315 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM315 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4911] The complementary binding of GAM315 RNA, herein designated GAM RNA, to target binding sites on GAM315 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM315 target RNA, herein designated GAM TARGET RNA, into GAM315 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4912] It is appreciated that GAM315 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM315 target genes. The mRNA of each one of this plurality of GAM315 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM315 RNA, herein designated GAM RNA, and which when bound by GAM315 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM315 target proteins.

[4913] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM315 gene, herein designated GAM GENE, on one or more GAM315 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4914] It is yet further appreciated that specific functions, and accordingly utilities, of GAM315 correlate with, and may be deduced from, the identity of the target genes which GAM315 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4915] Nucleotide sequences of the GAM315 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM315 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM315 are further described hereinbelow with reference to Table Table1.

[4916] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM315 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4917] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 316 (GAM316) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4918] GAM316 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM316 was detected is described hereinabove with reference to Figs. 2-8.

[4919] GAM316 gene, herein designated GAM GENE, and GAM316 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4920] GAM316 gene, herein designated GAM GENE, encodes a GAM316 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM316 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM316 precursor RNA is designated SEQ ID:288, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:288 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[4921] GAM316 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4922] An enzyme complex designated DICER COMPLEX, dices the GAM316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM316 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM316 RNA is designated SEQ ID:1964, and is provided hereinbelow with reference to the sequence listing part.

[4923] GAM316 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM316 target RNA, herein designated GAM TARGET RNA.

GAM316 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4924] GAM316 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM316 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM316 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM316 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM316 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4925] The complementary binding of GAM316 RNA, herein designated GAM RNA, to target binding sites on GAM316 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM316 target RNA, herein designated GAM TARGET RNA, into GAM316 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4926] It is appreciated that GAM316 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM316 target genes. The mRNA of each one of this plurality of GAM316 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM316 RNA, herein designated GAM RNA, and which when bound by GAM316 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM316 target proteins.

[4927] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM316 gene, herein designated GAM GENE, on one or more GAM316 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4928] It is yet further appreciated that specific functions, and accordingly utilities, of GAM316 correlate with, and may be deduced from, the identity of the target genes which GAM316 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4929] Nucleotide sequences of the GAM316 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM316 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM316 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM316 are further described hereinbelow with reference to Table Table1.

[4930] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM316 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4931] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 317 (GAM317) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4932] GAM317 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM317 was detected is described hereinabove with reference to Figs. 2-8.

[4933] GAM317 gene, herein designated GAM GENE, and GAM317 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4934] GAM317 gene, herein designated GAM GENE, encodes a GAM317 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM317 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM317 precursor RNA is designated SEQ ID:289, and is provided hereinbelow with reference to the sequence listing part.

[4935] GAM317 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4936] An enzyme complex designated DICER COMPLEX, dices the GAM317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM317 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM317 RNA is designated SEQ ID:1965, and is provided hereinbelow with reference to the sequence listing part.

[4937] GAM317 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM317 target RNA, herein designated GAM TARGET RNA. GAM317 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4938] GAM317 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM317 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM317 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM317 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM317 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4939] The complementary binding of GAM317 RNA, herein designated GAM RNA, to target binding sites on GAM317 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM317 target RNA, herein designated GAM TARGET RNA, into GAM317 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4940] It is appreciated that GAM317 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM317 target genes. The mRNA of each one of this plurality of GAM317 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM317 RNA, herein designated GAM RNA, and which when bound by GAM317 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM317 target proteins.

[4941] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM317 gene, herein designated GAM GENE, on one or more GAM317 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4942] It is yet further appreciated that specific functions, and accordingly utilities, of GAM317 correlate with, and may

be deduced from, the identity of the target genes which GAM317 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4943] Nucleotide sequences of the GAM317 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM317 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM317 are further described hereinbelow with reference to Table Table1.

[4944] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM317 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4945] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 318 (GAM318) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4946] GAM318 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM318 was detected is described hereinabove with reference to Figs. 2-8.

[4947] GAM318 gene, herein designated GAM GENE, and GAM318 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4948] GAM318 gene, herein designated GAM GENE, encodes a GAM318 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM318 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM318 precursor RNA is designated SEQ ID:290, and is provided hereinbelow with reference to the sequence listing part.

[4949] GAM318 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[4950] An enzyme complex designated DICER COMPLEX, dices the GAM318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM318 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM318 RNA is designated SEQ ID:1966, and is provided hereinbelow with reference to the sequence listing part.

[4951] GAM318 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM318 target RNA, herein designated GAM TARGET RNA. GAM318 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4952] GAM318 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM318 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM318 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM318 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM318 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4953] The complementary binding of GAM318 RNA, herein designated GAM RNA, to target binding sites on GAM318 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM318 target RNA, herein desig-

nated GAM TARGET RNA, into GAM318 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4954] It is appreciated that GAM318 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM318 target genes. The mRNA of each one of this plurality of GAM318 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM318 RNA, herein designated GAM RNA, and which when bound by GAM318 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM318 target proteins.

[4955] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM318 gene, herein designated GAM GENE, on one or more GAM318 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4956] It is yet further appreciated that specific functions, and accordingly utilities, of GAM318 correlate with, and may be deduced from, the identity of the target genes which GAM318 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4957] Nucleotide sequences of the GAM318 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM318 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM318 are further described hereinbelow with reference to Table Table1.

[4958] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM318 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[4959] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 319 (GAM319) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4960] GAM319 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM319 was detected is described hereinabove with reference to Figs. 2-8.

[4961] GAM319 gene, herein designated GAM GENE, and GAM319 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4962] GAM319 gene, herein designated GAM GENE, encodes a GAM319 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM319 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM319 precursor RNA is designated SEQ ID:291, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:291 is located at position 4173070 relative to contig NT_022517.13, on chromosome 3.

[4963] GAM319 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4964] An enzyme complex designated DICER COMPLEX, dices the GAM319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM319 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM319 RNA is designated SEQ ID:1967, and is provided hereinbelow with reference to the sequence listing part.

[4965] GAM319 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM319 target RNA, herein designated GAM TARGET RNA. GAM319 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4966] GAM319 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM319 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM319 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM319 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM319

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4967] The complementary binding of GAM319 RNA, herein designated GAM RNA, to target binding sites on GAM319 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM319 target RNA, herein designated GAM TARGET RNA, into GAM319 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4968] It is appreciated that GAM319 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM319 target genes. The mRNA of each one of this plurality of GAM319 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM319 RNA, herein designated GAM RNA, and which when bound by GAM319 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM319 target proteins.

[4969] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM319 gene, herein designated GAM GENE, on one or more GAM319 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4970] It is yet further appreciated that specific functions, and accordingly utilities, of GAM319 correlate with, and may be deduced from, the identity of the target genes which GAM319 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4971] Nucleotide sequences of the GAM319 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM319 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM319 are further described hereinbelow with reference to Table Table1.

[4972] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM319 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4973] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 320 (GAM320) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[4974] GAM320 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM320 was detected is described hereinabove with reference to Figs. 2-8.

[4975] GAM320 gene, herein designated GAM GENE, and GAM320 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[4976] GAM320 gene, herein designated GAM GENE, encodes a GAM320 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM320 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM320 precursor RNA is designated SEQ ID:292, and is provided hereinbelow with reference to the sequence listing part.

[4977] GAM320 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4978] An enzyme complex designated DICER COMPLEX, dices the GAM320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM320 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM320 RNA is designated SEQ ID:1968, and is provided hereinbelow with reference to the sequence listing part.

[4979] GAM320 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM320 target RNA, herein designated GAM TARGET RNA. GAM320 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4980] GAM320 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM320 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM320 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM320 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM320 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4981] The complementary binding of GAM320 RNA, herein designated GAM RNA, to target binding sites on GAM320 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM320 target RNA, herein designated GAM TARGET RNA, into GAM320 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4982] It is appreciated that GAM320 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM320 target genes. The mRNA of each one of this plurality of GAM320 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM320 RNA, herein designated GAM RNA, and which when bound by GAM320 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM320 target proteins.

[4983] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM320 gene, herein designated GAM GENE, on one or more GAM320 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[4984] It is yet further appreciated that specific functions, and accordingly utilities, of GAM320 correlate with, and may be deduced from, the identity of the target genes which GAM320 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4985] Nucleotide sequences of the GAM320 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM320 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM320 are further described hereinbelow with reference to Table Table1.

[4986] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM320 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[4987] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 321 (GAM321) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[4988] GAM321 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM321 was detected is described hereinabove with reference to Figs. 2-8.

[4989] GAM321 gene, herein designated GAM GENE, and GAM321 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[4990] GAM321 gene, herein designated GAM GENE, encodes a GAM321 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM321 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM321 precursor RNA is designated SEQ ID:293, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:293 is located at position 58159291 relative to contig NT_026437.9, on chromosome 14.

[4991] GAM321 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[4992] An enzyme complex designated DICER COMPLEX, dices the GAM321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM321 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM321 RNA is designated SEQ ID:1969, and is provided hereinbelow with reference to the sequence listing part.

[4993] GAM321 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM321 target RNA, herein designated GAM TARGET RNA. GAM321 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[4994] GAM321 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM321 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM321 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM321 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM321 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[4995] The complementary binding of GAM321 RNA, herein designated GAM RNA, to target binding sites on GAM321 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM321 target RNA, herein designated GAM TARGET RNA, into GAM321 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[4996] It is appreciated that GAM321 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM321 target genes. The mRNA of each one of this plurality of GAM321 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM321 RNA, herein designated GAM RNA, and which when bound by GAM321 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM321 target proteins.

[4997] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM321 gene, herein designated GAM GENE, on one or more GAM321 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[4998] It is yet further appreciated that specific functions, and accordingly utilities, of GAM321 correlate with, and may be deduced from, the identity of the target genes which GAM321 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[4999] Nucleotide sequences of the GAM321 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM321 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM321 are further described hereinbelow with reference to Table Table1.

[5000] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM321 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5001] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 322 (GAM322) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5002] GAM322 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM322 was detected is described hereinabove with reference to Figs. 2-8.

[5003] GAM322 gene, herein designated GAM GENE, and GAM322 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5004] GAM322 gene, herein designated GAM GENE, encodes a GAM322 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM322 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM322 precursor RNA is designated SEQ ID:294, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:294 is located at position 58159295 relative to contig NT_026437.9, on chromosome 14.

[5005] GAM322 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5006] An enzyme complex designated DICER COMPLEX, dices the GAM322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM322 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM322 RNA is designated SEQ ID:1970, and is provided hereinbelow with reference to the sequence listing part.

[5007] GAM322 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM322 target RNA, herein designated GAM TARGET RNA. GAM322 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5008] GAM322 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM322 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM322 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM322 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM322 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5009] The complementary binding of GAM322 RNA, herein designated GAM RNA, to target binding sites on GAM322 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM322 target RNA, herein designated GAM TARGET RNA, into GAM322 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5010] It is appreciated that GAM322 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM322 target genes. The mRNA of each one of this plurality of GAM322 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM322 RNA, herein designated GAM RNA, and which when bound by GAM322 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM322 target proteins.

[5011] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM322 gene, herein designated GAM GENE, on one or more GAM322 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5012] It is yet further appreciated that specific functions, and accordingly utilities, of GAM322 correlate with, and may

be deduced from, the identity of the target genes which GAM322 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5013] Nucleotide sequences of the GAM322 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM322 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM322 are further described hereinbelow with reference to Table Table1.

[5014] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM322 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5015] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 323 (GAM323) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5016] GAM323 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM323 was detected is described hereinabove with reference to Figs. 2-8.

[5017] GAM323 gene, herein designated GAM GENE, and GAM323 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5018] GAM323 gene, herein designated GAM GENE, encodes a GAM323 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM323 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM323 precursor RNA is designated SEQ ID:295, and is provided hereinbelow with reference to the sequence listing part.

[5019] GAM323 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[5020] An enzyme complex designated DICER COMPLEX, dices the GAM323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM323 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM323 RNA is designated SEQ ID:1971, and is provided hereinbelow with reference to the sequence listing part.

[5021] GAM323 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM323 target RNA, herein designated GAM TARGET RNA.
GAM323 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5022] GAM323 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM323 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM323 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM323 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM323 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5023] The complementary binding of GAM323 RNA, herein designated GAM RNA, to target binding sites on GAM323 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM323 target RNA, herein desig-

nated GAM TARGET RNA, into GAM323 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5024] It is appreciated that GAM323 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM323 target genes. The mRNA of each one of this plurality of GAM323 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM323 RNA, herein designated GAM RNA, and which when bound by GAM323 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM323 target proteins.

[5025] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM323 gene, herein designated GAM GENE, on one or more GAM323 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5026] It is yet further appreciated that specific functions, and accordingly utilities, of GAM323 correlate with, and may be deduced from, the identity of the target genes which GAM323 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5027] Nucleotide sequences of the GAM323 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM323 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM323 are further described hereinbelow with reference to Table Table1.

[5028] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM323 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[5029] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 324 (GAM324) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5030] GAM324 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM324 was detected is described hereinabove with reference to Figs. 2-8.

[5031] GAM324 gene, herein designated GAM GENE, and GAM324 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5032] GAM324 gene, herein designated GAM GENE, encodes a GAM324 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM324 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM324 precursor RNA is designated SEQ ID:296, and is provided hereinbelow with reference to the sequence listing part.

[5033] GAM324 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5034] An enzyme complex designated DICER COMPLEX, dices the GAM324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM324 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 96%) nucleotide sequence of GAM324 RNA is designated SEQ ID:1972, and is provided hereinbelow with reference to the sequence listing part.

[5035] GAM324 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM324

target RNA, herein designated GAM TARGET RNA.

GAM324 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5036] GAM324 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM324 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM324 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM324 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM324 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5037] The complementary binding of GAM324 RNA, herein designated GAM RNA, to target binding sites on GAM324 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM324 target RNA, herein designated GAM TARGET RNA, into GAM324 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5038] It is appreciated that GAM324 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM324 target genes. The mRNA of each one of this plurality of GAM324 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM324 RNA, herein designated GAM RNA, and which when bound by GAM324 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM324 target proteins.

[5039] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM324 gene, herein designated GAM GENE, on one or more GAM324 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5040] It is yet further appreciated that specific functions, and accordingly utilities, of GAM324 correlate with, and may be deduced from, the identity of the target genes which GAM324 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5041] Nucleotide sequences of the GAM324 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM324 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM324 are further described hereinbelow with reference to Table Table1.

[5042] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM324 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5043] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 325 (GAM325) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5044] GAM325 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM325 was detected is described hereinabove with reference to Figs. 2-8.

[5045] GAM325 gene, herein designated GAM GENE, and GAM325 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5046] GAM325 gene, herein designated GAM GENE, encodes a

GAM325 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM325 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM325 precursor RNA is designated SEQ ID:297, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:297 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[5047] GAM325 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5048] An enzyme complex designated DICER COMPLEX, dices the GAM325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM325 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM325 RNA is designated SEQ ID:1973, and is provided hereinbelow with reference to the sequence listing part.

[5049] GAM325 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM325 target RNA, herein designated GAM TARGET RNA. GAM325 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5050] GAM325 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM325 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM325 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM325 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM325 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5051] The complementary binding of GAM325 RNA, herein designated GAM RNA, to target binding sites on GAM325 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM325 target RNA, herein designated GAM TARGET RNA, into GAM325 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5052] It is appreciated that GAM325 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM325 target genes. The mRNA of each one of this plurality of GAM325 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM325 RNA, herein designated GAM RNA, and which when bound by GAM325 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM325 target proteins.

[5053] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM325 gene, herein designated GAM GENE, on one or more GAM325 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[5054] It is yet further appreciated that specific functions, and accordingly utilities, of GAM325 correlate with, and may be deduced from, the identity of the target genes which GAM325 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5055] Nucleotide sequences of the GAM325 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM325 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM325 are further described hereinbelow with reference to Table Table1.

[5056] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM325 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5057] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 326 (GAM326) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[5058] GAM326 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM326 was detected is described hereinabove with reference to Figs. 2-8.

[5059] GAM326 gene, herein designated GAM GENE, and GAM326 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5060] GAM326 gene, herein designated GAM GENE, encodes a GAM326 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM326 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM326 precursor RNA is designated SEQ ID:298, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:298 is located at position 58159291 relative to contig NT_026437.9, on chromosome 14.

[5061] GAM326 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5062] An enzyme complex designated DICER COMPLEX, dices the GAM326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM326 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM326 RNA is designated SEQ ID:1974, and is provided hereinbelow with reference to the sequence listing part.

[5063] GAM326 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM326 target RNA, herein designated GAM TARGET RNA. GAM326 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5064] GAM326 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM326 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM326 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM326 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM326 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5065] The complementary binding of GAM326 RNA, herein designated GAM RNA, to target binding sites on GAM326 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM326 target RNA, herein designated GAM TARGET RNA, into GAM326 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5066] It is appreciated that GAM326 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM326 target genes. The mRNA of each one of this plurality of GAM326 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM326 RNA, herein designated GAM RNA, and which when bound by GAM326 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM326 target proteins.

[5067] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM326 gene, herein designated GAM GENE, on one or more GAM326 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5068] It is yet further appreciated that specific functions, and accordingly utilities, of GAM326 correlate with, and may be deduced from, the identity of the target genes which GAM326 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5069] Nucleotide sequences of the GAM326 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM326 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM326 are further described hereinbelow with reference to Table Table1.

[5070] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM326 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5071] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 327 (GAM327) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5072] GAM327 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM327 was detected is described hereinabove with reference to Figs. 2-8.

[5073] GAM327 gene, herein designated GAM GENE, and GAM327 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5074] GAM327 gene, herein designated GAM GENE, encodes a GAM327 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM327 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM327 precursor RNA is designated SEQ ID:299, and is provided hereinbelow with reference to the sequence listing part.

[5075] GAM327 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[5076] SEQ ID:98615 detected in mouse EST Accession AL022643.1.

[5077] SEQ ID:98616 detected in mouse EST Accession BI453661.1.

[5078] SEQ ID:98621 detected in mouse EST Accession AI060752.1.

[5079] SEQ ID:98622 detected in mouse EST Accession BF452099.1.

[5080] SEQ ID:98624 detected in mouse EST Accession BE531895.1.

[5081] SEQ ID:98625 detected in mouse EST Accession AA546767.1.

[5082] SEQ ID:98626 detected in mouse EST Accession

AA184326.1.

[5083] GAM327 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5084] An enzyme complex designated DICER COMPLEX, dices the GAM327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM327 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM327 RNA is designated SEQ ID:1975, and is provided hereinbelow with reference to the sequence listing part.

[5085] GAM327 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM327 target RNA, herein designated GAM TARGET RNA.

GAM327 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5086] GAM327 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM327 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM327 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM327 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM327 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5087] The complementary binding of GAM327 RNA, herein designated GAM RNA, to target binding sites on GAM327 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM327 target RNA, herein designated GAM TARGET RNA, into GAM327 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5088] It is appreciated that GAM327 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM327 target genes. The mRNA of each one of this plurality of GAM327 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM327 RNA, herein designated GAM RNA, and which when bound by GAM327 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM327 target proteins.

[5089] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM327 gene, herein designated GAM GENE, on one or more GAM327 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5090] It is yet further appreciated that specific functions, and accordingly utilities, of GAM327 correlate with, and may be deduced from, the identity of the target genes which GAM327 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5091] Nucleotide sequences of the GAM327 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM327 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM327 are further described hereinbelow with reference to Table Table1.

[5092] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM327 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5093] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 328 (GAM328) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5094] GAM328 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM328 was detected is described hereinabove with reference to Figs. 2-8.

[5095] GAM328 gene, herein designated GAM GENE, and GAM328 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5096] GAM328 gene, herein designated GAM GENE, encodes a GAM328 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM328 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM328 precursor RNA is designated SEQ ID:300, and is provided hereinbelow with reference to the sequence listing part.

[5097] GAM328 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5098] An enzyme complex designated DICER COMPLEX, dices the GAM328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM328 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM328 RNA is designated SEQ ID:1976, and is provided hereinbelow with reference to the sequence listing part.

[5099] GAM328 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM328 target RNA, herein designated GAM TARGET RNA. GAM328 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5100] GAM328 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM328 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM328 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM328 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM328 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5101] The complementary binding of GAM328 RNA, herein designated GAM RNA, to target binding sites on GAM328 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM328 target RNA, herein designated GAM TARGET RNA, into GAM328 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5102] It is appreciated that GAM328 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM328 target genes. The mRNA of each one of this plu-

rality of GAM328 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM328 RNA, herein designated GAM RNA, and which when bound by GAM328 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM328 target proteins.

[5103] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM328 gene, herein designated GAM GENE, on one or more GAM328 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5104] It is yet further appreciated that specific functions, and accordingly utilities, of GAM328 correlate with, and may be deduced from, the identity of the target genes which GAM328 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5105] Nucleotide sequences of the GAM328 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM328 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM328 are further described hereinbelow with reference to Table Table1.

[5106] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM328 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5107] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 329 (GAM329) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[5108] GAM329 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM329 was detected is described hereinabove with reference to Figs. 2-8.

[5109] GAM329 gene, herein designated GAM GENE, and GAM329 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5110] GAM329 gene, herein designated GAM GENE, encodes a GAM329 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM329 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM329 precursor RNA is designated SEQ ID:301, and is provided hereinbelow with reference to the sequence listing part.

[5111] GAM329 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5112] An enzyme complex designated DICER COMPLEX, dices the GAM329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM329 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM329 RNA is designated SEQ ID:1977, and is provided hereinbelow with reference to the sequence listing part.

[5113] GAM329 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM329 target RNA, herein designated GAM TARGET RNA. GAM329 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5114] GAM329 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM329 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM329 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM329 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM329 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5115] The complementary binding of GAM329 RNA, herein designated GAM RNA, to target binding sites on GAM329 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM329 target RNA, herein designated GAM TARGET RNA, into GAM329 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5116] It is appreciated that GAM329 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM329 target genes. The mRNA of each one of this plurality of GAM329 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM329 RNA, herein designated GAM RNA, and which when bound by GAM329 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM329 target proteins.

[5117] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM329 gene, herein designated GAM GENE, on one or more GAM329 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5118] It is yet further appreciated that specific functions, and accordingly utilities, of GAM329 correlate with, and may be deduced from, the identity of the target genes which GAM329 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5119] Nucleotide sequences of the GAM329 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM329 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM329 are further described hereinbelow with reference to Table Table1.

[5120] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM329 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5121] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 330 (GAM330) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5122] GAM330 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM330 was detected is described hereinabove with reference to Figs. 2-8.

[5123] GAM330 gene, herein designated GAM GENE, and GAM330 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5124] GAM330 gene, herein designated GAM GENE, encodes a GAM330 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM330 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM330 precursor RNA is designated SEQ ID:302, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:302 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[5125] GAM330 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5126] An enzyme complex designated DICER COMPLEX, dices the GAM330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM330 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM330 RNA is designated SEQ ID:1978, and is provided hereinbelow with reference to the sequence listing part.

[5127] GAM330 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM330 target RNA, herein designated GAM TARGET RNA.
GAM330 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[5128] GAM330 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM330 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM330 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM330 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM330 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5129] The complementary binding of GAM330 RNA, herein designated GAM RNA, to target binding sites on GAM330 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM330 target RNA, herein designated GAM TARGET RNA, into GAM330 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5130] It is appreciated that GAM330 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM330 target genes. The mRNA of each one of this plurality of GAM330 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM330 RNA, herein designated GAM RNA, and which when bound by GAM330 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM330 target proteins.

[5131] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM330 gene, herein designated GAM GENE, on one or more GAM330 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5132] It is yet further appreciated that specific functions, and accordingly utilities, of GAM330 correlate with, and may be deduced from, the identity of the target genes which GAM330 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5133] Nucleotide sequences of the GAM330 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM330 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM330 are further described hereinbelow with reference to Table Table1.

[5134] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM330 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5135] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 331 (GAM331) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5136] GAM331 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM331 was detected is described hereinabove with reference to Figs. 2-8.

[5137] GAM331 gene, herein designated GAM GENE, and GAM331 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5138] GAM331 gene, herein designated GAM GENE, encodes a GAM331 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM331 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM331 precursor RNA is designated SEQ ID:303, and is provided hereinbelow with reference to the sequence listing part.

[5139] GAM331 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5140] An enzyme complex designated DICER COMPLEX, dices the GAM331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM331 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM331 RNA is designated SEQ ID:1979, and is provided

hereinbelow with reference to the sequence listing part.

[5141] GAM331 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM331 target RNA, herein designated GAM TARGET RNA.
GAM331 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5142] GAM331 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM331 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM331 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM331 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM331 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5143] The complementary binding of GAM331 RNA, herein designated GAM RNA, to target binding sites on GAM331 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM331 target RNA, herein designated GAM TARGET RNA, into GAM331 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5144] It is appreciated that GAM331 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM331 target genes. The mRNA of each one of this plurality of GAM331 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM331 RNA, herein designated GAM RNA, and which when bound by GAM331 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM331 tar-

get proteins.

[5145] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM331 gene, herein designated GAM GENE, on one or more GAM331 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5146] It is yet further appreciated that specific functions, and accordingly utilities, of GAM331 correlate with, and may be deduced from, the identity of the target genes which GAM331 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5147] Nucleotide sequences of the GAM331 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM331 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM331 are further described hereinbelow with reference to Table Table1.

[5148] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM331 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5149] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 332 (GAM332) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5150] GAM332 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM332 was detected is described hereinabove with reference to Figs. 2-8.

[5151] GAM332 gene, herein designated GAM GENE, and

GAM332 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5152] GAM332 gene, herein designated GAM GENE, encodes a GAM332 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM332 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM332 precursor RNA is designated SEQ ID:304, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:304 is located at position 2025400 relative to contig NT_005832.12, on chromosome 3.

[5153] GAM332 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5154] An enzyme complex designated DICER COMPLEX, dices the GAM332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM332 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM332 RNA is designated SEQ ID:1980, and is provided hereinbelow with reference to the sequence listing part.

[5155] GAM332 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM332 target RNA, herein designated GAM TARGET RNA. GAM332 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5156] GAM332 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM332 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM332 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM332 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM332 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5157] The complementary binding of GAM332 RNA, herein designated GAM RNA, to target binding sites on GAM332 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM332 target RNA, herein designated GAM TARGET RNA, into GAM332 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[5158] It is appreciated that GAM332 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM332 target genes. The mRNA of each one of this plurality of GAM332 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM332 RNA, herein designated GAM RNA, and which when bound by GAM332 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM332 target proteins.

[5159] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM332 gene, herein designated GAM GENE, on one or more GAM332 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5160] It is yet further appreciated that specific functions, and accordingly utilities, of GAM332 correlate with, and may be deduced from, the identity of the target genes which GAM332 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5161] Nucleotide sequences of the GAM332 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM332 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM332 are further described hereinbelow with reference to Table Table1.

[5162] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM332 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5163] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 333 (GAM333) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5164] GAM333 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM333 was detected is described hereinabove with reference to Figs. 2-8.

[5165] GAM333 gene, herein designated GAM GENE, and GAM333 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5166] GAM333 gene, herein designated GAM GENE, encodes a GAM333 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM333 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM333 precursor RNA is designated SEQ ID:305, and is provided hereinbelow with reference to the sequence listing part.

[5167] GAM333 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM333 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5168] An enzyme complex designated DICER COMPLEX, dices the GAM333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM333 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM333 RNA is designated SEQ ID:1981, and is provided hereinbelow with reference to the sequence listing part.

[5169] GAM333 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM333 target RNA, herein designated GAM TARGET RNA. GAM333 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5170] GAM333 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM333 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM333 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM333 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM333 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[5171] The complementary binding of GAM333 RNA, herein designated GAM RNA, to target binding sites on GAM333 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM333 target RNA, herein designated GAM TARGET RNA, into GAM333 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5172] It is appreciated that GAM333 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM333 target genes. The mRNA of each one of this plurality of GAM333 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM333 RNA, herein designated GAM RNA, and which when bound by GAM333 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM333 target proteins.

[5173] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM333 gene, herein designated GAM GENE, on one or

more GAM333 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5174] It is yet further appreciated that specific functions, and accordingly utilities, of GAM333 correlate with, and may be deduced from, the identity of the target genes which GAM333 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5175] Nucleotide sequences of the GAM333 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM333 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM333 are further de-

scribed hereinbelow with reference to Table Table1.

[5176] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM333 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5177] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 334 (GAM334) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5178] GAM334 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM334 was detected is described hereinabove with reference to Figs. 2-8.

[5179] GAM334 gene, herein designated GAM GENE, and GAM334 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5180] GAM334 gene, herein designated GAM GENE, encodes a GAM334 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM334 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM334 precursor RNA is designated SEQ ID:306, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:306 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[5181] GAM334 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5182] An enzyme complex designated DICER COMPLEX, dices the GAM334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM334 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM334 RNA is designated SEQ ID:1982, and is provided hereinbelow with reference to the sequence listing part.

[5183] GAM334 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM334 target RNA, herein designated GAM TARGET RNA. GAM334 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5184] GAM334 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM334 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM334 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM334 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM334 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5185] The complementary binding of GAM334 RNA, herein designated GAM RNA, to target binding sites on GAM334 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM334 target RNA, herein designated GAM TARGET RNA, into GAM334 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5186] It is appreciated that GAM334 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM334 target genes. The mRNA of each one of this plurality of GAM334 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM334 RNA, herein designated GAM RNA, and which when bound by GAM334 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM334 target proteins.

[5187] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM334 gene, herein designated GAM GENE, on one or more GAM334 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5188] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM334 correlate with, and may be deduced from, the identity of the target genes which GAM334 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5189] Nucleotide sequences of the GAM334 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM334 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM334 are further described hereinbelow with reference to Table Table1.

[5190] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM334 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5191] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 335 (GAM335) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5192] GAM335 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM335 was detected is described hereinabove with reference to Figs. 2-8.

[5193] GAM335 gene, herein designated GAM GENE, and GAM335 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5194] GAM335 gene, herein designated GAM GENE, encodes a GAM335 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM335 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM335 precursor RNA is designated SEQ ID:307, and is provided hereinbelow with reference to the sequence listing part.

[5195] GAM335 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5196] An enzyme complex designated DICER COMPLEX, dices the GAM335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM335 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM335 RNA is designated SEQ ID:1983, and is provided hereinbelow with reference to the sequence listing part.

[5197] GAM335 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM335 target RNA, herein designated GAM TARGET RNA. GAM335 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5198] GAM335 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM335 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM335 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM335 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM335 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5199] The complementary binding of GAM335 RNA, herein designated GAM RNA, to target binding sites on GAM335 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM335 target RNA, herein designated GAM TARGET RNA, into GAM335 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5200] It is appreciated that GAM335 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM335 target genes. The mRNA of each one of this plurality of GAM335 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM335 RNA, herein designated GAM RNA, and which when bound by GAM335 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM335 target proteins.

[5201] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM335 gene, herein designated GAM GENE, on one or more GAM335 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5202] It is yet further appreciated that specific functions, and accordingly utilities, of GAM335 correlate with, and may be deduced from, the identity of the target genes which GAM335 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5203] Nucleotide sequences of the GAM335 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM335 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM335 are further described hereinbelow with reference to Table Table1.

[5204] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM335 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5205] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 336 (GAM336) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5206] GAM336 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM336 was detected is described hereinabove with reference to Figs. 2-8.

[5207] GAM336 gene, herein designated GAM GENE, and GAM336 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5208] GAM336 gene, herein designated GAM GENE, encodes a GAM336 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM336 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM336 precursor RNA is designated SEQ ID:308, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:308 is located at position 22523325 relative to contig NT_011362.7, on chromosome 20.

[5209] GAM336 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5210] An enzyme complex designated DICER COMPLEX, dices the GAM336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM336 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM336 RNA is designated SEQ ID:1984, and is provided

hereinbelow with reference to the sequence listing part.

[5211] GAM336 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM336 target RNA, herein designated GAM TARGET RNA.
GAM336 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5212] GAM336 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM336 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM336 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM336 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM336 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5213] The complementary binding of GAM336 RNA, herein designated GAM RNA, to target binding sites on GAM336 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM336 target RNA, herein designated GAM TARGET RNA, into GAM336 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5214] It is appreciated that GAM336 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM336 target genes. The mRNA of each one of this plurality of GAM336 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM336 RNA, herein designated GAM RNA, and which when bound by GAM336 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM336 tar-

get proteins.

[5215] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM336 gene, herein designated GAM GENE, on one or more GAM336 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5216] It is yet further appreciated that specific functions, and accordingly utilities, of GAM336 correlate with, and may be deduced from, the identity of the target genes which GAM336 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5217] Nucleotide sequences of the GAM336 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM336 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM336 are further described hereinbelow with reference to Table Table1.

[5218] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM336 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5219] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 337 (GAM337) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5220] GAM337 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM337 was detected is described hereinabove with reference to Figs. 2-8.

[5221] GAM337 gene, herein designated GAM GENE, and

GAM337 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5222] GAM337 gene, herein designated GAM GENE, encodes a GAM337 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM337 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM337 precursor RNA is designated SEQ ID:309, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:309 is located at position 2812807 relative to contig NT_033903.3, on chromosome 11.

[5223] GAM337 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5224] An enzyme complex designated DICER COMPLEX, dices the GAM337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM337 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM337 RNA is designated SEQ ID:1985, and is provided hereinbelow with reference to the sequence listing part.

[5225] GAM337 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM337 target RNA, herein designated GAM TARGET RNA. GAM337 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5226] GAM337 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM337 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM337 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM337 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM337 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5227] The complementary binding of GAM337 RNA, herein designated GAM RNA, to target binding sites on GAM337 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM337 target RNA, herein designated GAM TARGET RNA, into GAM337 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[5228] It is appreciated that GAM337 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM337 target genes. The mRNA of each one of this plurality of GAM337 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM337 RNA, herein designated GAM RNA, and which when bound by GAM337 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM337 target proteins.

[5229] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM337 gene, herein designated GAM GENE, on one or more GAM337 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5230] It is yet further appreciated that specific functions, and accordingly utilities, of GAM337 correlate with, and may be deduced from, the identity of the target genes which GAM337 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5231] Nucleotide sequences of the GAM337 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM337 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM337 are further described hereinbelow with reference to Table Table1.

[5232] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM337 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5233] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 338 (GAM338) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5234] GAM338 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM338 was detected is described hereinabove with reference to Figs. 2-8.

[5235] GAM338 gene, herein designated GAM GENE, and GAM338 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5236] GAM338 gene, herein designated GAM GENE, encodes a GAM338 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM338 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM338 precursor RNA is designated SEQ ID:310, and is provided hereinbelow with reference to the sequence listing part.

[5237] GAM338 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's.

Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[5238] SEQ ID:98217 detected in mouse EST Accession BE862202.1.

[5239] SEQ ID:98218 detected in mouse EST Accession AW229351.1.

[5240] SEQ ID:98219 detected in mouse EST Accession BI413638.1.

[5241] SEQ ID:98220 detected in mouse EST Accession BG242453.1.

[5242] GAM338 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5243] An enzyme complex designated DICER COMPLEX, dices the GAM338 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM338 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM338 RNA is designated SEQ ID:1986, and is provided hereinbelow with reference to the sequence listing part.

[5244] GAM338 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM338 target RNA, herein designated GAM TARGET RNA. GAM338 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5245] GAM338 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM338 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM338 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM338 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM338 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5246] The complementary binding of GAM338 RNA, herein designated GAM RNA, to target binding sites on GAM338 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM338 target RNA, herein designated GAM TARGET RNA, into GAM338 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5247] It is appreciated that GAM338 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM338 target genes. The mRNA of each one of this plurality of GAM338 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM338 RNA, herein designated GAM RNA, and which when bound by GAM338 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM338 target proteins.

[5248] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM338 gene, herein designated GAM GENE, on one or more GAM338 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5249] It is yet further appreciated that specific functions, and accordingly utilities, of GAM338 correlate with, and may be deduced from, the identity of the target genes which GAM338 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5250] Nucleotide sequences of the GAM338 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM338 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM338 are further described hereinbelow with reference to Table Table1.

[5251] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM338 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5252] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

339 (GAM339) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5253] GAM339 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM339 was detected is described hereinabove with reference to Figs. 2-8.

[5254] GAM339 gene, herein designated GAM GENE, and GAM339 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5255] GAM339 gene, herein designated GAM GENE, encodes a GAM339 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM339 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM339 precursor RNA is designated SEQ ID:311, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:311 is located at position 154787 relative to contig NT_034776.2, on chromosome 5.

[5256] GAM339 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM339 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5257] An enzyme complex designated DICER COMPLEX, dices the GAM339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM339 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM339 RNA is designated SEQ ID:1987, and is provided hereinbelow with reference to the sequence listing part.

[5258] GAM339 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM339 target RNA, herein designated GAM TARGET RNA. GAM339 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5259] GAM339 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM339 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM339 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM339 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM339 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[5260] The complementary binding of GAM339 RNA, herein designated GAM RNA, to target binding sites on GAM339 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM339 target RNA, herein designated GAM TARGET RNA, into GAM339 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5261] It is appreciated that GAM339 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM339 target genes. The mRNA of each one of this plurality of GAM339 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM339 RNA, herein designated GAM RNA, and which when bound by GAM339 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM339 target proteins.

[5262] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM339 gene, herein designated GAM GENE, on one or

more GAM339 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5263] It is yet further appreciated that specific functions, and accordingly utilities, of GAM339 correlate with, and may be deduced from, the identity of the target genes which GAM339 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5264] Nucleotide sequences of the GAM339 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM339 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM339 are further de-

scribed hereinbelow with reference to Table Table1.

[5265] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM339 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5266] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 340 (GAM340) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5267] GAM340 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM340 was detected is described hereinabove with reference to Figs. 2-8.

[5268] GAM340 gene, herein designated GAM GENE, and GAM340 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5269] GAM340 gene, herein designated GAM GENE, encodes a GAM340 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM340 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM340 precursor RNA is designated SEQ ID:312, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:312 is located at position 1235058 relative to contig NT_009526.11, on chromosome 12.

[5270] GAM340 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[5271] SEQ ID:99183 detected in mouse EST Accession BI965972.1.

[5272] SEQ ID:99184 detected in mouse EST Accession AI326210.1.

[5273] SEQ ID:99185 detected in mouse EST Accession BI965652.1.

[5274] GAM340 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5275] An enzyme complex designated DICER COMPLEX, dices the GAM340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM340 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM340 RNA is designated SEQ ID:1988, and is provided hereinbelow with reference to the sequence listing part.

[5276] GAM340 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM340 target RNA, herein designated GAM TARGET RNA. GAM340 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5277] GAM340 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM340 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM340 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM340 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM340 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5278] The complementary binding of GAM340 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM340 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM340 target RNA, herein designated GAM TARGET RNA, into GAM340 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5279] It is appreciated that GAM340 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM340 target genes. The mRNA of each one of this plurality of GAM340 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM340 RNA, herein designated GAM RNA, and which when bound by GAM340 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM340 target proteins.

[5280] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM340 gene, herein designated GAM GENE, on one or more GAM340 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5281] It is yet further appreciated that specific functions, and accordingly utilities, of GAM340 correlate with, and may be deduced from, the identity of the target genes which GAM340 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5282] Nucleotide sequences of the GAM340 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM340 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM340 are further described hereinbelow with reference to Table Table1.

[5283] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM340 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5284] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 341 (GAM341) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5285] GAM341 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM341 was detected is described hereinabove with reference to Figs. 2-8.

[5286] GAM341 gene, herein designated GAM GENE, and GAM341 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5287] GAM341 gene, herein designated GAM GENE, encodes a GAM341 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM341 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM341 precursor RNA is designated SEQ ID:313, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:313 is located at position 7678826 relative to contig NT_004852.13, on chromosome 1.

[5288] GAM341 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5289] An enzyme complex designated DICER COMPLEX, dices the GAM341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM341 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM341 RNA is designated SEQ ID:1989, and is provided hereinbelow with reference to the sequence listing part.

[5290] GAM341 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM341 target RNA, herein designated GAM TARGET RNA. GAM341 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5291] GAM341 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM341 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM341 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM341 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM341 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5292] The complementary binding of GAM341 RNA, herein designated GAM RNA, to target binding sites on GAM341 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM341 target RNA, herein designated GAM TARGET RNA, into GAM341 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5293] It is appreciated that GAM341 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM341 target genes. The mRNA of each one of this plurality of GAM341 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM341 RNA,

herein designated GAM RNA, and which when bound by GAM341 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM341 target proteins.

[5294] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM341 gene, herein designated GAM GENE, on one or more GAM341 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5295] It is yet further appreciated that specific functions, and accordingly utilities, of GAM341 correlate with, and may be deduced from, the identity of the target genes which

GAM341 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5296] Nucleotide sequences of the GAM341 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM341 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM341 are further described hereinbelow with reference to Table Table1.

[5297] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM341 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5298] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 342 (GAM342) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5299] GAM342 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM342 was detected is described hereinabove with reference to Figs. 2-8.

[5300] GAM342 gene, herein designated GAM GENE, and GAM342 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5301] GAM342 gene, herein designated GAM GENE, encodes a GAM342 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM342 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM342 precursor RNA is designated SEQ ID:314, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:314 is located at position 8271492 relative to contig NT_011109.13, on chromosome 19.

[5302] GAM342 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5303] An enzyme complex designated DICER COMPLEX, dices the GAM342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM342 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM342 RNA is designated SEQ ID:1990, and is provided hereinbelow with reference to the sequence listing part.

[5304] GAM342 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM342 target RNA, herein designated GAM TARGET RNA. GAM342 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5305] GAM342 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM342 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM342 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM342 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM342 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5306] The complementary binding of GAM342 RNA, herein designated GAM RNA, to target binding sites on GAM342 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM342 target RNA, herein designated GAM TARGET RNA, into GAM342 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5307] It is appreciated that GAM342 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM342 target genes. The mRNA of each one of this plurality of GAM342 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM342 RNA, herein designated GAM RNA, and which when bound by GAM342 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM342 target proteins.

[5308] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM342 gene, herein designated GAM GENE, on one or more GAM342 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5309] It is yet further appreciated that specific functions, and accordingly utilities, of GAM342 correlate with, and may be deduced from, the identity of the target genes which GAM342 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5310] Nucleotide sequences of the GAM342 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM342 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM342 are further described hereinbelow with reference to Table Table1.

[5311] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM342 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5312] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 343 (GAM343) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5313] GAM343 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM343 was detected is described hereinabove with reference to Figs. 2-8.

[5314] GAM343 gene, herein designated GAM GENE, and GAM343 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5315] GAM343 gene, herein designated GAM GENE, encodes a GAM343 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM343 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM343 precursor RNA is designated SEQ ID:315, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:315 is located at position 2045037 relative to contig NT_011176.13, on chromosome 19.

[5316] GAM343 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5317] An enzyme complex designated DICER COMPLEX, dices the GAM343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM343 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM343 RNA is designated SEQ ID:1991, and is provided

hereinbelow with reference to the sequence listing part.

[5318] GAM343 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM343 target RNA, herein designated GAM TARGET RNA.
GAM343 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5319] GAM343 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM343 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM343 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM343 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM343 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5320] The complementary binding of GAM343 RNA, herein designated GAM RNA, to target binding sites on GAM343 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM343 target RNA, herein designated GAM TARGET RNA, into GAM343 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5321] It is appreciated that GAM343 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM343 target genes. The mRNA of each one of this plurality of GAM343 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM343 RNA, herein designated GAM RNA, and which when bound by GAM343 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM343 tar-

get proteins.

[5322] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM343 gene, herein designated GAM GENE, on one or more GAM343 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5323] It is yet further appreciated that specific functions, and accordingly utilities, of GAM343 correlate with, and may be deduced from, the identity of the target genes which GAM343 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5324] Nucleotide sequences of the GAM343 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM343 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM343 are further described hereinbelow with reference to Table Table1.

[5325] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM343 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5326] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 344 (GAM344) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5327] GAM344 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM344 was detected is described hereinabove with reference to Figs. 2-8.

[5328] GAM344 gene, herein designated GAM GENE, and

GAM344 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5329] GAM344 gene, herein designated GAM GENE, encodes a GAM344 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM344 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM344 precursor RNA is designated SEQ ID:316, and is provided hereinbelow with reference to the sequence listing part.

[5330] GAM344 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5331] An enzyme complex designated DICER COMPLEX, dices the GAM344 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM344 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM344 RNA is designated SEQ ID:1992, and is provided hereinbelow with reference to the sequence listing part.

[5332] GAM344 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM344 target RNA, herein designated GAM TARGET RNA. GAM344 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5333] GAM344 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM344 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM344 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM344 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM344 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5334] The complementary binding of GAM344 RNA, herein designated GAM RNA, to target binding sites on GAM344 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM344 target RNA, herein designated GAM TARGET RNA, into GAM344 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5335] It is appreciated that GAM344 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM344 target genes. The mRNA of each one of this plurality of GAM344 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM344 RNA, herein designated GAM RNA, and which when bound by GAM344 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM344 target proteins.

[5336] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM344 gene, herein designated GAM GENE, on one or more GAM344 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5337] It is yet further appreciated that specific functions, and accordingly utilities, of GAM344 correlate with, and may be deduced from, the identity of the target genes which GAM344 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5338] Nucleotide sequences of the GAM344 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM344 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM344 are further described hereinbelow with reference to Table Table1.

[5339] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM344 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5340] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

345 (GAM345) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5341] GAM345 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM345 was detected is described hereinabove with reference to Figs. 2-8.

[5342] GAM345 gene, herein designated GAM GENE, and GAM345 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5343] GAM345 gene, herein designated GAM GENE, encodes a GAM345 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM345 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM345 precursor RNA is designated SEQ ID:317, and is provided hereinbelow with reference to the sequence listing part.

[5344] GAM345 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5345] An enzyme complex designated DICER COMPLEX, dices the GAM345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM345 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM345 RNA is designated SEQ ID:1993, and is provided hereinbelow with reference to the sequence listing part.

[5346] GAM345 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM345 target RNA, herein designated GAM TARGET RNA. GAM345 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5347] GAM345 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM345 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM345 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM345 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM345 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5348] The complementary binding of GAM345 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM345 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM345 target RNA, herein designated GAM TARGET RNA, into GAM345 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5349] It is appreciated that GAM345 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM345 target genes. The mRNA of each one of this plurality of GAM345 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM345 RNA, herein designated GAM RNA, and which when bound by GAM345 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM345 target proteins.

[5350] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM345 gene, herein designated GAM GENE, on one or more GAM345 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5351] It is yet further appreciated that specific functions, and accordingly utilities, of GAM345 correlate with, and may be deduced from, the identity of the target genes which GAM345 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5352] Nucleotide sequences of the GAM345 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM345 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM345 are further described hereinbelow with reference to Table Table1.

[5353] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM345 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5354] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 346 (GAM346) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5355] GAM346 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM346 was detected is described hereinabove with reference to Figs. 2-8.

[5356] GAM346 gene, herein designated GAM GENE, and GAM346 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5357] GAM346 gene, herein designated GAM GENE, encodes a GAM346 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM346 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM346 precursor RNA is designated SEQ ID:318, and is provided hereinbelow with reference to the sequence listing part.

[5358] GAM346 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5359] An enzyme complex designated DICER COMPLEX, dices the GAM346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM346 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of

GAM346 RNA is designated SEQ ID:1994, and is provided hereinbelow with reference to the sequence listing part.

[5360] GAM346 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM346 target RNA, herein designated GAM TARGET RNA. GAM346 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5361] GAM346 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM346 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM346 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM346 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM346 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5362] The complementary binding of GAM346 RNA, herein designated GAM RNA, to target binding sites on GAM346 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM346 target RNA, herein designated GAM TARGET RNA, into GAM346 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5363] It is appreciated that GAM346 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM346 target genes. The mRNA of each one of this plurality of GAM346 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM346 RNA, herein designated GAM RNA, and which when bound by GAM346 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM346 target proteins.

[5364] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM346 gene, herein designated GAM GENE, on one or more GAM346 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5365] It is yet further appreciated that specific functions, and accordingly utilities, of GAM346 correlate with, and may be deduced from, the identity of the target genes which GAM346 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5366] Nucleotide sequences of the GAM346 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM346 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM346 are further described hereinbelow with reference to Table Table1.

[5367] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM346 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5368] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 347 (GAM347) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5369] GAM347 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM347 was detected is described hereinabove with reference to Figs. 2-8.

[5370] GAM347 gene, herein designated GAM GENE, and GAM347 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5371] GAM347 gene, herein designated GAM GENE, encodes a GAM347 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM347 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM347 precursor RNA is designated SEQ ID:319, and is provided hereinbelow with reference to the sequence listing part.

[5372] GAM347 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5373] An enzyme complex designated DICER COMPLEX, dices

the GAM347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM347 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM347 RNA is designated SEQ ID:1995, and is provided hereinbelow with reference to the sequence listing part.

[5374] GAM347 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM347 target RNA, herein designated GAM TARGET RNA. GAM347 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5375] GAM347 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM347 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM347

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM347 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM347 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5376] The complementary binding of GAM347 RNA, herein designated GAM RNA, to target binding sites on GAM347 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM347 target RNA, herein designated GAM TARGET RNA, into GAM347 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5377] It is appreciated that GAM347 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM347 target genes. The mRNA of each one of this plurality of GAM347 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM347 RNA, herein designated GAM RNA, and which when bound by GAM347 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM347 target proteins.

[5378] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM347 gene, herein designated GAM GENE, on one or more GAM347 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5379] It is yet further appreciated that specific functions, and accordingly utilities, of GAM347 correlate with, and may be deduced from, the identity of the target genes which GAM347 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5380] Nucleotide sequences of the GAM347 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM347 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM347 are further described hereinbelow with reference to Table Table1.

[5381] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM347 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5382] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 348 (GAM348) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5383] GAM348 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM348 was detected is described hereinabove with reference to Figs. 2-8.

[5384] GAM348 gene, herein designated GAM GENE, and GAM348 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5385] GAM348 gene, herein designated GAM GENE, encodes a GAM348 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM348 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM348 precursor RNA is designated SEQ ID:320, and is provided hereinbelow with reference to the sequence listing part.

[5386] GAM348 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5387] An enzyme complex designated DICER COMPLEX, dices the GAM348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM348 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM348 RNA is designated SEQ ID:1996, and is provided hereinbelow with reference to the sequence listing part.

[5388] GAM348 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM348 target RNA, herein designated GAM TARGET RNA. GAM348 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5389] GAM348 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM348 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM348 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM348 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM348 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5390] The complementary binding of GAM348 RNA, herein designated GAM RNA, to target binding sites on GAM348 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM348 target RNA, herein designated GAM TARGET RNA, into GAM348 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5391] It is appreciated that GAM348 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM348 target genes. The mRNA of each one of this plurality of GAM348 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM348 RNA, herein designated GAM RNA, and which when bound by GAM348 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM348 target proteins.

[5392] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM348 gene, herein designated GAM GENE, on one or more GAM348 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5393] It is yet further appreciated that specific functions, and accordingly utilities, of GAM348 correlate with, and may be deduced from, the identity of the target genes which GAM348 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5394] Nucleotide sequences of the GAM348 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM348 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM348 are further described hereinbelow with reference to Table Table1.

[5395] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM348 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5396] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 349 (GAM349) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5397] GAM349 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM349 was detected is described hereinabove with reference to Figs. 2-8.

[5398] GAM349 gene, herein designated GAM GENE, and GAM349 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5399] GAM349 gene, herein designated GAM GENE, encodes a GAM349 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM349 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM349 precursor RNA is designated SEQ ID:321, and is provided hereinbelow with reference to the sequence listing part.

[5400] GAM349 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5401] An enzyme complex designated DICER COMPLEX, dices the GAM349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM349 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM349 RNA is designated SEQ ID:1997, and is provided hereinbelow with reference to the sequence listing part.

[5402] GAM349 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM349 target RNA, herein designated GAM TARGET RNA. GAM349 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5403] GAM349 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM349 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM349 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM349 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM349 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5404] The complementary binding of GAM349 RNA, herein designated GAM RNA, to target binding sites on GAM349 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM349 target RNA, herein designated GAM TARGET RNA, into GAM349 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5405] It is appreciated that GAM349 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM349 target genes. The mRNA of each one of this plurality of GAM349 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM349 RNA, herein designated GAM RNA, and which when bound by

GAM349 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM349 target proteins.

[5406] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM349 gene, herein designated GAM GENE, on one or more GAM349 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5407] It is yet further appreciated that specific functions, and accordingly utilities, of GAM349 correlate with, and may be deduced from, the identity of the target genes which GAM349 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[5408] Nucleotide sequences of the GAM349 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM349 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM349 are further described hereinbelow with reference to Table Table1.

[5409] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM349 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5410] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 350 (GAM350) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5411] GAM350 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM350 was detected is described hereinabove

with reference to Figs. 2-8.

[5412] GAM350 gene, herein designated GAM GENE, and GAM350 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5413] GAM350 gene, herein designated GAM GENE, encodes a GAM350 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM350 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM350 precursor RNA is designated SEQ ID:322, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:322 is located at position 1558797 relative to contig NT_030801.7, on chromosome 11.

[5414] GAM350 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[5415] An enzyme complex designated DICER COMPLEX, dices the GAM350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM350 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM350 RNA is designated SEQ ID:1998, and is provided hereinbelow with reference to the sequence listing part.

[5416] GAM350 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM350 target RNA, herein designated GAM TARGET RNA.
GAM350 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5417] GAM350 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM350 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM350 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM350 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM350 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5418] The complementary binding of GAM350 RNA, herein designated GAM RNA, to target binding sites on GAM350 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM350 target RNA, herein desig-

nated GAM TARGET RNA, into GAM350 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5419] It is appreciated that GAM350 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM350 target genes. The mRNA of each one of this plurality of GAM350 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM350 RNA, herein designated GAM RNA, and which when bound by GAM350 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM350 target proteins.

[5420] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM350 gene, herein designated GAM GENE, on one or more GAM350 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5421] It is yet further appreciated that specific functions, and accordingly utilities, of GAM350 correlate with, and may be deduced from, the identity of the target genes which GAM350 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5422] Nucleotide sequences of the GAM350 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM350 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM350 are further described hereinbelow with reference to Table Table1.

[5423] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM350 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[5424] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 351 (GAM351) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5425] GAM351 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM351 was detected is described hereinabove with reference to Figs. 2-8.

[5426] GAM351 gene, herein designated GAM GENE, and GAM351 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5427] GAM351 gene, herein designated GAM GENE, encodes a GAM351 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM351 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM351 precursor RNA is designated SEQ ID:323, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:323 is located at position 8520882 relative to contig NT_034880.2, on chromosome 6.

[5428] GAM351 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5429] An enzyme complex designated DICER COMPLEX, dices the GAM351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM351 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM351 RNA is designated SEQ ID:1999, and is provided hereinbelow with reference to the sequence listing part.

[5430] GAM351 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM351 target RNA, herein designated GAM TARGET RNA. GAM351 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5431] GAM351 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM351 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM351 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM351 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM351

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5432] The complementary binding of GAM351 RNA, herein designated GAM RNA, to target binding sites on GAM351 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM351 target RNA, herein designated GAM TARGET RNA, into GAM351 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5433] It is appreciated that GAM351 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM351 target genes. The mRNA of each one of this plurality of GAM351 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM351 RNA, herein designated GAM RNA, and which when bound by GAM351 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM351 target proteins.

[5434] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM351 gene, herein designated GAM GENE, on one or more GAM351 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5435] It is yet further appreciated that specific functions, and accordingly utilities, of GAM351 correlate with, and may be deduced from, the identity of the target genes which GAM351 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5436] Nucleotide sequences of the GAM351 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM351 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM351 are further described hereinbelow with reference to Table Table1.

[5437] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM351 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5438] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 352 (GAM352) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5439] GAM352 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM352 was detected is described hereinabove with reference to Figs. 2-8.

[5440] GAM352 gene, herein designated GAM GENE, and GAM352 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[5441] GAM352 gene, herein designated GAM GENE, encodes a GAM352 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM352 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM352 precursor RNA is designated SEQ ID:324, and is provided hereinbelow with reference to the sequence listing part.

[5442] GAM352 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5443] An enzyme complex designated DICER COMPLEX, dices the GAM352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM352 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM352 RNA is designated SEQ ID:2000, and is provided hereinbelow with reference to the sequence listing part.

[5444] GAM352 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM352 target RNA, herein designated GAM TARGET RNA. GAM352 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5445] GAM352 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM352 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM352 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM352 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM352 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5446] The complementary binding of GAM352 RNA, herein designated GAM RNA, to target binding sites on GAM352 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM352 target RNA, herein designated GAM TARGET RNA, into GAM352 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5447] It is appreciated that GAM352 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM352 target genes. The mRNA of each one of this plurality of GAM352 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM352 RNA, herein designated GAM RNA, and which when bound by GAM352 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM352 target proteins.

[5448] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM352 gene, herein designated GAM GENE, on one or more GAM352 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[5449] It is yet further appreciated that specific functions, and accordingly utilities, of GAM352 correlate with, and may be deduced from, the identity of the target genes which GAM352 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5450] Nucleotide sequences of the GAM352 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM352 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM352 are further described hereinbelow with reference to Table Table1.

[5451] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM352 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5452] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 353 (GAM353) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[5453] GAM353 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM353 was detected is described hereinabove with reference to Figs. 2-8.

[5454] GAM353 gene, herein designated GAM GENE, and GAM353 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5455] GAM353 gene, herein designated GAM GENE, encodes a GAM353 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM353 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM353 precursor RNA is designated SEQ ID:325, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:325 is located at position 58159291 relative to contig NT_026437.9, on chromosome 14.

[5456] GAM353 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5457] An enzyme complex designated DICER COMPLEX, dices the GAM353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM353 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM353 RNA is designated SEQ ID:2001, and is provided hereinbelow with reference to the sequence listing part.

[5458] GAM353 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM353 target RNA, herein designated GAM TARGET RNA. GAM353 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5459] GAM353 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM353 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM353 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM353 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM353 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5460] The complementary binding of GAM353 RNA, herein designated GAM RNA, to target binding sites on GAM353 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM353 target RNA, herein designated GAM TARGET RNA, into GAM353 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5461] It is appreciated that GAM353 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM353 target genes. The mRNA of each one of this plurality of GAM353 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM353 RNA, herein designated GAM RNA, and which when bound by GAM353 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM353 target proteins.

[5462] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM353 gene, herein designated GAM GENE, on one or more GAM353 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5463] It is yet further appreciated that specific functions, and accordingly utilities, of GAM353 correlate with, and may be deduced from, the identity of the target genes which GAM353 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5464] Nucleotide sequences of the GAM353 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM353 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM353 are further described hereinbelow with reference to Table Table1.

[5465] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM353 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5466] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 354 (GAM354) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5467] GAM354 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM354 was detected is described hereinabove with reference to Figs. 2-8.

[5468] GAM354 gene, herein designated GAM GENE, and GAM354 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5469] GAM354 gene, herein designated GAM GENE, encodes a GAM354 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM354 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM354 precursor RNA is designated SEQ ID:326, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:326 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[5470] GAM354 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5471] An enzyme complex designated DICER COMPLEX, dices the GAM354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM354 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM354 RNA is designated SEQ ID:2002, and is provided hereinbelow with reference to the sequence listing part.

[5472] GAM354 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM354 target RNA, herein designated GAM TARGET RNA. GAM354 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5473] GAM354 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM354 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM354 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM354 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM354 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5474] The complementary binding of GAM354 RNA, herein designated GAM RNA, to target binding sites on GAM354 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM354 target RNA, herein designated GAM TARGET RNA, into GAM354 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5475] It is appreciated that GAM354 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM354 target genes. The mRNA of each one of this plurality of GAM354 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM354 RNA, herein designated GAM RNA, and which when bound by GAM354 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM354 target proteins.

[5476] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM354 gene, herein designated GAM GENE, on one or more GAM354 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5477] It is yet further appreciated that specific functions, and accordingly utilities, of GAM354 correlate with, and may

be deduced from, the identity of the target genes which GAM354 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5478] Nucleotide sequences of the GAM354 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM354 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM354 are further described hereinbelow with reference to Table Table1.

[5479] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM354 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5480] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 355 (GAM355) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5481] GAM355 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM355 was detected is described hereinabove with reference to Figs. 2-8.

[5482] GAM355 gene, herein designated GAM GENE, and GAM355 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5483] GAM355 gene, herein designated GAM GENE, encodes a GAM355 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM355 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM355 precursor RNA is designated SEQ ID:327, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:327 is located at position 5139123 relative to contig NT_033254.3, on chromosome 12.

[5484] GAM355 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5485] An enzyme complex designated DICER COMPLEX, dices the GAM355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM355 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM355 RNA is designated SEQ ID:2003, and is provided hereinbelow with reference to the sequence listing part.

[5486] GAM355 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM355 target RNA, herein designated GAM TARGET RNA. GAM355 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5487] GAM355 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM355 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM355 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM355 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM355 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5488] The complementary binding of GAM355 RNA, herein designated GAM RNA, to target binding sites on GAM355 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM355 target RNA, herein designated GAM TARGET RNA, into GAM355 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5489] It is appreciated that GAM355 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM355 target genes. The mRNA of each one of this plurality of GAM355 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM355 RNA, herein designated GAM RNA, and which when bound by GAM355 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM355 target proteins.

[5490] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM355 gene, herein designated GAM GENE, on one or more GAM355 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5491] It is yet further appreciated that specific functions, and accordingly utilities, of GAM355 correlate with, and may be deduced from, the identity of the target genes which GAM355 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5492] Nucleotide sequences of the GAM355 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM355 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM355 are further described hereinbelow with reference to Table Table1.

[5493] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM355 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5494] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 356 (GAM356) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5495] GAM356 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM356 was detected is described hereinabove with reference to Figs. 2-8.

[5496] GAM356 gene, herein designated GAM GENE, and GAM356 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5497] GAM356 gene, herein designated GAM GENE, encodes a GAM356 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM356 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM356 precursor RNA is desig-

nated SEQ ID:328, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:328 is located at position 5139123 relative to contig NT_033254.3, on chromosome 12.

[5498] GAM356 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5499] An enzyme complex designated DICER COMPLEX, dices the GAM356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM356 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM356 RNA is designated SEQ ID:2004, and is provided hereinbelow with reference to the sequence listing part.

[5500] GAM356 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM356 target RNA, herein designated GAM TARGET RNA. GAM356 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5501] GAM356 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM356 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM356 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM356 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM356 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5502] The complementary binding of GAM356 RNA, herein designated GAM RNA, to target binding sites on GAM356 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM356 target RNA, herein designated GAM TARGET RNA, into GAM356 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5503] It is appreciated that GAM356 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM356 target genes. The mRNA of each one of this plurality of GAM356 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM356 RNA, herein designated GAM RNA, and which when bound by GAM356 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM356 target proteins.

[5504] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM356 gene, herein designated GAM GENE, on one or more GAM356 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5505] It is yet further appreciated that specific functions, and accordingly utilities, of GAM356 correlate with, and may be deduced from, the identity of the target genes which GAM356 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5506] Nucleotide sequences of the GAM356 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM356 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM356 are further described hereinbelow with reference to Table Table1.

[5507] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM356 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5508] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 357 (GAM357) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5509] GAM357 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM357 was detected is described hereinabove with reference to Figs. 2-8.

[5510] GAM357 gene, herein designated GAM GENE, and GAM357 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5511] GAM357 gene, herein designated GAM GENE, encodes a GAM357 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM357 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM357 precursor RNA is designated SEQ ID:329, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:329 is located at position 3910585 relative to contig NT_029289.7, on chromosome 5.

[5512] GAM357 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[5513] An enzyme complex designated DICER COMPLEX, dices the GAM357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM357 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM357 RNA is designated SEQ ID:2005, and is provided hereinbelow with reference to the sequence listing part.

[5514] GAM357 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM357 target RNA, herein designated GAM TARGET RNA. GAM357 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5515] GAM357 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM357 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM357 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM357 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM357 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5516] The complementary binding of GAM357 RNA, herein designated GAM RNA, to target binding sites on GAM357 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM357 target RNA, herein designated GAM TARGET RNA, into GAM357 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5517] It is appreciated that GAM357 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM357 target genes. The mRNA of each one of this plurality of GAM357 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM357 RNA, herein designated GAM RNA, and which when bound by GAM357 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM357 target proteins.

[5518] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM357 gene, herein designated GAM GENE, on one or more GAM357 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5519] It is yet further appreciated that specific functions, and accordingly utilities, of GAM357 correlate with, and may be deduced from, the identity of the target genes which GAM357 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5520] Nucleotide sequences of the GAM357 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM357 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM357 are further described hereinbelow with reference to Table Table1.

[5521] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM357 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5522] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 358 (GAM358) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5523] GAM358 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM358 was detected is described hereinabove with reference to Figs. 2-8.

[5524] GAM358 gene, herein designated GAM GENE, and GAM358 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5525] GAM358 gene, herein designated GAM GENE, encodes a GAM358 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM358 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM358 precursor RNA is designated SEQ ID:330, and is provided hereinbelow with reference to the sequence listing part.

[5526] GAM358 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5527] An enzyme complex designated DICER COMPLEX, dices the GAM358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM358 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM358 RNA is designated SEQ ID:2006, and is provided hereinbelow with reference to the sequence listing part.

[5528] GAM358 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM358 target RNA, herein designated GAM TARGET RNA.

GAM358 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5529] GAM358 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM358 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM358 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM358 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM358 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5530] The complementary binding of GAM358 RNA, herein designated GAM RNA, to target binding sites on GAM358 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM358 target RNA, herein designated GAM TARGET RNA, into GAM358 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5531] It is appreciated that GAM358 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM358 target genes. The mRNA of each one of this plurality of GAM358 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM358 RNA, herein designated GAM RNA, and which when bound by GAM358 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM358 target proteins.

[5532] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM358 gene, herein designated GAM GENE, on one or more GAM358 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5533] It is yet further appreciated that specific functions, and accordingly utilities, of GAM358 correlate with, and may be deduced from, the identity of the target genes which GAM358 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5534] Nucleotide sequences of the GAM358 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM358 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM358 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM358 are further described hereinbelow with reference to Table Table1.

[5535] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM358 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5536] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 359 (GAM359) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5537] GAM359 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM359 was detected is described hereinabove with reference to Figs. 2-8.

[5538] GAM359 gene, herein designated GAM GENE, and GAM359 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5539] GAM359 gene, herein designated GAM GENE, encodes a GAM359 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM359 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM359 precursor RNA is designated SEQ ID:331, and is provided hereinbelow with reference to the sequence listing part.

[5540] GAM359 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[5541] SEQ ID:99356 detected in mouse EST Accession BI714485.1.

[5542] SEQ ID:99357 detected in mouse EST Accession BE368829.1.

[5543] GAM359 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5544] An enzyme complex designated DICER COMPLEX, dices the GAM359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM359 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM359 RNA is designated SEQ ID:2007, and is provided hereinbelow with reference to the sequence listing part.

[5545] GAM359 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM359 target RNA, herein designated GAM TARGET RNA. GAM359 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5546] GAM359 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM359 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM359 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM359 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM359 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5547] The complementary binding of GAM359 RNA, herein designated GAM RNA, to target binding sites on GAM359 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM359 target RNA, herein designated GAM TARGET RNA, into GAM359 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5548] It is appreciated that GAM359 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM359 target genes. The mRNA of each one of this plurality of GAM359 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM359 RNA, herein designated GAM RNA, and which when bound by GAM359 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM359 target proteins.

[5549] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM359 gene, herein designated GAM GENE, on one or more GAM359 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5550] It is yet further appreciated that specific functions, and accordingly utilities, of GAM359 correlate with, and may be deduced from, the identity of the target genes which GAM359 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5551] Nucleotide sequences of the GAM359 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM359 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM359 are further described hereinbelow with reference to Table Table1.

[5552] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM359 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5553] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 360 (GAM360) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5554] GAM360 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM360 was detected is described hereinabove with reference to Figs. 2-8.

[5555] GAM360 gene, herein designated GAM GENE, and GAM360 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5556] GAM360 gene, herein designated GAM GENE, encodes a GAM360 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM360 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM360 precursor RNA is designated SEQ ID:332, and is provided hereinbelow with refer-

ence to the sequence listing part.

[5557] GAM360 has 61 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[5558] SEQ ID:100540 detected in mouse EST Accession W16182.1.

[5559] SEQ ID:100541 detected in mouse EST Accession AA237404.1.

[5560] SEQ ID:100542 detected in mouse EST Accession AW240449.1.

[5561] SEQ ID:100543 detected in mouse EST Accession BE624221.1.

[5562] SEQ ID:100544 detected in mouse EST Accession AW113760.1.

[5563] SEQ ID:100545 detected in mouse EST Accession BF450285.1.

[5564] SEQ ID:100546 detected in mouse EST Accession BE851242.1.

[5565] SEQ ID:100547 detected in mouse EST Accession AA397121.1.

[5566] SEQ ID:100548 detected in mouse EST Accession

BE690148.1.

[5567] SEQ ID:100549 detected in mouse EST Accession BE692663.1.

[5568] SEQ ID:100550 detected in mouse EST Accession AA237479.1.

[5569] SEQ ID:100551 detected in mouse EST Accession BF020203.1.

[5570] SEQ ID:100552 detected in mouse EST Accession AI152470.1.

[5571] SEQ ID:100553 detected in mouse EST Accession AW241043.1.

[5572] SEQ ID:100554 detected in mouse EST Accession BI110254.1.

[5573] SEQ ID:100555 detected in mouse EST Accession AW989706.1.

[5574] SEQ ID:100556 detected in mouse EST Accession AW987156.1.

[5575] SEQ ID:100557 detected in mouse EST Accession AW322040.1.

[5576] SEQ ID:100558 detected in mouse EST Accession AW324490.1.

[5577] SEQ ID:100559 detected in mouse EST Accession BE335469.1.

[5578] SEQ ID:100560 detected in mouse EST Accession AA270973.1.

[5579] SEQ ID:100561 detected in mouse EST Accession AI303167.1.

[5580] SEQ ID:100562 detected in mouse EST Accession BE199228.1.

[5581] SEQ ID:100563 detected in mouse EST Accession BE689588.1.

[5582] SEQ ID:100564 detected in mouse EST Accession AW018407.1.

[5583] SEQ ID:100565 detected in mouse EST Accession BE650065.1.

[5584] SEQ ID:100566 detected in mouse EST Accession BF227510.1.

[5585] SEQ ID:100605 detected in mouse EST Accession BE689976.1.

[5586] SEQ ID:100606 detected in mouse EST Accession BF116785.1.

[5587] SEQ ID:100607 detected in mouse EST Accession BE690578.1.

[5588] SEQ ID:100608 detected in mouse EST Accession AW908422.1.

[5589] SEQ ID:100609 detected in mouse EST Accession

AA239428.1.

[5590] SEQ ID:100610 detected in mouse EST Accession BF226299.1.

[5591] SEQ ID:100611 detected in mouse EST Accession AW909366.1.

[5592] SEQ ID:100612 detected in mouse EST Accession BE199152.1.

[5593] SEQ ID:100613 detected in mouse EST Accession BF227614.1.

[5594] SEQ ID:100614 detected in mouse EST Accession AI785459.1.

[5595] SEQ ID:100615 detected in mouse EST Accession AW209037.1.

[5596] SEQ ID:100616 detected in mouse EST Accession AI195467.1.

[5597] SEQ ID:100617 detected in mouse EST Accession AI114892.1.

[5598] SEQ ID:100618 detected in mouse EST Accession AI194959.1.

[5599] SEQ ID:100619 detected in mouse EST Accession AW110985.1.

[5600] SEQ ID:100620 detected in mouse EST Accession AW018398.1.

[5601] SEQ ID:100621 detected in mouse EST Accession AA238246.1.

[5602] SEQ ID:100622 detected in mouse EST Accession BG068359.1.

[5603] SEQ ID:100623 detected in mouse EST Accession AA230354.1.

[5604] SEQ ID:100624 detected in mouse EST Accession AU022691.1.

[5605] SEQ ID:100625 detected in mouse EST Accession BI111409.1.

[5606] SEQ ID:100626 detected in mouse EST Accession AI255679.1.

[5607] SEQ ID:100627 detected in mouse EST Accession BI248794.1.

[5608] SEQ ID:100628 detected in mouse EST Accession AW212849.1.

[5609] SEQ ID:100629 detected in mouse EST Accession AI646857.1.

[5610] SEQ ID:100630 detected in mouse EST Accession AW701118.1.

[5611] SEQ ID:100631 detected in mouse EST Accession BI246484.1.

[5612] SEQ ID:100632 detected in mouse EST Accession

AI747413.1.

[5613] SEQ ID:100633 detected in mouse EST Accession AW113761.1.

[5614] SEQ ID:100634 detected in mouse EST Accession AW110984.1.

[5615] SEQ ID:100635 detected in mouse EST Accession BF179498.1.

[5616] SEQ ID:100636 detected in mouse EST Accession BB009037.2.

[5617] SEQ ID:100637 detected in mouse EST Accession AI323769.1.

[5618] SEQ ID:100638 detected in mouse EST Accession AA764472.1.

[5619] GAM360 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5620] An enzyme complex designated DICER COMPLEX, dices the GAM360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM360 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM360 RNA is designated SEQ ID:2008, and is provided hereinbelow with reference to the sequence listing part.

[5621] GAM360 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM360 target RNA, herein designated GAM TARGET RNA. GAM360 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5622] GAM360 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM360 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM360 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM360 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM360 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5623] The complementary binding of GAM360 RNA, herein designated GAM RNA, to target binding sites on GAM360 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM360 target RNA, herein designated GAM TARGET RNA, into GAM360 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[5624] It is appreciated that GAM360 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM360 target genes. The mRNA of each one of this plurality of GAM360 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM360 RNA, herein designated GAM RNA, and which when bound by GAM360 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM360 target proteins.

[5625] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM360 gene, herein designated GAM GENE, on one or more GAM360 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5626] It is yet further appreciated that specific functions, and accordingly utilities, of GAM360 correlate with, and may be deduced from, the identity of the target genes which GAM360 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5627] Nucleotide sequences of the GAM360 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM360 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM360 are further described hereinbelow with reference to Table Table1.

[5628] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM360 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5629] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 361 (GAM361) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5630] GAM361 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM361 was detected is described hereinabove with reference to Figs. 2-8.

[5631] GAM361 gene, herein designated GAM GENE, and GAM361 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5632] GAM361 gene, herein designated GAM GENE, encodes a GAM361 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM361 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM361 precursor RNA is designated SEQ ID:333, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:333 is located at position 6294455 relative to contig NT_024981.11, on chromosome 18.

[5633] GAM361 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5634] An enzyme complex designated DICER COMPLEX, dices the GAM361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM361 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM361 RNA is designated SEQ ID:2009, and is provided hereinbelow with reference to the sequence listing part.

[5635] GAM361 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM361

target RNA, herein designated GAM TARGET RNA.

GAM361 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5636] GAM361 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM361 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM361 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM361 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM361 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5637] The complementary binding of GAM361 RNA, herein designated GAM RNA, to target binding sites on GAM361 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM361 target RNA, herein designated GAM TARGET RNA, into GAM361 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5638] It is appreciated that GAM361 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM361 target genes. The mRNA of each one of this plurality of GAM361 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM361 RNA, herein designated GAM RNA, and which when bound by GAM361 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM361 target proteins.

[5639] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM361 gene, herein designated GAM GENE, on one or more GAM361 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5640] It is yet further appreciated that specific functions, and accordingly utilities, of GAM361 correlate with, and may be deduced from, the identity of the target genes which GAM361 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5641] Nucleotide sequences of the GAM361 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM361 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM361 are further described hereinbelow with reference to Table Table1.

[5642] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM361 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5643] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 362 (GAM362) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5644] GAM362 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM362 was detected is described hereinabove with reference to Figs. 2-8.

[5645] GAM362 gene, herein designated GAM GENE, and GAM362 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5646] GAM362 gene, herein designated GAM GENE, encodes a

GAM362 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM362 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM362 precursor RNA is designated SEQ ID:334, and is provided hereinbelow with reference to the sequence listing part.

[5647] GAM362 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5648] An enzyme complex designated DICER COMPLEX, dices the GAM362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM362 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM362 RNA is designated SEQ ID:2010, and is provided hereinbelow with reference to the sequence listing part.

[5649] GAM362 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM362 target RNA, herein designated GAM TARGET RNA. GAM362 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5650] GAM362 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM362 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM362 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM362 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM362 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5651] The complementary binding of GAM362 RNA, herein designated GAM RNA, to target binding sites on GAM362 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM362 target RNA, herein designated GAM TARGET RNA, into GAM362 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5652] It is appreciated that GAM362 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM362 target genes. The mRNA of each one of this plurality of GAM362 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM362 RNA, herein designated GAM RNA, and which when bound by GAM362 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM362 target proteins.

[5653] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM362 gene, herein designated GAM GENE, on one or more GAM362 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5654] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM362 correlate with, and may be deduced from, the identity of the target genes which GAM362 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5655] Nucleotide sequences of the GAM362 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM362 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM362 are further described hereinbelow with reference to Table Table1.

[5656] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM362 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5657] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 363 (GAM363) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5658] GAM363 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM363 was detected is described hereinabove with reference to Figs. 2-8.

[5659] GAM363 gene, herein designated GAM GENE, and GAM363 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5660] GAM363 gene, herein designated GAM GENE, encodes a GAM363 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM363 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM363 precursor RNA is designated SEQ ID:335, and is provided hereinbelow with reference to the sequence listing part.

[5661] GAM363 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5662] An enzyme complex designated DICER COMPLEX, dices the GAM363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM363 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM363 RNA is designated SEQ ID:2011, and is provided hereinbelow with reference to the sequence listing part.

[5663] GAM363 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM363 target RNA, herein designated GAM TARGET RNA.
GAM363 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5664] GAM363 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM363 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM363 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM363 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM363 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5665] The complementary binding of GAM363 RNA, herein designated GAM RNA, to target binding sites on GAM363 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM363 target RNA, herein designated GAM TARGET RNA, into GAM363 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5666] It is appreciated that GAM363 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM363 target genes. The mRNA of each one of this plurality of GAM363 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM363 RNA, herein designated GAM RNA, and which when bound by GAM363 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM363 target proteins.

[5667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM363 gene, herein designated GAM GENE, on one or more GAM363 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5668] It is yet further appreciated that specific functions, and accordingly utilities, of GAM363 correlate with, and may be deduced from, the identity of the target genes which GAM363 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5669] Nucleotide sequences of the GAM363 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM363 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM363 are further described hereinbelow with reference to Table Table1.

[5670] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM363 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5671] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 364 (GAM364) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5672] GAM364 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM364 was detected is described hereinabove with reference to Figs. 2-8.

[5673] GAM364 gene, herein designated GAM GENE, and GAM364 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5674] GAM364 gene, herein designated GAM GENE, encodes a GAM364 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM364 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM364 precursor RNA is designated SEQ ID:336, and is provided hereinbelow with refer-

ence to the sequence listing part.

[5675] GAM364 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5676] An enzyme complex designated DICER COMPLEX, dices the GAM364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM364 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM364 RNA is designated SEQ ID:2012, and is provided hereinbelow with reference to the sequence listing part.

[5677] GAM364 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM364 target RNA, herein designated GAM TARGET RNA.

GAM364 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5678] GAM364 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM364 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM364 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM364 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM364 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5679] The complementary binding of GAM364 RNA, herein designated GAM RNA, to target binding sites on GAM364 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM364 target RNA, herein designated GAM TARGET RNA, into GAM364 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5680] It is appreciated that GAM364 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM364 target genes. The mRNA of each one of this plurality of GAM364 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM364 RNA, herein designated GAM RNA, and which when bound by GAM364 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM364 target proteins.

[5681] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM364 gene, herein designated GAM GENE, on one or more GAM364 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5682] It is yet further appreciated that specific functions, and accordingly utilities, of GAM364 correlate with, and may be deduced from, the identity of the target genes which GAM364 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5683] Nucleotide sequences of the GAM364 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM364 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM364 are further described hereinbelow with reference to Table Table1.

[5684] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM364 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5685] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 365 (GAM365) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5686] GAM365 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM365 was detected is described hereinabove with reference to Figs. 2-8.

[5687] GAM365 gene, herein designated GAM GENE, and GAM365 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5688] GAM365 gene, herein designated GAM GENE, encodes a GAM365 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM365 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM365 precursor RNA is designated SEQ ID:337, and is provided hereinbelow with reference to the sequence listing part.

[5689] GAM365 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5690] An enzyme complex designated DICER COMPLEX, dices the GAM365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM365 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM365 RNA is designated SEQ ID:2013, and is provided hereinbelow with reference to the sequence listing part.

[5691] GAM365 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM365 target RNA, herein designated GAM TARGET RNA. GAM365 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5692] GAM365 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM365 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM365 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM365 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM365 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5693] The complementary binding of GAM365 RNA, herein designated GAM RNA, to target binding sites on GAM365 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM365 target RNA, herein designated GAM TARGET RNA, into GAM365 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5694] It is appreciated that GAM365 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM365 target genes. The mRNA of each one of this plu-

rality of GAM365 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM365 RNA, herein designated GAM RNA, and which when bound by GAM365 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM365 target proteins.

[5695] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM365 gene, herein designated GAM GENE, on one or more GAM365 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5696] It is yet further appreciated that specific functions, and accordingly utilities, of GAM365 correlate with, and may be deduced from, the identity of the target genes which GAM365 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5697] Nucleotide sequences of the GAM365 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM365 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM365 are further described hereinbelow with reference to Table Table1.

[5698] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM365 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5699] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 366 (GAM366) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[5700] GAM366 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM366 was detected is described hereinabove with reference to Figs. 2-8.

[5701] GAM366 gene, herein designated GAM GENE, and GAM366 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5702] GAM366 gene, herein designated GAM GENE, encodes a GAM366 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM366 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM366 precursor RNA is designated SEQ ID:338, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:338 is located at position 58159291 relative to contig NT_026437.9, on chromosome 14.

[5703] GAM366 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5704] An enzyme complex designated DICER COMPLEX, dices the GAM366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM366 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM366 RNA is designated SEQ ID:2014, and is provided hereinbelow with reference to the sequence listing part.

[5705] GAM366 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM366 target RNA, herein designated GAM TARGET RNA. GAM366 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5706] GAM366 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM366 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM366 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM366 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM366 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5707] The complementary binding of GAM366 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM366 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM366 target RNA, herein designated GAM TARGET RNA, into GAM366 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5708] It is appreciated that GAM366 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM366 target genes. The mRNA of each one of this plurality of GAM366 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM366 RNA, herein designated GAM RNA, and which when bound by GAM366 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM366 target proteins.

[5709] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM366 gene, herein designated GAM GENE, on one or more GAM366 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5710] It is yet further appreciated that specific functions, and accordingly utilities, of GAM366 correlate with, and may be deduced from, the identity of the target genes which GAM366 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5711] Nucleotide sequences of the GAM366 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM366 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM366 are further described hereinbelow with reference to Table Table1.

[5712] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM366 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5713] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 367 (GAM367) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5714] GAM367 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM367 was detected is described hereinabove with reference to Figs. 2-8.

[5715] GAM367 gene, herein designated GAM GENE, and GAM367 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5716] GAM367 gene, herein designated GAM GENE, encodes a GAM367 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM367 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM367 precursor RNA is designated SEQ ID:339, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:339 is located at position 58159307 relative to contig NT_026437.9, on chromosome 14.

[5717] GAM367 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5718] An enzyme complex designated DICER COMPLEX, dices the GAM367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM367 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM367 RNA is designated SEQ ID:2015, and is provided hereinbelow with reference to the sequence listing part.

[5719] GAM367 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM367 target RNA, herein designated GAM TARGET RNA. GAM367 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5720] GAM367 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM367 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM367 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM367 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM367 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5721] The complementary binding of GAM367 RNA, herein designated GAM RNA, to target binding sites on GAM367 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM367 target RNA, herein designated GAM TARGET RNA, into GAM367 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5722] It is appreciated that GAM367 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM367 target genes. The mRNA of each one of this plurality of GAM367 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM367 RNA,

herein designated GAM RNA, and which when bound by GAM367 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM367 target proteins.

[5723] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM367 gene, herein designated GAM GENE, on one or more GAM367 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5724] It is yet further appreciated that specific functions, and accordingly utilities, of GAM367 correlate with, and may be deduced from, the identity of the target genes which

GAM367 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5725] Nucleotide sequences of the GAM367 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM367 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM367 are further described hereinbelow with reference to Table Table1.

[5726] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM367 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5727] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 368 (GAM368) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5728] GAM368 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM368 was detected is described hereinabove with reference to Figs. 2-8.

[5729] GAM368 gene, herein designated GAM GENE, and GAM368 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5730] GAM368 gene, herein designated GAM GENE, encodes a GAM368 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM368 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM368 precursor RNA is designated SEQ ID:340, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:340 is located at position 2071068 relative to contig NT_008183.13, on chromosome 8.

[5731] GAM368 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5732] An enzyme complex designated DICER COMPLEX, dices the GAM368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM368 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM368 RNA is designated SEQ ID:2016, and is provided hereinbelow with reference to the sequence listing part.

[5733] GAM368 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM368 target RNA, herein designated GAM TARGET RNA. GAM368 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5734] GAM368 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM368 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM368 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM368 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM368 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5735] The complementary binding of GAM368 RNA, herein designated GAM RNA, to target binding sites on GAM368 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM368 target RNA, herein designated GAM TARGET RNA, into GAM368 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5736] It is appreciated that GAM368 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM368 target genes. The mRNA of each one of this plurality of GAM368 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM368 RNA, herein designated GAM RNA, and which when bound by GAM368 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM368 target proteins.

[5737] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM368 gene, herein designated GAM GENE, on one or more GAM368 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5738] It is yet further appreciated that specific functions, and accordingly utilities, of GAM368 correlate with, and may be deduced from, the identity of the target genes which GAM368 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5739] Nucleotide sequences of the GAM368 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM368 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM368 are further described hereinbelow with reference to Table Table1.

[5740] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM368 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5741] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 369 (GAM369) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5742] GAM369 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM369 was detected is described hereinabove with reference to Figs. 2-8.

[5743] GAM369 gene, herein designated GAM GENE, and GAM369 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5744] GAM369 gene, herein designated GAM GENE, encodes a GAM369 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM369 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM369 precursor RNA is designated SEQ ID:341, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:341 is located at position 12816622 relative to contig NT_011362.7, on chromosome 20.

[5745] GAM369 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5746] An enzyme complex designated DICER COMPLEX, dices the GAM369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM369 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM369 RNA is designated SEQ ID:2017, and is provided

hereinbelow with reference to the sequence listing part.

[5747] GAM369 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM369 target RNA, herein designated GAM TARGET RNA.

GAM369 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5748] GAM369 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM369 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM369 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM369 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM369 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5749] The complementary binding of GAM369 RNA, herein designated GAM RNA, to target binding sites on GAM369 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM369 target RNA, herein designated GAM TARGET RNA, into GAM369 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5750] It is appreciated that GAM369 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM369 target genes. The mRNA of each one of this plurality of GAM369 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM369 RNA, herein designated GAM RNA, and which when bound by GAM369 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM369 tar-

get proteins.

[5751] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM369 gene, herein designated GAM GENE, on one or more GAM369 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5752] It is yet further appreciated that specific functions, and accordingly utilities, of GAM369 correlate with, and may be deduced from, the identity of the target genes which GAM369 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5753] Nucleotide sequences of the GAM369 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM369 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM369 are further described hereinbelow with reference to Table Table1.

[5754] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM369 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5755] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 370 (GAM370) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5756] GAM370 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM370 was detected is described hereinabove with reference to Figs. 2-8.

[5757] GAM370 gene, herein designated GAM GENE, and

GAM370 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5758] GAM370 gene, herein designated GAM GENE, encodes a GAM370 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM370 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM370 precursor RNA is designated SEQ ID:342, and is provided hereinbelow with reference to the sequence listing part.

[5759] GAM370 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5760] An enzyme complex designated DICER COMPLEX, dices the GAM370 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM370 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM370 RNA is designated SEQ ID:2018, and is provided hereinbelow with reference to the sequence listing part.

[5761] GAM370 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM370 target RNA, herein designated GAM TARGET RNA. GAM370 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5762] GAM370 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM370 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM370 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM370 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM370 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5763] The complementary binding of GAM370 RNA, herein designated GAM RNA, to target binding sites on GAM370 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM370 target RNA, herein designated GAM TARGET RNA, into GAM370 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5764] It is appreciated that GAM370 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM370 target genes. The mRNA of each one of this plurality of GAM370 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM370 RNA, herein designated GAM RNA, and which when bound by GAM370 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM370 target proteins.

[5765] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM370 gene, herein designated GAM GENE, on one or more GAM370 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5766] It is yet further appreciated that specific functions, and accordingly utilities, of GAM370 correlate with, and may be deduced from, the identity of the target genes which GAM370 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5767] Nucleotide sequences of the GAM370 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM370 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM370 are further described hereinbelow with reference to Table Table1.

[5768] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM370 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5769] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

371 (GAM371) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5770] GAM371 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM371 was detected is described hereinabove with reference to Figs. 2-8.

[5771] GAM371 gene, herein designated GAM GENE, and GAM371 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5772] GAM371 gene, herein designated GAM GENE, encodes a GAM371 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM371 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM371 precursor RNA is designated SEQ ID:343, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:343 is located at position 12969073 relative to contig NT_011512.7, on chromosome 21.

[5773] GAM371 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM371 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5774] An enzyme complex designated DICER COMPLEX, dices the GAM371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM371 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM371 RNA is designated SEQ ID:2019, and is provided hereinbelow with reference to the sequence listing part.

[5775] GAM371 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM371 target RNA, herein designated GAM TARGET RNA. GAM371 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5776] GAM371 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM371 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM371 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM371 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM371 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[5777] The complementary binding of GAM371 RNA, herein designated GAM RNA, to target binding sites on GAM371 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM371 target RNA, herein designated GAM TARGET RNA, into GAM371 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5778] It is appreciated that GAM371 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM371 target genes. The mRNA of each one of this plurality of GAM371 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM371 RNA, herein designated GAM RNA, and which when bound by GAM371 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM371 target proteins.

[5779] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM371 gene, herein designated GAM GENE, on one or

more GAM371 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5780] It is yet further appreciated that specific functions, and accordingly utilities, of GAM371 correlate with, and may be deduced from, the identity of the target genes which GAM371 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5781] Nucleotide sequences of the GAM371 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM371 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM371 are further de-

scribed hereinbelow with reference to Table Table1.

[5782] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM371 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5783] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 372 (GAM372) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5784] GAM372 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM372 was detected is described hereinabove with reference to Figs. 2-8.

[5785] GAM372 gene, herein designated GAM GENE, and GAM372 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5786] GAM372 gene, herein designated GAM GENE, encodes a GAM372 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM372 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM372 precursor RNA is designated SEQ ID:344, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:344 is located at position 881711 relative to contig NT_024812.8, on chromosome 16.

[5787] GAM372 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5788] An enzyme complex designated DICER COMPLEX, dices the GAM372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM372 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM372 RNA is designated SEQ ID:2020, and is provided hereinbelow with reference to the sequence listing part.

[5789] GAM372 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM372 target RNA, herein designated GAM TARGET RNA. GAM372 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5790] GAM372 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM372 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM372 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM372 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM372 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5791] The complementary binding of GAM372 RNA, herein designated GAM RNA, to target binding sites on GAM372 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM372 target RNA, herein designated GAM TARGET RNA, into GAM372 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5792] It is appreciated that GAM372 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM372 target genes. The mRNA of each one of this plurality of GAM372 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM372 RNA, herein designated GAM RNA, and which when bound by GAM372 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM372 target proteins.

[5793] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM372 gene, herein designated GAM GENE, on one or more GAM372 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5794] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM372 correlate with, and may be deduced from, the identity of the target genes which GAM372 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5795] Nucleotide sequences of the GAM372 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM372 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM372 are further described hereinbelow with reference to Table Table1.

[5796] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM372 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5797] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 373 (GAM373) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5798] GAM373 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM373 was detected is described hereinabove with reference to Figs. 2-8.

[5799] GAM373 gene, herein designated GAM GENE, and GAM373 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5800] GAM373 gene, herein designated GAM GENE, encodes a GAM373 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM373 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM373 precursor RNA is designated SEQ ID:345, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:345 is located at position 58159306 relative to contig NT_026437.9, on chromosome 14.

[5801] GAM373 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5802] An enzyme complex designated DICER COMPLEX, dices the GAM373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM373 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM373 RNA is designated SEQ ID:2021, and is provided hereinbelow with reference to the sequence listing part.

[5803] GAM373 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM373 target RNA, herein designated GAM TARGET RNA.
GAM373 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[5804] GAM373 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM373 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM373 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM373 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM373 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5805] The complementary binding of GAM373 RNA, herein designated GAM RNA, to target binding sites on GAM373 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM373 target RNA, herein designated GAM TARGET RNA, into GAM373 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5806] It is appreciated that GAM373 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM373 target genes. The mRNA of each one of this plurality of GAM373 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM373 RNA, herein designated GAM RNA, and which when bound by GAM373 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM373 target proteins.

[5807] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM373 gene, herein designated GAM GENE, on one or more GAM373 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5808] It is yet further appreciated that specific functions, and accordingly utilities, of GAM373 correlate with, and may be deduced from, the identity of the target genes which GAM373 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5809] Nucleotide sequences of the GAM373 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM373 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM373 are further described hereinbelow with reference to Table Table1.

[5810] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM373 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5811] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 374 (GAM374) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5812] GAM374 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM374 was detected is described hereinabove with reference to Figs. 2-8.

[5813] GAM374 gene, herein designated GAM GENE, and GAM374 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5814] GAM374 gene, herein designated GAM GENE, encodes a GAM374 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM374 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM374 precursor RNA is designated SEQ ID:346, and is provided hereinbelow with reference to the sequence listing part.

[5815] GAM374 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5816] An enzyme complex designated DICER COMPLEX, dices the GAM374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM374 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM374 RNA is designated SEQ ID:2022, and is provided

hereinbelow with reference to the sequence listing part.

[5817] GAM374 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM374 target RNA, herein designated GAM TARGET RNA. GAM374 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5818] GAM374 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM374 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM374 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM374 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM374 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5819] The complementary binding of GAM374 RNA, herein designated GAM RNA, to target binding sites on GAM374 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM374 target RNA, herein designated GAM TARGET RNA, into GAM374 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5820] It is appreciated that GAM374 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM374 target genes. The mRNA of each one of this plurality of GAM374 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM374 RNA, herein designated GAM RNA, and which when bound by GAM374 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM374 tar-

get proteins.

[5821] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM374 gene, herein designated GAM GENE, on one or more GAM374 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5822] It is yet further appreciated that specific functions, and accordingly utilities, of GAM374 correlate with, and may be deduced from, the identity of the target genes which GAM374 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5823] Nucleotide sequences of the GAM374 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM374 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM374 are further described hereinbelow with reference to Table Table1.

[5824] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM374 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5825] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 375 (GAM375) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5826] GAM375 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM375 was detected is described hereinabove with reference to Figs. 2-8.

[5827] GAM375 gene, herein designated GAM GENE, and

GAM375 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5828] GAM375 gene, herein designated GAM GENE, encodes a GAM375 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM375 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM375 precursor RNA is designated SEQ ID:347, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:347 is located at position 58159291 relative to contig NT_026437.9, on chromosome 14.

[5829] GAM375 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5830] An enzyme complex designated DICER COMPLEX, dices the GAM375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM375 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM375 RNA is designated SEQ ID:2023, and is provided hereinbelow with reference to the sequence listing part.

[5831] GAM375 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM375 target RNA, herein designated GAM TARGET RNA. GAM375 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5832] GAM375 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM375 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM375 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM375 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM375 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5833] The complementary binding of GAM375 RNA, herein designated GAM RNA, to target binding sites on GAM375 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM375 target RNA, herein designated GAM TARGET RNA, into GAM375 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[5834] It is appreciated that GAM375 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM375 target genes. The mRNA of each one of this plurality of GAM375 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM375 RNA, herein designated GAM RNA, and which when bound by GAM375 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM375 target proteins.

[5835] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM375 gene, herein designated GAM GENE, on one or more GAM375 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5836] It is yet further appreciated that specific functions, and accordingly utilities, of GAM375 correlate with, and may be deduced from, the identity of the target genes which GAM375 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5837] Nucleotide sequences of the GAM375 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM375 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM375 are further described hereinbelow with reference to Table Table1.

[5838] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM375 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5839] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 376 (GAM376) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5840] GAM376 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM376 was detected is described hereinabove with reference to Figs. 2-8.

[5841] GAM376 gene, herein designated GAM GENE, and GAM376 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5842] GAM376 gene, herein designated GAM GENE, encodes a GAM376 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM376 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM376 precursor RNA is designated SEQ ID:348, and is provided hereinbelow with reference to the sequence listing part.

[5843] GAM376 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM376 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5844] An enzyme complex designated DICER COMPLEX, dices the GAM376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM376 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM376 RNA is designated SEQ ID:2024, and is provided hereinbelow with reference to the sequence listing part.

[5845] GAM376 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM376 target RNA, herein designated GAM TARGET RNA. GAM376 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5846] GAM376 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM376 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM376 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM376 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM376 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[5847] The complementary binding of GAM376 RNA, herein designated GAM RNA, to target binding sites on GAM376 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM376 target RNA, herein designated GAM TARGET RNA, into GAM376 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5848] It is appreciated that GAM376 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM376 target genes. The mRNA of each one of this plurality of GAM376 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM376 RNA, herein designated GAM RNA, and which when bound by GAM376 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM376 target proteins.

[5849] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM376 gene, herein designated GAM GENE, on one or

more GAM376 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5850] It is yet further appreciated that specific functions, and accordingly utilities, of GAM376 correlate with, and may be deduced from, the identity of the target genes which GAM376 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5851] Nucleotide sequences of the GAM376 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM376 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM376 are further de-

scribed hereinbelow with reference to Table Table1.

[5852] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM376 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5853] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 377 (GAM377) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5854] GAM377 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM377 was detected is described hereinabove with reference to Figs. 2-8.

[5855] GAM377 gene, herein designated GAM GENE, and GAM377 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5856] GAM377 gene, herein designated GAM GENE, encodes a GAM377 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM377 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM377 precursor RNA is designated SEQ ID:349, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:349 is located at position 1235053 relative to contig NT_009526.11, on chromosome 12.

[5857] GAM377 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[5858] SEQ ID:100063 detected in mouse EST Accession BI965972.1.

[5859] SEQ ID:100181 detected in mouse EST Accession AI326210.1.

[5860] SEQ ID:100182 detected in mouse EST Accession BI965652.1.

[5861] GAM377 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5862] An enzyme complex designated DICER COMPLEX, dices the GAM377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM377 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM377 RNA is designated SEQ ID:2025, and is provided hereinbelow with reference to the sequence listing part.

[5863] GAM377 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM377 target RNA, herein designated GAM TARGET RNA. GAM377 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5864] GAM377 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM377 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM377 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM377 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM377 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5865] The complementary binding of GAM377 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM377 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM377 target RNA, herein designated GAM TARGET RNA, into GAM377 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5866] It is appreciated that GAM377 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM377 target genes. The mRNA of each one of this plurality of GAM377 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM377 RNA, herein designated GAM RNA, and which when bound by GAM377 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM377 target proteins.

[5867] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM377 gene, herein designated GAM GENE, on one or more GAM377 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5868] It is yet further appreciated that specific functions, and accordingly utilities, of GAM377 correlate with, and may be deduced from, the identity of the target genes which GAM377 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5869] Nucleotide sequences of the GAM377 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM377 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM377 are further described hereinbelow with reference to Table Table1.

[5870] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM377 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5871] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 378 (GAM378) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5872] GAM378 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM378 was detected is described hereinabove with reference to Figs. 2-8.

[5873] GAM378 gene, herein designated GAM GENE, and GAM378 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5874] GAM378 gene, herein designated GAM GENE, encodes a GAM378 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM378 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM378 precursor RNA is designated SEQ ID:350, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:350 is located at position 2907490 relative to contig NT_015805.11, on chromosome 2.

[5875] GAM378 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5876] An enzyme complex designated DICER COMPLEX, dices the GAM378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM378 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM378 RNA is designated SEQ ID:2026, and is provided hereinbelow with reference to the sequence listing part.

[5877] GAM378 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM378 target RNA, herein designated GAM TARGET RNA. GAM378 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5878] GAM378 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM378 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM378 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM378 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM378 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5879] The complementary binding of GAM378 RNA, herein designated GAM RNA, to target binding sites on GAM378 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM378 target RNA, herein designated GAM TARGET RNA, into GAM378 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5880] It is appreciated that GAM378 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM378 target genes. The mRNA of each one of this plurality of GAM378 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM378 RNA,

herein designated GAM RNA, and which when bound by GAM378 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM378 target proteins.

[5881] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM378 gene, herein designated GAM GENE, on one or more GAM378 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5882] It is yet further appreciated that specific functions, and accordingly utilities, of GAM378 correlate with, and may be deduced from, the identity of the target genes which

GAM378 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5883] Nucleotide sequences of the GAM378 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM378 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM378 are further described hereinbelow with reference to Table Table1.

[5884] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM378 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5885] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 379 (GAM379) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5886] GAM379 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM379 was detected is described hereinabove with reference to Figs. 2-8.

[5887] GAM379 gene, herein designated GAM GENE, and GAM379 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5888] GAM379 gene, herein designated GAM GENE, encodes a GAM379 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM379 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM379 precursor RNA is designated SEQ ID:351, and is provided hereinbelow with reference to the sequence listing part.

[5889] GAM379 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[5890] An enzyme complex designated DICER COMPLEX, dices the GAM379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM379 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM379 RNA is designated SEQ ID:2027, and is provided hereinbelow with reference to the sequence listing part.

[5891] GAM379 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM379 target RNA, herein designated GAM TARGET RNA. GAM379 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5892] GAM379 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM379 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM379 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM379 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM379 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5893] The complementary binding of GAM379 RNA, herein designated GAM RNA, to target binding sites on GAM379 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM379 target RNA, herein designated GAM TARGET RNA, into GAM379 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5894] It is appreciated that GAM379 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM379 target genes. The mRNA of each one of this plurality of GAM379 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM379 RNA, herein designated GAM RNA, and which when bound by GAM379 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM379 target proteins.

[5895] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM379 gene, herein designated GAM GENE, on one or more GAM379 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5896] It is yet further appreciated that specific functions, and accordingly utilities, of GAM379 correlate with, and may be deduced from, the identity of the target genes which GAM379 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5897] Nucleotide sequences of the GAM379 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM379 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM379 are further described hereinbelow with reference to Table Table1.

[5898] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM379 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5899] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 380 (GAM380) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5900] GAM380 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM380 was detected is described hereinabove with reference to Figs. 2-8.

[5901] GAM380 gene, herein designated GAM GENE, and GAM380 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5902] GAM380 gene, herein designated GAM GENE, encodes a GAM380 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM380 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM380 precursor RNA is designated SEQ ID:352, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:352 is located at position 4413739 relative to con-

tig NT_033951.3, on chromosome 6.

[5903] GAM380 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5904] An enzyme complex designated DICER COMPLEX, dices the GAM380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM380 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM380 RNA is designated SEQ ID:2028, and is provided hereinbelow with reference to the sequence listing part.

[5905] GAM380 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM380 target RNA, herein designated GAM TARGET RNA.

GAM380 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5906] GAM380 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM380 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM380 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM380 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM380 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5907] The complementary binding of GAM380 RNA, herein designated GAM RNA, to target binding sites on GAM380 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM380 target RNA, herein designated GAM TARGET RNA, into GAM380 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5908] It is appreciated that GAM380 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM380 target genes. The mRNA of each one of this plurality of GAM380 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM380 RNA, herein designated GAM RNA, and which when bound by GAM380 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM380 target proteins.

[5909] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM380 gene, herein designated GAM GENE, on one or more GAM380 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5910] It is yet further appreciated that specific functions, and accordingly utilities, of GAM380 correlate with, and may be deduced from, the identity of the target genes which GAM380 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5911] Nucleotide sequences of the GAM380 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM380 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM380 are further described hereinbelow with reference to Table Table1.

[5912] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM380 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5913] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 381 (GAM381) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5914] GAM381 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM381 was detected is described hereinabove with reference to Figs. 2-8.

[5915] GAM381 gene, herein designated GAM GENE, and GAM381 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5916] GAM381 gene, herein designated GAM GENE, encodes a GAM381 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM381 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM381 precursor RNA is designated SEQ ID:353, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:353 is located at position 1235058 relative to contig NT_009526.11, on chromosome 12.

[5917] GAM381 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[5918] SEQ ID:98036 detected in mouse EST Accession BI965972.1.

[5919] SEQ ID:98037 detected in mouse EST Accession AI326210.1.

[5920] SEQ ID:98493 detected in mouse EST Accession BI965652.1.

[5921] GAM381 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5922] An enzyme complex designated DICER COMPLEX, dices the GAM381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM381 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM381 RNA is designated SEQ ID:2029, and is provided hereinbelow with reference to the sequence listing part.

[5923] GAM381 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM381 target RNA, herein designated GAM TARGET RNA.

GAM381 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5924] GAM381 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM381 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM381 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM381 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM381 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5925] The complementary binding of GAM381 RNA, herein designated GAM RNA, to target binding sites on GAM381 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM381 target RNA, herein designated GAM TARGET RNA, into GAM381 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5926] It is appreciated that GAM381 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM381 target genes. The mRNA of each one of this plurality of GAM381 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM381 RNA, herein designated GAM RNA, and which when bound by GAM381 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM381 target proteins.

[5927] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM381 gene, herein designated GAM GENE, on one or more GAM381 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5928] It is yet further appreciated that specific functions, and accordingly utilities, of GAM381 correlate with, and may be deduced from, the identity of the target genes which GAM381 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5929] Nucleotide sequences of the GAM381 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM381 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM381 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM381 are further described hereinbelow with reference to Table Table1.

[5930] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM381 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5931] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 382 (GAM382) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5932] GAM382 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM382 was detected is described hereinabove with reference to Figs. 2-8.

[5933] GAM382 gene, herein designated GAM GENE, and GAM382 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5934] GAM382 gene, herein designated GAM GENE, encodes a GAM382 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM382 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM382 precursor RNA is designated SEQ ID:354, and is provided hereinbelow with reference to the sequence listing part.

[5935] GAM382 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[5936] SEQ ID:99215 detected in mouse EST Accession BF450182.1.

[5937] SEQ ID:99216 detected in mouse EST Accession BG964017.1.

[5938] SEQ ID:100156 detected in mouse EST Accession BE369926.1.

[5939] SEQ ID:100157 detected in mouse EST Accession BE371634.1.

[5940] SEQ ID:100158 detected in mouse EST Accession BF162728.1.

[5941] SEQ ID:100159 detected in mouse EST Accession

BE572790.1.

[5942] SEQ ID:100160 detected in mouse EST Accession BE291495.1.

[5943] GAM382 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5944] An enzyme complex designated DICER COMPLEX, dices the GAM382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM382 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM382 RNA is designated SEQ ID:2030, and is provided

hereinbelow with reference to the sequence listing part.

[5945] GAM382 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM382 target RNA, herein designated GAM TARGET RNA.

GAM382 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5946] GAM382 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM382 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM382 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM382 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM382 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5947] The complementary binding of GAM382 RNA, herein designated GAM RNA, to target binding sites on GAM382 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM382 target RNA, herein designated GAM TARGET RNA, into GAM382 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5948] It is appreciated that GAM382 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM382 target genes. The mRNA of each one of this plurality of GAM382 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM382 RNA, herein designated GAM RNA, and which when bound by GAM382 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM382 tar-

get proteins.

[5949] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM382 gene, herein designated GAM GENE, on one or more GAM382 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5950] It is yet further appreciated that specific functions, and accordingly utilities, of GAM382 correlate with, and may be deduced from, the identity of the target genes which GAM382 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5951] Nucleotide sequences of the GAM382 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM382 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM382 are further described hereinbelow with reference to Table Table1.

[5952] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM382 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5953] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 383 (GAM383) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5954] GAM383 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM383 was detected is described hereinabove with reference to Figs. 2-8.

[5955] GAM383 gene, herein designated GAM GENE, and

GAM383 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5956] GAM383 gene, herein designated GAM GENE, encodes a GAM383 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM383 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM383 precursor RNA is designated SEQ ID:355, and is provided hereinbelow with reference to the sequence listing part.

[5957] GAM383 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5958] An enzyme complex designated DICER COMPLEX, dices the GAM383 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM383 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM383 RNA is designated SEQ ID:2031, and is provided hereinbelow with reference to the sequence listing part.

[5959] GAM383 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM383 target RNA, herein designated GAM TARGET RNA. GAM383 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5960] GAM383 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM383 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM383 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM383 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM383 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5961] The complementary binding of GAM383 RNA, herein designated GAM RNA, to target binding sites on GAM383 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM383 target RNA, herein designated GAM TARGET RNA, into GAM383 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5962] It is appreciated that GAM383 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM383 target genes. The mRNA of each one of this plurality of GAM383 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM383 RNA, herein designated GAM RNA, and which when bound by GAM383 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM383 target proteins.

[5963] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM383 gene, herein designated GAM GENE, on one or more GAM383 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5964] It is yet further appreciated that specific functions, and accordingly utilities, of GAM383 correlate with, and may be deduced from, the identity of the target genes which GAM383 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5965] Nucleotide sequences of the GAM383 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM383 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM383 are further described hereinbelow with reference to Table Table1.

[5966] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM383 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5967] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

384 (GAM384) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5968] GAM384 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM384 was detected is described hereinabove with reference to Figs. 2-8.

[5969] GAM384 gene, herein designated GAM GENE, and GAM384 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5970] GAM384 gene, herein designated GAM GENE, encodes a GAM384 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM384 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM384 precursor RNA is designated SEQ ID:356, and is provided hereinbelow with reference to the sequence listing part.

[5971] GAM384 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[5972] An enzyme complex designated DICER COMPLEX, dices the GAM384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM384 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM384 RNA is designated SEQ ID:2032, and is provided hereinbelow with reference to the sequence listing part.

[5973] GAM384 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM384 target RNA, herein designated GAM TARGET RNA. GAM384 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[5974] GAM384 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM384 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM384 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM384 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM384 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[5975] The complementary binding of GAM384 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM384 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM384 target RNA, herein designated GAM TARGET RNA, into GAM384 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[5976] It is appreciated that GAM384 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM384 target genes. The mRNA of each one of this plurality of GAM384 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM384 RNA, herein designated GAM RNA, and which when bound by GAM384 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM384 target proteins.

[5977] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM384 gene, herein designated GAM GENE, on one or more GAM384 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[5978] It is yet further appreciated that specific functions, and accordingly utilities, of GAM384 correlate with, and may be deduced from, the identity of the target genes which GAM384 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[5979] Nucleotide sequences of the GAM384 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM384 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM384 are further described hereinbelow with reference to Table Table1.

[5980] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM384 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[5981] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 385 (GAM385) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[5982] GAM385 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM385 was detected is described hereinabove with reference to Figs. 2-8.

[5983] GAM385 gene, herein designated GAM GENE, and GAM385 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[5984] GAM385 gene, herein designated GAM GENE, encodes a GAM385 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM385 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM385 precursor RNA is designated SEQ ID:357, and is provided hereinbelow with reference to the sequence listing part.

[5985] GAM385 has 78 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[5986] SEQ ID:99263 detected in mouse EST Accession BF160960.1.

[5987] SEQ ID:99264 detected in mouse EST Accession BF138727.1.

[5988] SEQ ID:99265 detected in mouse EST Accession BF166442.1.

[5989] SEQ ID:99266 detected in mouse EST Accession BF782233.1.

[5990] SEQ ID:99267 detected in mouse EST Accession BF535580.1.

[5991] SEQ ID:99268 detected in mouse EST Accession BG916852.1.

[5992] SEQ ID:99269 detected in mouse EST Accession BI081856.1.

[5993] SEQ ID:99270 detected in mouse EST Accession BG922649.1.

[5994] SEQ ID:100246 detected in mouse EST Accession BF659317.1.

[5995] SEQ ID:100247 detected in mouse EST Accession N38728.1.

[5996] SEQ ID:100248 detected in mouse EST Accession BF117629.1.

[5997] SEQ ID:100249 detected in mouse EST Accession AA221726.1.

[5998] SEQ ID:100250 detected in mouse EST Accession BG801294.1.

[5999] SEQ ID:100251 detected in mouse EST Accession AA596917.1.

[6000] SEQ ID:100252 detected in mouse EST Accession AA693078.1.

[6001] SEQ ID:100253 detected in mouse EST Accession AA474248.1.

[6002] SEQ ID:100254 detected in mouse EST Accession W33955.1.

[6003] SEQ ID:100255 detected in mouse EST Accession AW475822.1.

[6004] SEQ ID:100256 detected in mouse EST Accession

AI892624.1.

[6005] SEQ ID:100257 detected in mouse EST Accession AA681470.1.

[6006] SEQ ID:100258 detected in mouse EST Accession AA237242.1.

[6007] SEQ ID:100259 detected in mouse EST Accession BI348925.1.

[6008] SEQ ID:100261 detected in mouse EST Accession AA389407.1.

[6009] SEQ ID:100262 detected in mouse EST Accession BE369890.1.

[6010] SEQ ID:100263 detected in mouse EST Accession AA475478.1.

[6011] SEQ ID:100264 detected in mouse EST Accession BG798526.1.

[6012] SEQ ID:100265 detected in mouse EST Accession AA289293.1.

[6013] SEQ ID:100266 detected in mouse EST Accession BG145499.1.

[6014] SEQ ID:100267 detected in mouse EST Accession BF022103.1.

[6015] SEQ ID:100268 detected in mouse EST Accession AA154971.1.

[6016] SEQ ID:100269 detected in mouse EST Accession AA592513.1.

[6017] SEQ ID:100270 detected in mouse EST Accession AA271180.1.

[6018] SEQ ID:100271 detected in mouse EST Accession AA691903.1.

[6019] SEQ ID:100272 detected in mouse EST Accession BI151694.1.

[6020] SEQ ID:100273 detected in mouse EST Accession AW414331.1.

[6021] SEQ ID:100274 detected in mouse EST Accession BF452313.1.

[6022] SEQ ID:100275 detected in mouse EST Accession BG806253.1.

[6023] SEQ ID:100276 detected in mouse EST Accession BI986866.1.

[6024] SEQ ID:100277 detected in mouse EST Accession BG806266.1.

[6025] SEQ ID:100278 detected in mouse EST Accession BI653740.1.

[6026] SEQ ID:100279 detected in mouse EST Accession AU035796.1.

[6027] SEQ ID:100280 detected in mouse EST Accession

AW519600.1.

[6028] SEQ ID:100281 detected in mouse EST Accession AA690129.1.

[6029] SEQ ID:100282 detected in mouse EST Accession BF138335.1.

[6030] SEQ ID:100285 detected in mouse EST Accession AA636573.1.

[6031] SEQ ID:100286 detected in mouse EST Accession BF787914.1.

[6032] SEQ ID:100287 detected in mouse EST Accession AA162923.1.

[6033] SEQ ID:100288 detected in mouse EST Accession AW106705.1.

[6034] SEQ ID:100289 detected in mouse EST Accession AA208925.1.

[6035] SEQ ID:100290 detected in mouse EST Accession BG924108.1.

[6036] SEQ ID:100291 detected in mouse EST Accession BF167547.1.

[6037] SEQ ID:100292 detected in mouse EST Accession BI654443.1.

[6038] SEQ ID:100293 detected in mouse EST Accession BE368360.1.

[6039] SEQ ID:100294 detected in mouse EST Accession AW741972.1.

[6040] SEQ ID:100295 detected in mouse EST Accession AI006184.1.

[6041] SEQ ID:100296 detected in mouse EST Accession BG864247.1.

[6042] SEQ ID:100297 detected in mouse EST Accession BI663578.1.

[6043] SEQ ID:100298 detected in mouse EST Accession BF181848.1.

[6044] SEQ ID:100299 detected in mouse EST Accession BI409527.1.

[6045] SEQ ID:100300 detected in mouse EST Accession BF538922.1.

[6046] SEQ ID:100301 detected in mouse EST Accession BF135054.1.

[6047] SEQ ID:100302 detected in mouse EST Accession BI415290.1.

[6048] SEQ ID:100303 detected in mouse EST Accession BG922635.1.

[6049] SEQ ID:100304 detected in mouse EST Accession BI248051.1.

[6050] SEQ ID:100305 detected in mouse EST Accession

BF719109.1.

[6051] SEQ ID:100306 detected in mouse EST Accession AA823879.1.

[6052] SEQ ID:100307 detected in mouse EST Accession BI645584.1.

[6053] SEQ ID:100308 detected in mouse EST Accession AW106884.1.

[6054] SEQ ID:100309 detected in mouse EST Accession BI103848.1.

[6055] SEQ ID:100310 detected in mouse EST Accession BI647997.1.

[6056] SEQ ID:100311 detected in mouse EST Accession AA161790.1.

[6057] SEQ ID:100312 detected in mouse EST Accession BI688868.1.

[6058] SEQ ID:100313 detected in mouse EST Accession BF536229.1.

[6059] SEQ ID:100314 detected in mouse EST Accession BF168730.1.

[6060] SEQ ID:100315 detected in mouse EST Accession BI151389.1.

[6061] SEQ ID:100316 detected in mouse EST Accession AU080964.1.

[6062] SEQ ID:100317 detected in mouse EST Accession BI737416.1.

[6063] SEQ ID:100318 detected in mouse EST Accession BF140767.1.

[6064] GAM385 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6065] An enzyme complex designated DICER COMPLEX, dices the GAM385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM385 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM385 RNA is designated SEQ ID:2033, and is provided hereinbelow with reference to the sequence listing part.

[6066] GAM385 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM385 target RNA, herein designated GAM TARGET RNA. GAM385 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6067] GAM385 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM385 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM385 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM385 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM385 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6068] The complementary binding of GAM385 RNA, herein designated GAM RNA, to target binding sites on GAM385 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM385 target RNA, herein designated GAM TARGET RNA, into GAM385 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6069] It is appreciated that GAM385 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM385 target genes. The mRNA of each one of this plurality of GAM385 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM385 RNA, herein designated GAM RNA, and which when bound by GAM385 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM385 target proteins.

[6070] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM385 gene, herein designated GAM GENE, on one or more GAM385 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6071] It is yet further appreciated that specific functions, and accordingly utilities, of GAM385 correlate with, and may be deduced from, the identity of the target genes which GAM385 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6072] Nucleotide sequences of the GAM385 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM385 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM385 are further described hereinbelow with reference to Table Table1.

[6073] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM385 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6074] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 386 (GAM386) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6075] GAM386 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM386 was detected is described hereinabove with reference to Figs. 2-8.

[6076] GAM386 gene, herein designated GAM GENE, and GAM386 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6077] GAM386 gene, herein designated GAM GENE, encodes a GAM386 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM386 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM386 precursor RNA is designated SEQ ID:358, and is provided hereinbelow with reference to the sequence listing part.

[6078] GAM386 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6079] An enzyme complex designated DICER COMPLEX, dices

the GAM386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM386 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM386 RNA is designated SEQ ID:2034, and is provided hereinbelow with reference to the sequence listing part.

[6080] GAM386 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM386 target RNA, herein designated GAM TARGET RNA. GAM386 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6081] GAM386 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM386 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM386

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM386 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM386 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6082] The complementary binding of GAM386 RNA, herein designated GAM RNA, to target binding sites on GAM386 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM386 target RNA, herein designated GAM TARGET RNA, into GAM386 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6083] It is appreciated that GAM386 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM386 target genes. The mRNA of each one of this plurality of GAM386 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM386 RNA, herein designated GAM RNA, and which when bound by GAM386 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM386 target proteins.

[6084] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM386 gene, herein designated GAM GENE, on one or more GAM386 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6085] It is yet further appreciated that specific functions, and accordingly utilities, of GAM386 correlate with, and may be deduced from, the identity of the target genes which GAM386 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6086] Nucleotide sequences of the GAM386 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM386 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM386 are further described hereinbelow with reference to Table Table1.

[6087] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM386 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6088] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 387 (GAM387) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6089] GAM387 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM387 was detected is described hereinabove with reference to Figs. 2-8.

[6090] GAM387 gene, herein designated GAM GENE, and GAM387 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6091] GAM387 gene, herein designated GAM GENE, encodes a GAM387 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM387 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM387 precursor RNA is designated SEQ ID:359, and is provided hereinbelow with reference to the sequence listing part.

[6092] GAM387 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6093] An enzyme complex designated DICER COMPLEX, dices the GAM387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM387 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM387 RNA is designated SEQ ID:2035, and is provided hereinbelow with reference to the sequence listing part.

[6094] GAM387 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM387 target RNA, herein designated GAM TARGET RNA. GAM387 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6095] GAM387 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM387 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM387 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM387 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM387 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6096] The complementary binding of GAM387 RNA, herein designated GAM RNA, to target binding sites on GAM387 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM387 target RNA, herein designated GAM TARGET RNA, into GAM387 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6097] It is appreciated that GAM387 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM387 target genes. The mRNA of each one of this plurality of GAM387 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM387 RNA, herein designated GAM RNA, and which when bound by GAM387 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM387 target proteins.

[6098] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM387 gene, herein designated GAM GENE, on one or more GAM387 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6099] It is yet further appreciated that specific functions, and accordingly utilities, of GAM387 correlate with, and may be deduced from, the identity of the target genes which GAM387 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6100] Nucleotide sequences of the GAM387 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM387 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM387 are further described hereinbelow with reference to Table Table1.

[6101] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM387 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6102] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 388 (GAM388) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6103] GAM388 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM388 was detected is described hereinabove with reference to Figs. 2-8.

[6104] GAM388 gene, herein designated GAM GENE, and GAM388 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6105] GAM388 gene, herein designated GAM GENE, encodes a GAM388 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM388 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM388 precursor RNA is designated SEQ ID:360, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:360 is located at position 281879 relative to contig NT_007995.11, on chromosome 8.

[6106] GAM388 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6107] An enzyme complex designated DICER COMPLEX, dices the GAM388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM388 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM388 RNA is designated SEQ ID:2036, and is provided hereinbelow with reference to the sequence listing part.

[6108] GAM388 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM388 target RNA, herein designated GAM TARGET RNA. GAM388 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6109] GAM388 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM388 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM388 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM388 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM388 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6110] The complementary binding of GAM388 RNA, herein designated GAM RNA, to target binding sites on GAM388 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM388 target RNA, herein designated GAM TARGET RNA, into GAM388 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6111] It is appreciated that GAM388 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM388 target genes. The mRNA of each one of this plurality of GAM388 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM388 RNA, herein designated GAM RNA, and which when bound by GAM388 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM388 target proteins.

[6112] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM388 gene, herein designated GAM GENE, on one or more GAM388 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6113] It is yet further appreciated that specific functions, and accordingly utilities, of GAM388 correlate with, and may

be deduced from, the identity of the target genes which GAM388 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6114] Nucleotide sequences of the GAM388 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM388 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM388 are further described hereinbelow with reference to Table Table1.

[6115] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM388 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6116] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 389 (GAM389) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6117] GAM389 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM389 was detected is described hereinabove with reference to Figs. 2-8.

[6118] GAM389 gene, herein designated GAM GENE, and GAM389 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6119] GAM389 gene, herein designated GAM GENE, encodes a GAM389 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM389 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM389 precursor RNA is designated SEQ ID:361, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:361 is located at position 5750768 relative to contig NT_010966.11, on chromosome 18.

[6120] GAM389 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6121] An enzyme complex designated DICER COMPLEX, dices the GAM389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM389 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM389 RNA is designated SEQ ID:2037, and is provided hereinbelow with reference to the sequence listing part.

[6122] GAM389 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM389 target RNA, herein designated GAM TARGET RNA. GAM389 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6123] GAM389 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM389 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM389 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM389 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM389 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6124] The complementary binding of GAM389 RNA, herein designated GAM RNA, to target binding sites on GAM389 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM389 target RNA, herein designated GAM TARGET RNA, into GAM389 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6125] It is appreciated that GAM389 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM389 target genes. The mRNA of each one of this plurality of GAM389 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM389 RNA, herein designated GAM RNA, and which when bound by GAM389 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM389 target proteins.

[6126] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM389 gene, herein designated GAM GENE, on one or more GAM389 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6127] It is yet further appreciated that specific functions, and accordingly utilities, of GAM389 correlate with, and may be deduced from, the identity of the target genes which GAM389 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6128] Nucleotide sequences of the GAM389 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM389 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM389 are further described hereinbelow with reference to Table Table1.

[6129] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM389 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6130] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 390 (GAM390) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6131] GAM390 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM390 was detected is described hereinabove with reference to Figs. 2-8.

[6132] GAM390 gene, herein designated GAM GENE, and GAM390 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6133] GAM390 gene, herein designated GAM GENE, encodes a GAM390 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM390 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM390 precursor RNA is desig-

nated SEQ ID:362, and is provided hereinbelow with reference to the sequence listing part.

[6134] GAM390 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6135] An enzyme complex designated DICER COMPLEX, dices the GAM390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM390 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM390 RNA is designated SEQ ID:2038, and is provided hereinbelow with reference to the sequence listing part.

[6136] GAM390 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM390 target RNA, herein designated GAM TARGET RNA. GAM390 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6137] GAM390 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM390 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM390 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM390 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM390

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6138] The complementary binding of GAM390 RNA, herein designated GAM RNA, to target binding sites on GAM390 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM390 target RNA, herein designated GAM TARGET RNA, into GAM390 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6139] It is appreciated that GAM390 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM390 target genes. The mRNA of each one of this plurality of GAM390 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM390 RNA, herein designated GAM RNA, and which when bound by GAM390 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM390 target proteins.

[6140] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM390 gene, herein designated GAM GENE, on one or more GAM390 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6141] It is yet further appreciated that specific functions, and accordingly utilities, of GAM390 correlate with, and may be deduced from, the identity of the target genes which GAM390 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6142] Nucleotide sequences of the GAM390 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM390 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM390 are further described hereinbelow with reference to Table Table1.

[6143] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM390 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6144] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 391 (GAM391) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[6145] GAM391 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM391 was detected is described hereinabove with reference to Figs. 2-8.

[6146] GAM391 gene, herein designated GAM GENE, and GAM391 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6147] GAM391 gene, herein designated GAM GENE, encodes a GAM391 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM391 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM391 precursor RNA is designated SEQ ID:363, and is provided hereinbelow with reference to the sequence listing part.

[6148] GAM391 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6149] An enzyme complex designated DICER COMPLEX, dices the GAM391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM391 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM391 RNA is designated SEQ ID:2039, and is provided hereinbelow with reference to the sequence listing part.

[6150] GAM391 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM391 target RNA, herein designated GAM TARGET RNA. GAM391 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6151] GAM391 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM391 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM391 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM391 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM391 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6152] The complementary binding of GAM391 RNA, herein designated GAM RNA, to target binding sites on GAM391 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM391 target RNA, herein designated GAM TARGET RNA, into GAM391 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6153] It is appreciated that GAM391 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM391 target genes. The mRNA of each one of this plurality of GAM391 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM391 RNA, herein designated GAM RNA, and which when bound by GAM391 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM391 target proteins.

[6154] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM391 gene, herein designated GAM GENE, on one or more GAM391 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6155] It is yet further appreciated that specific functions, and accordingly utilities, of GAM391 correlate with, and may be deduced from, the identity of the target genes which GAM391 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6156] Nucleotide sequences of the GAM391 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM391 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM391 are further described hereinbelow with reference to Table Table1.

[6157] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM391 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6158] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 392 (GAM392) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6159] GAM392 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM392 was detected is described hereinabove with reference to Figs. 2-8.

[6160] GAM392 gene, herein designated GAM GENE, and GAM392 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6161] GAM392 gene, herein designated GAM GENE, encodes a GAM392 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM392 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM392 precursor RNA is desig-

nated SEQ ID:364, and is provided hereinbelow with reference to the sequence listing part.

[6162] GAM392 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6163] An enzyme complex designated DICER COMPLEX, dices the GAM392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM392 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM392 RNA is designated SEQ ID:2040, and is provided hereinbelow with reference to the sequence listing part.

[6164] GAM392 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM392 target RNA, herein designated GAM TARGET RNA. GAM392 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6165] GAM392 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM392 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM392 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM392 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM392

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6166] The complementary binding of GAM392 RNA, herein designated GAM RNA, to target binding sites on GAM392 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM392 target RNA, herein designated GAM TARGET RNA, into GAM392 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6167] It is appreciated that GAM392 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM392 target genes. The mRNA of each one of this plurality of GAM392 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM392 RNA, herein designated GAM RNA, and which when bound by GAM392 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM392 target proteins.

[6168] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM392 gene, herein designated GAM GENE, on one or more GAM392 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6169] It is yet further appreciated that specific functions, and accordingly utilities, of GAM392 correlate with, and may be deduced from, the identity of the target genes which GAM392 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6170] Nucleotide sequences of the GAM392 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM392 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM392 are further described hereinbelow with reference to Table Table1.

[6171] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM392 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6172] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 393 (GAM393) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6173] GAM393 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM393 was detected is described hereinabove with reference to Figs. 2-8.

[6174] GAM393 gene, herein designated GAM GENE, and GAM393 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[6175] GAM393 gene, herein designated GAM GENE, encodes a GAM393 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM393 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM393 precursor RNA is designated SEQ ID:365, and is provided hereinbelow with reference to the sequence listing part.

[6176] GAM393 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6177] An enzyme complex designated DICER COMPLEX, dices the GAM393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM393 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM393 RNA is designated SEQ ID:2041, and is provided hereinbelow with reference to the sequence listing part.

[6178] GAM393 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM393 target RNA, herein designated GAM TARGET RNA. GAM393 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6179] GAM393 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM393 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM393 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM393 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM393 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6180] The complementary binding of GAM393 RNA, herein designated GAM RNA, to target binding sites on GAM393 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM393 target RNA, herein designated GAM TARGET RNA, into GAM393 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6181] It is appreciated that GAM393 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM393 target genes. The mRNA of each one of this plurality of GAM393 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM393 RNA, herein designated GAM RNA, and which when bound by GAM393 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM393 target proteins.

[6182] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM393 gene, herein designated GAM GENE, on one or more GAM393 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[6183] It is yet further appreciated that specific functions, and accordingly utilities, of GAM393 correlate with, and may be deduced from, the identity of the target genes which GAM393 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6184] Nucleotide sequences of the GAM393 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM393 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM393 are further described hereinbelow with reference to Table Table1.

[6185] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM393 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6186] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 394 (GAM394) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[6187] GAM394 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM394 was detected is described hereinabove with reference to Figs. 2-8.

[6188] GAM394 gene, herein designated GAM GENE, and GAM394 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6189] GAM394 gene, herein designated GAM GENE, encodes a GAM394 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM394 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM394 precursor RNA is designated SEQ ID:366, and is provided hereinbelow with reference to the sequence listing part.

[6190] GAM394 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99234, which mouse homolog is detected in mouse EST accession AA881786.1.

[6191] GAM394 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6192] An enzyme complex designated DICER COMPLEX, dices the GAM394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM394 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 96%) nucleotide sequence of GAM394 RNA is designated SEQ ID:2042, and is provided hereinbelow with reference to the sequence listing part.

[6193] GAM394 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM394

target RNA, herein designated GAM TARGET RNA.

GAM394 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6194] GAM394 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM394 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM394 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM394 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM394 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6195] The complementary binding of GAM394 RNA, herein designated GAM RNA, to target binding sites on GAM394 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM394 target RNA, herein designated GAM TARGET RNA, into GAM394 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6196] It is appreciated that GAM394 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM394 target genes. The mRNA of each one of this plurality of GAM394 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM394 RNA, herein designated GAM RNA, and which when bound by GAM394 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM394 target proteins.

[6197] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM394 gene, herein designated GAM GENE, on one or more GAM394 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6198] It is yet further appreciated that specific functions, and accordingly utilities, of GAM394 correlate with, and may be deduced from, the identity of the target genes which GAM394 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6199] Nucleotide sequences of the GAM394 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM394 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM394 are further described hereinbelow with reference to Table Table1.

[6200] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM394 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6201] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 395 (GAM395) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6202] GAM395 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM395 was detected is described hereinabove with reference to Figs. 2-8.

[6203] GAM395 gene, herein designated GAM GENE, and GAM395 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6204] GAM395 gene, herein designated GAM GENE, encodes a

GAM395 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM395 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM395 precursor RNA is designated SEQ ID:367, and is provided hereinbelow with reference to the sequence listing part.

[6205] GAM395 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6206] An enzyme complex designated DICER COMPLEX, dices the GAM395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM395 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM395 RNA is designated SEQ ID:2043, and is provided hereinbelow with reference to the sequence listing part.

[6207] GAM395 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM395 target RNA, herein designated GAM TARGET RNA. GAM395 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6208] GAM395 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM395 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM395 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM395 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM395 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6209] The complementary binding of GAM395 RNA, herein designated GAM RNA, to target binding sites on GAM395 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM395 target RNA, herein designated GAM TARGET RNA, into GAM395 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6210] It is appreciated that GAM395 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM395 target genes. The mRNA of each one of this plurality of GAM395 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM395 RNA, herein designated GAM RNA, and which when bound by GAM395 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM395 target proteins.

[6211] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM395 gene, herein designated GAM GENE, on one or more GAM395 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6212] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM395 correlate with, and may be deduced from, the identity of the target genes which GAM395 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6213] Nucleotide sequences of the GAM395 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM395 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM395 are further described hereinbelow with reference to Table Table1.

[6214] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM395 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6215] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 396 (GAM396) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6216] GAM396 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM396 was detected is described hereinabove with reference to Figs. 2-8.

[6217] GAM396 gene, herein designated GAM GENE, and GAM396 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6218] GAM396 gene, herein designated GAM GENE, encodes a GAM396 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM396 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM396 precursor RNA is designated SEQ ID:368, and is provided hereinbelow with reference to the sequence listing part.

[6219] GAM396 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6220] An enzyme complex designated DICER COMPLEX, dices the GAM396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM396 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM396 RNA is designated SEQ ID:2044, and is provided hereinbelow with reference to the sequence listing part.

[6221] GAM396 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM396 target RNA, herein designated GAM TARGET RNA. GAM396 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6222] GAM396 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM396 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM396 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM396 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM396 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6223] The complementary binding of GAM396 RNA, herein designated GAM RNA, to target binding sites on GAM396 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM396 target RNA, herein designated GAM TARGET RNA, into GAM396 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6224] It is appreciated that GAM396 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM396 target genes. The mRNA of each one of this plurality of GAM396 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM396 RNA, herein designated GAM RNA, and which when bound by GAM396 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM396 target proteins.

[6225] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM396 gene, herein designated GAM GENE, on one or more GAM396 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6226] It is yet further appreciated that specific functions, and accordingly utilities, of GAM396 correlate with, and may be deduced from, the identity of the target genes which GAM396 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6227] Nucleotide sequences of the GAM396 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM396 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM396 are further described hereinbelow with reference to Table Table1.

[6228] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM396 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6229] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 397 (GAM397) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6230] GAM397 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM397 was detected is described hereinabove with reference to Figs. 2-8.

[6231] GAM397 gene, herein designated GAM GENE, and GAM397 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6232] GAM397 gene, herein designated GAM GENE, encodes a GAM397 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM397 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM397 precursor RNA is designated SEQ ID:369, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:369 is located at position 1122805 relative to contig NT_011512.7, on chromosome 21.

[6233] GAM397 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6234] An enzyme complex designated DICER COMPLEX, dices the GAM397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM397 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM397 RNA is designated SEQ ID:2045, and is provided

hereinbelow with reference to the sequence listing part.

[6235] GAM397 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM397 target RNA, herein designated GAM TARGET RNA. GAM397 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6236] GAM397 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM397 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM397 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM397 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM397 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6237] The complementary binding of GAM397 RNA, herein designated GAM RNA, to target binding sites on GAM397 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM397 target RNA, herein designated GAM TARGET RNA, into GAM397 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6238] It is appreciated that GAM397 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM397 target genes. The mRNA of each one of this plurality of GAM397 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM397 RNA, herein designated GAM RNA, and which when bound by GAM397 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM397 tar-

get proteins.

[6239] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM397 gene, herein designated GAM GENE, on one or more GAM397 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6240] It is yet further appreciated that specific functions, and accordingly utilities, of GAM397 correlate with, and may be deduced from, the identity of the target genes which GAM397 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6241] Nucleotide sequences of the GAM397 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM397 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM397 are further described hereinbelow with reference to Table Table1.

[6242] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM397 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6243] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 398 (GAM398) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6244] GAM398 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM398 was detected is described hereinabove with reference to Figs. 2-8.

[6245] GAM398 gene, herein designated GAM GENE, and

GAM398 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6246] GAM398 gene, herein designated GAM GENE, encodes a GAM398 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM398 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM398 precursor RNA is designated SEQ ID:370, and is provided hereinbelow with reference to the sequence listing part.

[6247] GAM398 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[6248] SEQ ID:98425 detected in mouse EST Accession BE369926.1.

[6249] SEQ ID:98426 detected in mouse EST Accession BF450182.1.

[6250] SEQ ID:98427 detected in mouse EST Accession BE371634.1.

[6251] SEQ ID:98428 detected in mouse EST Accession

BE291495.1.

[6252] SEQ ID:98429 detected in mouse EST Accession BF162728.1.

[6253] SEQ ID:98430 detected in mouse EST Accession BE572790.1.

[6254] SEQ ID:98431 detected in mouse EST Accession BG964017.1.

[6255] GAM398 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6256] An enzyme complex designated DICER COMPLEX, dices the GAM398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM398 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM398 RNA is designated SEQ ID:2046, and is provided hereinbelow with reference to the sequence listing part.

[6257] GAM398 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM398 target RNA, herein designated GAM TARGET RNA. GAM398 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6258] GAM398 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM398 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM398 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM398 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM398 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6259] The complementary binding of GAM398 RNA, herein designated GAM RNA, to target binding sites on GAM398 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM398 target RNA, herein designated GAM TARGET RNA, into GAM398 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6260] It is appreciated that GAM398 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM398 target genes. The mRNA of each one of this plurality of GAM398 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM398 RNA, herein designated GAM RNA, and which when bound by GAM398 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM398 target proteins.

[6261] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM398 gene, herein designated GAM GENE, on one or more GAM398 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6262] It is yet further appreciated that specific functions, and accordingly utilities, of GAM398 correlate with, and may

be deduced from, the identity of the target genes which GAM398 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6263] Nucleotide sequences of the GAM398 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM398 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM398 are further described hereinbelow with reference to Table Table1.

[6264] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM398 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6265] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 399 (GAM399) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6266] GAM399 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM399 was detected is described hereinabove with reference to Figs. 2-8.

[6267] GAM399 gene, herein designated GAM GENE, and GAM399 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6268] GAM399 gene, herein designated GAM GENE, encodes a GAM399 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM399 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM399 precursor RNA is designated SEQ ID:371, and is provided hereinbelow with reference to the sequence listing part.

[6269] GAM399 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[6270] An enzyme complex designated DICER COMPLEX, dices the GAM399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM399 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM399 RNA is designated SEQ ID:2047, and is provided hereinbelow with reference to the sequence listing part.

[6271] GAM399 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM399 target RNA, herein designated GAM TARGET RNA.
GAM399 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6272] GAM399 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM399 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM399 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM399 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM399 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6273] The complementary binding of GAM399 RNA, herein designated GAM RNA, to target binding sites on GAM399 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM399 target RNA, herein desig-

nated GAM TARGET RNA, into GAM399 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6274] It is appreciated that GAM399 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM399 target genes. The mRNA of each one of this plurality of GAM399 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM399 RNA, herein designated GAM RNA, and which when bound by GAM399 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM399 target proteins.

[6275] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM399 gene, herein designated GAM GENE, on one or more GAM399 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6276] It is yet further appreciated that specific functions, and accordingly utilities, of GAM399 correlate with, and may be deduced from, the identity of the target genes which GAM399 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6277] Nucleotide sequences of the GAM399 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM399 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM399 are further described hereinbelow with reference to Table Table1.

[6278] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM399 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[6279] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 400 (GAM400) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6280] GAM400 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM400 was detected is described hereinabove with reference to Figs. 2-8.

[6281] GAM400 gene, herein designated GAM GENE, and GAM400 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6282] GAM400 gene, herein designated GAM GENE, encodes a GAM400 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM400 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM400 precursor RNA is designated SEQ ID:372, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:372 is located at position 1235058 relative to contig NT_009526.11, on chromosome 12.

[6283] GAM400 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[6284] SEQ ID:100213 detected in mouse EST Accession BI965972.1.

[6285] SEQ ID:100214 detected in mouse EST Accession AI326210.1.

[6286] SEQ ID:100215 detected in mouse EST Accession BI965652.1.

[6287] GAM400 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6288] An enzyme complex designated DICER COMPLEX, dices the GAM400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM400 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM400 RNA is designated SEQ ID:2048, and is provided hereinbelow with reference to the sequence listing part.

[6289] GAM400 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM400 target RNA, herein designated GAM TARGET RNA. GAM400 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6290] GAM400 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM400 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM400 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM400 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM400 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6291] The complementary binding of GAM400 RNA, herein designated GAM RNA, to target binding sites on GAM400 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM400 target RNA, herein designated GAM TARGET RNA, into GAM400 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[6292] It is appreciated that GAM400 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM400 target genes. The mRNA of each one of this plurality of GAM400 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM400 RNA, herein designated GAM RNA, and which when bound by GAM400 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM400 target proteins.

[6293] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM400 gene, herein designated GAM GENE, on one or more GAM400 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6294] It is yet further appreciated that specific functions, and accordingly utilities, of GAM400 correlate with, and may be deduced from, the identity of the target genes which GAM400 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6295] Nucleotide sequences of the GAM400 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM400 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM400 are further described hereinbelow with reference to Table Table1.

[6296] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM400 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6297] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 401 (GAM401) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6298] GAM401 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM401 was detected is described hereinabove with reference to Figs. 2-8.

[6299] GAM401 gene, herein designated GAM GENE, and GAM401 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6300] GAM401 gene, herein designated GAM GENE, encodes a GAM401 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM401 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM401 precursor RNA is designated SEQ ID:373, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:373 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[6301] GAM401 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6302] An enzyme complex designated DICER COMPLEX, dices the GAM401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM401 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM401 RNA is designated SEQ ID:2049, and is provided hereinbelow with reference to the sequence listing part.

[6303] GAM401 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM401

target RNA, herein designated GAM TARGET RNA.

GAM401 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6304] GAM401 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM401 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM401 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM401 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM401 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6305] The complementary binding of GAM401 RNA, herein designated GAM RNA, to target binding sites on GAM401 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM401 target RNA, herein designated GAM TARGET RNA, into GAM401 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6306] It is appreciated that GAM401 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM401 target genes. The mRNA of each one of this plurality of GAM401 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM401 RNA, herein designated GAM RNA, and which when bound by GAM401 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM401 target proteins.

[6307] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM401 gene, herein designated GAM GENE, on one or more GAM401 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6308] It is yet further appreciated that specific functions, and accordingly utilities, of GAM401 correlate with, and may be deduced from, the identity of the target genes which GAM401 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6309] Nucleotide sequences of the GAM401 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM401 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM401 are further described hereinbelow with reference to Table Table1.

[6310] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM401 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6311] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 402 (GAM402) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6312] GAM402 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM402 was detected is described hereinabove with reference to Figs. 2-8.

[6313] GAM402 gene, herein designated GAM GENE, and GAM402 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6314] GAM402 gene, herein designated GAM GENE, encodes a

GAM402 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM402 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM402 precursor RNA is designated SEQ ID:374, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:374 is located at position 765366 relative to contig NT_005863.13, on chromosome 3.

[6315] GAM402 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[6316] SEQ ID:98929 detected in mouse EST Accession BI690616.1.

[6317] SEQ ID:98930 detected in mouse EST Accession BI688304.1.

[6318] SEQ ID:98931 detected in mouse EST Accession BI659161.1.

[6319] GAM402 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM402 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6320] An enzyme complex designated DICER COMPLEX, dices the GAM402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM402 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM402 RNA is designated SEQ ID:2050, and is provided hereinbelow with reference to the sequence listing part.

[6321] GAM402 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM402 target RNA, herein designated GAM TARGET RNA. GAM402 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6322] GAM402 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM402 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM402 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM402 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM402 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[6323] The complementary binding of GAM402 RNA, herein designated GAM RNA, to target binding sites on GAM402 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM402 target RNA, herein designated GAM TARGET RNA, into GAM402 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6324] It is appreciated that GAM402 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM402 target genes. The mRNA of each one of this plurality of GAM402 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM402 RNA, herein designated GAM RNA, and which when bound by GAM402 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM402 target proteins.

[6325] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM402 gene, herein designated GAM GENE, on one or

more GAM402 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6326] It is yet further appreciated that specific functions, and accordingly utilities, of GAM402 correlate with, and may be deduced from, the identity of the target genes which GAM402 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6327] Nucleotide sequences of the GAM402 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM402 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM402 are further de-

scribed hereinbelow with reference to Table Table1.

[6328] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM402 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6329] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 403 (GAM403) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6330] GAM403 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM403 was detected is described hereinabove with reference to Figs. 2-8.

[6331] GAM403 gene, herein designated GAM GENE, and GAM403 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6332] GAM403 gene, herein designated GAM GENE, encodes a GAM403 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM403 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM403 precursor RNA is designated SEQ ID:375, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:375 is located at position 58159291 relative to contig NT_026437.9, on chromosome 14.

[6333] GAM403 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6334] An enzyme complex designated DICER COMPLEX, dices the GAM403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM403 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM403 RNA is designated SEQ ID:2051, and is provided hereinbelow with reference to the sequence listing part.

[6335] GAM403 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM403 target RNA, herein designated GAM TARGET RNA. GAM403 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6336] GAM403 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM403 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM403 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM403 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM403 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6337] The complementary binding of GAM403 RNA, herein designated GAM RNA, to target binding sites on GAM403 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM403 target RNA, herein designated GAM TARGET RNA, into GAM403 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6338] It is appreciated that GAM403 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM403 target genes. The mRNA of each one of this plurality of GAM403 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM403 RNA, herein designated GAM RNA, and which when bound by GAM403 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM403 target proteins.

[6339] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM403 gene, herein designated GAM GENE, on one or more GAM403 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6340] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM403 correlate with, and may be deduced from, the identity of the target genes which GAM403 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6341] Nucleotide sequences of the GAM403 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM403 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM403 are further described hereinbelow with reference to Table Table1.

[6342] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM403 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6343] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 404 (GAM404) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6344] GAM404 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM404 was detected is described hereinabove with reference to Figs. 2-8.

[6345] GAM404 gene, herein designated GAM GENE, and GAM404 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6346] GAM404 gene, herein designated GAM GENE, encodes a GAM404 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM404 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM404 precursor RNA is designated SEQ ID:376, and is provided hereinbelow with reference to the sequence listing part.

[6347] GAM404 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6348] An enzyme complex designated DICER COMPLEX, dices the GAM404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM404 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM404 RNA is designated SEQ ID:2052, and is provided hereinbelow with reference to the sequence listing part.

[6349] GAM404 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM404 target RNA, herein designated GAM TARGET RNA. GAM404 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6350] GAM404 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM404 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM404 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM404 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM404 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6351] The complementary binding of GAM404 RNA, herein designated GAM RNA, to target binding sites on GAM404 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM404 target RNA, herein designated GAM TARGET RNA, into GAM404 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6352] It is appreciated that GAM404 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM404 target genes. The mRNA of each one of this plurality of GAM404 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM404 RNA, herein designated GAM RNA, and which when bound by GAM404 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM404 target proteins.

[6353] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM404 gene, herein designated GAM GENE, on one or more GAM404 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6354] It is yet further appreciated that specific functions, and accordingly utilities, of GAM404 correlate with, and may be deduced from, the identity of the target genes which GAM404 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6355] Nucleotide sequences of the GAM404 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM404 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM404 are further described hereinbelow with reference to Table Table1.

[6356] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM404 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6357] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 405 (GAM405) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6358] GAM405 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM405 was detected is described hereinabove with reference to Figs. 2-8.

[6359] GAM405 gene, herein designated GAM GENE, and GAM405 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6360] GAM405 gene, herein designated GAM GENE, encodes a GAM405 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM405 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM405 precursor RNA is designated SEQ ID:377, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:377 is located at position 12528241 relative to contig NT_008183.13, on chromosome 8.

[6361] GAM405 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6362] An enzyme complex designated DICER COMPLEX, dices the GAM405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM405 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM405 RNA is designated SEQ ID:2053, and is provided

hereinbelow with reference to the sequence listing part.

[6363] GAM405 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM405 target RNA, herein designated GAM TARGET RNA.
GAM405 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6364] GAM405 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM405 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM405 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM405 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM405 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6365] The complementary binding of GAM405 RNA, herein designated GAM RNA, to target binding sites on GAM405 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM405 target RNA, herein designated GAM TARGET RNA, into GAM405 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6366] It is appreciated that GAM405 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM405 target genes. The mRNA of each one of this plurality of GAM405 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM405 RNA, herein designated GAM RNA, and which when bound by GAM405 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM405 tar-

get proteins.

[6367] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM405 gene, herein designated GAM GENE, on one or more GAM405 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6368] It is yet further appreciated that specific functions, and accordingly utilities, of GAM405 correlate with, and may be deduced from, the identity of the target genes which GAM405 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6369] Nucleotide sequences of the GAM405 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM405 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM405 are further described hereinbelow with reference to Table Table1.

[6370] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM405 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6371] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 406 (GAM406) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6372] GAM406 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM406 was detected is described hereinabove with reference to Figs. 2-8.

[6373] GAM406 gene, herein designated GAM GENE, and

GAM406 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6374] GAM406 gene, herein designated GAM GENE, encodes a GAM406 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM406 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM406 precursor RNA is designated SEQ ID:378, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:378 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[6375] GAM406 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6376] An enzyme complex designated DICER COMPLEX, dices the GAM406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM406 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM406 RNA is designated SEQ ID:2054, and is provided hereinbelow with reference to the sequence listing part.

[6377] GAM406 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM406 target RNA, herein designated GAM TARGET RNA. GAM406 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6378] GAM406 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM406 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM406 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM406 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM406 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6379] The complementary binding of GAM406 RNA, herein designated GAM RNA, to target binding sites on GAM406 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM406 target RNA, herein designated GAM TARGET RNA, into GAM406 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[6380] It is appreciated that GAM406 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM406 target genes. The mRNA of each one of this plurality of GAM406 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM406 RNA, herein designated GAM RNA, and which when bound by GAM406 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM406 target proteins.

[6381] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM406 gene, herein designated GAM GENE, on one or more GAM406 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6382] It is yet further appreciated that specific functions, and accordingly utilities, of GAM406 correlate with, and may be deduced from, the identity of the target genes which GAM406 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6383] Nucleotide sequences of the GAM406 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM406 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM406 are further described hereinbelow with reference to Table Table1.

[6384] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM406 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6385] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 407 (GAM407) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6386] GAM407 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM407 was detected is described hereinabove with reference to Figs. 2-8.

[6387] GAM407 gene, herein designated GAM GENE, and GAM407 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6388] GAM407 gene, herein designated GAM GENE, encodes a GAM407 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM407 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM407 precursor RNA is designated SEQ ID:379, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:379 is located at position 3362161 relative to contig NT_023451.11, on chromosome 6.

[6389] GAM407 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6390] An enzyme complex designated DICER COMPLEX, dices the GAM407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM407 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM407 RNA is designated SEQ ID:2055, and is provided hereinbelow with reference to the sequence listing part.

[6391] GAM407 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM407

target RNA, herein designated GAM TARGET RNA.

GAM407 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6392] GAM407 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM407 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM407 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM407 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM407 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6393] The complementary binding of GAM407 RNA, herein designated GAM RNA, to target binding sites on GAM407 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM407 target RNA, herein designated GAM TARGET RNA, into GAM407 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6394] It is appreciated that GAM407 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM407 target genes. The mRNA of each one of this plurality of GAM407 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM407 RNA, herein designated GAM RNA, and which when bound by GAM407 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM407 target proteins.

[6395] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM407 gene, herein designated GAM GENE, on one or more GAM407 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6396] It is yet further appreciated that specific functions, and accordingly utilities, of GAM407 correlate with, and may be deduced from, the identity of the target genes which GAM407 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6397] Nucleotide sequences of the GAM407 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM407 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM407 are further described hereinbelow with reference to Table Table1.

[6398] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM407 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6399] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 408 (GAM408) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6400] GAM408 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM408 was detected is described hereinabove with reference to Figs. 2-8.

[6401] GAM408 gene, herein designated GAM GENE, and GAM408 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6402] GAM408 gene, herein designated GAM GENE, encodes a

GAM408 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM408 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM408 precursor RNA is designated SEQ ID:380, and is provided hereinbelow with reference to the sequence listing part.

[6403] GAM408 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6404] An enzyme complex designated DICER COMPLEX, dices the GAM408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM408 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM408 RNA is designated SEQ ID:2056, and is provided hereinbelow with reference to the sequence listing part.

[6405] GAM408 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM408 target RNA, herein designated GAM TARGET RNA. GAM408 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6406] GAM408 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM408 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM408 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM408 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM408 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6407] The complementary binding of GAM408 RNA, herein designated GAM RNA, to target binding sites on GAM408 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM408 target RNA, herein designated GAM TARGET RNA, into GAM408 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6408] It is appreciated that GAM408 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM408 target genes. The mRNA of each one of this plurality of GAM408 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM408 RNA, herein designated GAM RNA, and which when bound by GAM408 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM408 target proteins.

[6409] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM408 gene, herein designated GAM GENE, on one or more GAM408 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6410] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM408 correlate with, and may be deduced from, the identity of the target genes which GAM408 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6411] Nucleotide sequences of the GAM408 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM408 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM408 are further described hereinbelow with reference to Table Table1.

[6412] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM408 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6413] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 409 (GAM409) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6414] GAM409 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM409 was detected is described hereinabove with reference to Figs. 2-8.

[6415] GAM409 gene, herein designated GAM GENE, and GAM409 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6416] GAM409 gene, herein designated GAM GENE, encodes a GAM409 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM409 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM409 precursor RNA is designated SEQ ID:381, and is provided hereinbelow with reference to the sequence listing part.

[6417] GAM409 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6418] An enzyme complex designated DICER COMPLEX, dices the GAM409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM409 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM409 RNA is designated SEQ ID:2057, and is provided hereinbelow with reference to the sequence listing part.

[6419] GAM409 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM409 target RNA, herein designated GAM TARGET RNA. GAM409 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6420] GAM409 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM409 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM409 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM409 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM409 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6421] The complementary binding of GAM409 RNA, herein designated GAM RNA, to target binding sites on GAM409 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM409 target RNA, herein designated GAM TARGET RNA, into GAM409 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6422] It is appreciated that GAM409 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM409 target genes. The mRNA of each one of this plurality of GAM409 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM409 RNA, herein designated GAM RNA, and which when bound by GAM409 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM409 target proteins.

[6423] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM409 gene, herein designated GAM GENE, on one or more GAM409 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6424] It is yet further appreciated that specific functions, and accordingly utilities, of GAM409 correlate with, and may be deduced from, the identity of the target genes which GAM409 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6425] Nucleotide sequences of the GAM409 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM409 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM409 are further described hereinbelow with reference to Table Table1.

[6426] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM409 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6427] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 410 (GAM410) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6428] GAM410 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM410 was detected is described hereinabove with reference to Figs. 2-8.

[6429] GAM410 gene, herein designated GAM GENE, and GAM410 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6430] GAM410 gene, herein designated GAM GENE, encodes a GAM410 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM410 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM410 precursor RNA is designated SEQ ID:382, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:382 is located at position 2349685 relative to contig NT_021907.13, on chromosome 1.

[6431] GAM410 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6432] An enzyme complex designated DICER COMPLEX, dices the GAM410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM410 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM410 RNA is designated SEQ ID:2058, and is provided

hereinbelow with reference to the sequence listing part.

[6433] GAM410 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM410 target RNA, herein designated GAM TARGET RNA. GAM410 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6434] GAM410 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM410 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM410 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM410 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM410 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6435] The complementary binding of GAM410 RNA, herein designated GAM RNA, to target binding sites on GAM410 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM410 target RNA, herein designated GAM TARGET RNA, into GAM410 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6436] It is appreciated that GAM410 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM410 target genes. The mRNA of each one of this plurality of GAM410 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM410 RNA, herein designated GAM RNA, and which when bound by GAM410 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM410 tar-

get proteins.

[6437] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM410 gene, herein designated GAM GENE, on one or more GAM410 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6438] It is yet further appreciated that specific functions, and accordingly utilities, of GAM410 correlate with, and may be deduced from, the identity of the target genes which GAM410 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6439] Nucleotide sequences of the GAM410 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM410 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM410 are further described hereinbelow with reference to Table Table1.

[6440] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM410 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6441] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 411 (GAM411) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6442] GAM411 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM411 was detected is described hereinabove with reference to Figs. 2-8.

[6443] GAM411 gene, herein designated GAM GENE, and

GAM411 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6444] GAM411 gene, herein designated GAM GENE, encodes a GAM411 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM411 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM411 precursor RNA is designated SEQ ID:383, and is provided hereinbelow with reference to the sequence listing part.

[6445] GAM411 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6446] An enzyme complex designated DICER COMPLEX, dices the GAM411 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM411 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM411 RNA is designated SEQ ID:2059, and is provided hereinbelow with reference to the sequence listing part.

[6447] GAM411 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM411 target RNA, herein designated GAM TARGET RNA. GAM411 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6448] GAM411 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM411 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM411 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM411 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM411 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6449] The complementary binding of GAM411 RNA, herein designated GAM RNA, to target binding sites on GAM411 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM411 target RNA, herein designated GAM TARGET RNA, into GAM411 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6450] It is appreciated that GAM411 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM411 target genes. The mRNA of each one of this plurality of GAM411 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM411 RNA, herein designated GAM RNA, and which when bound by GAM411 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM411 target proteins.

[6451] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM411 gene, herein designated GAM GENE, on one or more GAM411 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6452] It is yet further appreciated that specific functions, and accordingly utilities, of GAM411 correlate with, and may be deduced from, the identity of the target genes which GAM411 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6453] Nucleotide sequences of the GAM411 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM411 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM411 are further described hereinbelow with reference to Table Table1.

[6454] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM411 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6455] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

412 (GAM412) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6456] GAM412 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM412 was detected is described hereinabove with reference to Figs. 2-8.

[6457] GAM412 gene, herein designated GAM GENE, and GAM412 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6458] GAM412 gene, herein designated GAM GENE, encodes a GAM412 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM412 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM412 precursor RNA is designated SEQ ID:384, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:384 is located at position 3288795 relative to contig NT_006713.11, on chromosome 5.

[6459] GAM412 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM412 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6460] An enzyme complex designated DICER COMPLEX, dices the GAM412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM412 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM412 RNA is designated SEQ ID:2060, and is provided hereinbelow with reference to the sequence listing part.

[6461] GAM412 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM412 target RNA, herein designated GAM TARGET RNA. GAM412 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6462] GAM412 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM412 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM412 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM412 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM412 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[6463] The complementary binding of GAM412 RNA, herein designated GAM RNA, to target binding sites on GAM412 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM412 target RNA, herein designated GAM TARGET RNA, into GAM412 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6464] It is appreciated that GAM412 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM412 target genes. The mRNA of each one of this plurality of GAM412 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM412 RNA, herein designated GAM RNA, and which when bound by GAM412 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM412 target proteins.

[6465] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM412 gene, herein designated GAM GENE, on one or

more GAM412 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6466] It is yet further appreciated that specific functions, and accordingly utilities, of GAM412 correlate with, and may be deduced from, the identity of the target genes which GAM412 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6467] Nucleotide sequences of the GAM412 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM412 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM412 are further de-

scribed hereinbelow with reference to Table Table1.

[6468] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM412 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6469] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 413 (GAM413) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6470] GAM413 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM413 was detected is described hereinabove with reference to Figs. 2-8.

[6471] GAM413 gene, herein designated GAM GENE, and GAM413 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6472] GAM413 gene, herein designated GAM GENE, encodes a GAM413 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM413 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM413 precursor RNA is designated SEQ ID:385, and is provided hereinbelow with reference to the sequence listing part.

[6473] GAM413 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6474] An enzyme complex designated DICER COMPLEX, dices the GAM413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM413 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM413 RNA is designated SEQ ID:2061, and is provided hereinbelow with reference to the sequence listing part.

[6475] GAM413 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM413 target RNA, herein designated GAM TARGET RNA. GAM413 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6476] GAM413 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM413 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM413 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM413 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM413 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6477] The complementary binding of GAM413 RNA, herein designated GAM RNA, to target binding sites on GAM413 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM413 target RNA, herein designated GAM TARGET RNA, into GAM413 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6478] It is appreciated that GAM413 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM413 target genes. The mRNA of each one of this plurality of GAM413 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM413 RNA,

herein designated GAM RNA, and which when bound by GAM413 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM413 target proteins.

[6479] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM413 gene, herein designated GAM GENE, on one or more GAM413 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6480] It is yet further appreciated that specific functions, and accordingly utilities, of GAM413 correlate with, and may be deduced from, the identity of the target genes which

GAM413 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6481] Nucleotide sequences of the GAM413 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM413 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM413 are further described hereinbelow with reference to Table Table1.

[6482] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM413 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6483] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 414 (GAM414) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6484] GAM414 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM414 was detected is described hereinabove with reference to Figs. 2-8.

[6485] GAM414 gene, herein designated GAM GENE, and GAM414 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6486] GAM414 gene, herein designated GAM GENE, encodes a GAM414 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM414 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM414 precursor RNA is designated SEQ ID:386, and is provided hereinbelow with reference to the sequence listing part.

[6487] GAM414 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[6488] An enzyme complex designated DICER COMPLEX, dices the GAM414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM414 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM414 RNA is designated SEQ ID:2062, and is provided hereinbelow with reference to the sequence listing part.

[6489] GAM414 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM414 target RNA, herein designated GAM TARGET RNA. GAM414 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6490] GAM414 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM414 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM414 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM414 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM414 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6491] The complementary binding of GAM414 RNA, herein designated GAM RNA, to target binding sites on GAM414 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM414 target RNA, herein designated GAM TARGET RNA, into GAM414 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6492] It is appreciated that GAM414 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM414 target genes. The mRNA of each one of this plurality of GAM414 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM414 RNA, herein designated GAM RNA, and which when bound by GAM414 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM414 target proteins.

[6493] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM414 gene, herein designated GAM GENE, on one or more GAM414 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6494] It is yet further appreciated that specific functions, and accordingly utilities, of GAM414 correlate with, and may be deduced from, the identity of the target genes which GAM414 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6495] Nucleotide sequences of the GAM414 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM414 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM414 are further described hereinbelow with reference to Table Table1.

[6496] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM414 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6497] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 415 (GAM415) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6498] GAM415 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM415 was detected is described hereinabove with reference to Figs. 2-8.

[6499] GAM415 gene, herein designated GAM GENE, and GAM415 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6500] GAM415 gene, herein designated GAM GENE, encodes a GAM415 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM415 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM415 precursor RNA is designated SEQ ID:387, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:387 is located at position 7933233 relative to con-

tig NT_033899.3, on chromosome 11.

[6501] GAM415 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98324, which mouse homolog is detected in mouse EST accession BI411194.1.

[6502] GAM415 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6503] An enzyme complex designated DICER COMPLEX, dices the GAM415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM415 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM415 RNA is designated SEQ ID:2063, and is provided hereinbelow with reference to the sequence listing part.

[6504] GAM415 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM415 target RNA, herein designated GAM TARGET RNA. GAM415 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6505] GAM415 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM415 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM415 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM415 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM415 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6506] The complementary binding of GAM415 RNA, herein designated GAM RNA, to target binding sites on GAM415 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM415 target RNA, herein designated GAM TARGET RNA, into GAM415 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6507] It is appreciated that GAM415 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM415 target genes. The mRNA of each one of this plurality of GAM415 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM415 RNA,

herein designated GAM RNA, and which when bound by GAM415 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM415 target proteins.

[6508] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM415 gene, herein designated GAM GENE, on one or more GAM415 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6509] It is yet further appreciated that specific functions, and accordingly utilities, of GAM415 correlate with, and may be deduced from, the identity of the target genes which

GAM415 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6510] Nucleotide sequences of the GAM415 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM415 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM415 are further described hereinbelow with reference to Table Table1.

[6511] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM415 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6512] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 416 (GAM416) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6513] GAM416 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM416 was detected is described hereinabove with reference to Figs. 2-8.

[6514] GAM416 gene, herein designated GAM GENE, and GAM416 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6515] GAM416 gene, herein designated GAM GENE, encodes a GAM416 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM416 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM416 precursor RNA is designated SEQ ID:388, and is provided hereinbelow with reference to the sequence listing part.

[6516] GAM416 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[6517] An enzyme complex designated DICER COMPLEX, dices the GAM416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM416 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM416 RNA is designated SEQ ID:2064, and is provided hereinbelow with reference to the sequence listing part.

[6518] GAM416 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM416 target RNA, herein designated GAM TARGET RNA. GAM416 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6519] GAM416 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM416 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM416 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM416 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM416 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6520] The complementary binding of GAM416 RNA, herein designated GAM RNA, to target binding sites on GAM416 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM416 target RNA, herein designated GAM TARGET RNA, into GAM416 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6521] It is appreciated that GAM416 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM416 target genes. The mRNA of each one of this plurality of GAM416 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM416 RNA, herein designated GAM RNA, and which when bound by GAM416 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM416 target proteins.

[6522] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM416 gene, herein designated GAM GENE, on one or more GAM416 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6523] It is yet further appreciated that specific functions, and accordingly utilities, of GAM416 correlate with, and may be deduced from, the identity of the target genes which GAM416 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6524] Nucleotide sequences of the GAM416 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM416 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM416 are further described hereinbelow with reference to Table Table1.

[6525] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM416 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6526] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 417 (GAM417) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6527] GAM417 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM417 was detected is described hereinabove with reference to Figs. 2-8.

[6528] GAM417 gene, herein designated GAM GENE, and GAM417 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6529] GAM417 gene, herein designated GAM GENE, encodes a GAM417 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM417 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM417 precursor RNA is designated SEQ ID:389, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:389 is located at position 5764678 relative to con-

tig NT_008984.13, on chromosome 11.

[6530] GAM417 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6531] An enzyme complex designated DICER COMPLEX, dices the GAM417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM417 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM417 RNA is designated SEQ ID:2065, and is provided hereinbelow with reference to the sequence listing part.

[6532] GAM417 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM417 target RNA, herein designated GAM TARGET RNA.

GAM417 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6533] GAM417 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM417 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM417 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM417 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM417 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6534] The complementary binding of GAM417 RNA, herein designated GAM RNA, to target binding sites on GAM417 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM417 target RNA, herein designated GAM TARGET RNA, into GAM417 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6535] It is appreciated that GAM417 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM417 target genes. The mRNA of each one of this plurality of GAM417 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM417 RNA, herein designated GAM RNA, and which when bound by GAM417 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM417 target proteins.

[6536] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM417 gene, herein designated GAM GENE, on one or more GAM417 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6537] It is yet further appreciated that specific functions, and accordingly utilities, of GAM417 correlate with, and may be deduced from, the identity of the target genes which GAM417 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6538] Nucleotide sequences of the GAM417 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM417 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM417 are further described hereinbelow with reference to Table Table1.

[6539] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM417 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6540] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 418 (GAM418) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6541] GAM418 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM418 was detected is described hereinabove with reference to Figs. 2-8.

[6542] GAM418 gene, herein designated GAM GENE, and GAM418 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6543] GAM418 gene, herein designated GAM GENE, encodes a GAM418 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM418 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM418 precursor RNA is designated SEQ ID:390, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:390 is located at position 3904213 relative to contig NT_030737.5, on chromosome 8.

[6544] GAM418 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6545] An enzyme complex designated DICER COMPLEX, dices the GAM418 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM418 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM418 RNA is designated SEQ ID:2066, and is provided hereinbelow with reference to the sequence listing part.

[6546] GAM418 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM418 target RNA, herein designated GAM TARGET RNA. GAM418 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6547] GAM418 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM418 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM418 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM418 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM418 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6548] The complementary binding of GAM418 RNA, herein designated GAM RNA, to target binding sites on GAM418 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM418 target RNA, herein designated GAM TARGET RNA, into GAM418 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6549] It is appreciated that GAM418 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM418 target genes. The mRNA of each one of this plurality of GAM418 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM418 RNA, herein designated GAM RNA, and which when bound by GAM418 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM418 target proteins.

[6550] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM418 gene, herein designated GAM GENE, on one or more GAM418 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6551] It is yet further appreciated that specific functions, and accordingly utilities, of GAM418 correlate with, and may be deduced from, the identity of the target genes which GAM418 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6552] Nucleotide sequences of the GAM418 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM418 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM418 are further described hereinbelow with reference to Table Table1.

[6553] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM418 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6554] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

419 (GAM419) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6555] GAM419 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM419 was detected is described hereinabove with reference to Figs. 2-8.

[6556] GAM419 gene, herein designated GAM GENE, and GAM419 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6557] GAM419 gene, herein designated GAM GENE, encodes a GAM419 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM419 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM419 precursor RNA is designated SEQ ID:391, and is provided hereinbelow with reference to the sequence listing part.

[6558] GAM419 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse

EST's in which these homologs were detected are:

[6559] SEQ ID:98038 detected in mouse EST Accession BG298762.1.

[6560] SEQ ID:98039 detected in mouse EST Accession AU051458.1.

[6561] GAM419 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6562] An enzyme complex designated DICER COMPLEX, dices the GAM419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM419 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM419 RNA is designated SEQ ID:2067, and is provided hereinbelow with reference to the sequence listing part.

[6563] GAM419 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM419 target RNA, herein designated GAM TARGET RNA. GAM419 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6564] GAM419 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM419 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM419 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM419 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM419 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6565] The complementary binding of GAM419 RNA, herein designated GAM RNA, to target binding sites on GAM419 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM419 target RNA, herein designated GAM TARGET RNA, into GAM419 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6566] It is appreciated that GAM419 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM419 target genes. The mRNA of each one of this plurality of GAM419 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM419 RNA, herein designated GAM RNA, and which when bound by

GAM419 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM419 target proteins.

[6567] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM419 gene, herein designated GAM GENE, on one or more GAM419 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6568] It is yet further appreciated that specific functions, and accordingly utilities, of GAM419 correlate with, and may be deduced from, the identity of the target genes which GAM419 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[6569] Nucleotide sequences of the GAM419 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM419 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM419 are further described hereinbelow with reference to Table Table1.

[6570] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM419 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6571] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 420 (GAM420) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6572] GAM420 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM420 was detected is described hereinabove

with reference to Figs. 2-8.

[6573] GAM420 gene, herein designated GAM GENE, and GAM420 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6574] GAM420 gene, herein designated GAM GENE, encodes a GAM420 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM420 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM420 precursor RNA is designated SEQ ID:392, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:392 is located at position 2045043 relative to contig NT_011176.13, on chromosome 19.

[6575] GAM420 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[6576] An enzyme complex designated DICER COMPLEX, dices the GAM420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM420 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM420 RNA is designated SEQ ID:2068, and is provided hereinbelow with reference to the sequence listing part.

[6577] GAM420 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM420 target RNA, herein designated GAM TARGET RNA.
GAM420 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6578] GAM420 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM420 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM420 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM420 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM420 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6579] The complementary binding of GAM420 RNA, herein designated GAM RNA, to target binding sites on GAM420 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM420 target RNA, herein desig-

nated GAM TARGET RNA, into GAM420 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6580] It is appreciated that GAM420 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM420 target genes. The mRNA of each one of this plurality of GAM420 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM420 RNA, herein designated GAM RNA, and which when bound by GAM420 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM420 target proteins.

[6581] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM420 gene, herein designated GAM GENE, on one or more GAM420 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6582] It is yet further appreciated that specific functions, and accordingly utilities, of GAM420 correlate with, and may be deduced from, the identity of the target genes which GAM420 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6583] Nucleotide sequences of the GAM420 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM420 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM420 are further described hereinbelow with reference to Table Table1.

[6584] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM420 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[6585] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 421 (GAM421) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6586] GAM421 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM421 was detected is described hereinabove with reference to Figs. 2-8.

[6587] GAM421 gene, herein designated GAM GENE, and GAM421 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6588] GAM421 gene, herein designated GAM GENE, encodes a GAM421 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM421 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM421 precursor RNA is designated SEQ ID:393, and is provided hereinbelow with reference to the sequence listing part.

[6589] GAM421 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[6590] SEQ ID:98085 detected in mouse EST Accession AA823029.1.

[6591] SEQ ID:98944 detected in mouse EST Accession AA068787.1.

[6592] SEQ ID:98945 detected in mouse EST Accession BE625629.1.

[6593] SEQ ID:98946 detected in mouse EST Accession BI792530.1.

[6594] SEQ ID:98947 detected in mouse EST Accession BE309708.1.

[6595] SEQ ID:98948 detected in mouse EST Accession BI100916.1.

[6596] SEQ ID:98951 detected in mouse EST Accession BE380224.1.

[6597] SEQ ID:98952 detected in mouse EST Accession BG296866.1.

[6598] GAM421 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM421 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6599] An enzyme complex designated DICER COMPLEX, dices the GAM421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM421 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 97%) nucleotide sequence of GAM421 RNA is designated SEQ ID:2069, and is provided hereinbelow with reference to the sequence listing part.

[6600] GAM421 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM421 target RNA, herein designated GAM TARGET RNA. GAM421 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6601] GAM421 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM421 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM421 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM421 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM421 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[6602] The complementary binding of GAM421 RNA, herein designated GAM RNA, to target binding sites on GAM421 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM421 target RNA, herein designated GAM TARGET RNA, into GAM421 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6603] It is appreciated that GAM421 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM421 target genes. The mRNA of each one of this plurality of GAM421 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM421 RNA, herein designated GAM RNA, and which when bound by GAM421 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM421 target proteins.

[6604] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM421 gene, herein designated GAM GENE, on one or

more GAM421 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6605] It is yet further appreciated that specific functions, and accordingly utilities, of GAM421 correlate with, and may be deduced from, the identity of the target genes which GAM421 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6606] Nucleotide sequences of the GAM421 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM421 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM421 are further de-

scribed hereinbelow with reference to Table Table1.

[6607] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM421 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6608] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 422 (GAM422) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6609] GAM422 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM422 was detected is described hereinabove with reference to Figs. 2-8.

[6610] GAM422 gene, herein designated GAM GENE, and GAM422 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6611] GAM422 gene, herein designated GAM GENE, encodes a GAM422 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM422 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM422 precursor RNA is designated SEQ ID:394, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:394 is located at position 7678827 relative to contig NT_004852.13, on chromosome 1.

[6612] GAM422 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6613] An enzyme complex designated DICER COMPLEX, dices the GAM422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM422 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM422 RNA is designated SEQ ID:2070, and is provided hereinbelow with reference to the sequence listing part.

[6614] GAM422 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM422 target RNA, herein designated GAM TARGET RNA. GAM422 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6615] GAM422 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM422 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM422 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM422 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM422 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6616] The complementary binding of GAM422 RNA, herein designated GAM RNA, to target binding sites on GAM422 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM422 target RNA, herein designated GAM TARGET RNA, into GAM422 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6617] It is appreciated that GAM422 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM422 target genes. The mRNA of each one of this plurality of GAM422 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM422 RNA, herein designated GAM RNA, and which when bound by GAM422 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM422 target proteins.

[6618] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM422 gene, herein designated GAM GENE, on one or more GAM422 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6619] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM422 correlate with, and may be deduced from, the identity of the target genes which GAM422 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6620] Nucleotide sequences of the GAM422 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM422 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM422 are further described hereinbelow with reference to Table Table1.

[6621] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM422 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6622] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 423 (GAM423) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6623] GAM423 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM423 was detected is described hereinabove with reference to Figs. 2-8.

[6624] GAM423 gene, herein designated GAM GENE, and GAM423 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6625] GAM423 gene, herein designated GAM GENE, encodes a GAM423 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM423 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM423 precursor RNA is designated SEQ ID:395, and is provided hereinbelow with reference to the sequence listing part.

[6626] GAM423 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6627] An enzyme complex designated DICER COMPLEX, dices the GAM423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM423 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM423 RNA is designated SEQ ID:2071, and is provided hereinbelow with reference to the sequence listing part.

[6628] GAM423 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM423 target RNA, herein designated GAM TARGET RNA. GAM423 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6629] GAM423 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM423 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM423 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM423 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM423 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6630] The complementary binding of GAM423 RNA, herein designated GAM RNA, to target binding sites on GAM423 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM423 target RNA, herein designated GAM TARGET RNA, into GAM423 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6631] It is appreciated that GAM423 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM423 target genes. The mRNA of each one of this plurality of GAM423 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM423 RNA, herein designated GAM RNA, and which when bound by GAM423 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM423 target proteins.

[6632] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM423 gene, herein designated GAM GENE, on one or more GAM423 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6633] It is yet further appreciated that specific functions, and accordingly utilities, of GAM423 correlate with, and may be deduced from, the identity of the target genes which GAM423 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6634] Nucleotide sequences of the GAM423 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM423 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM423 are further described hereinbelow with reference to Table Table1.

[6635] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM423 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6636] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 424 (GAM424) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6637] GAM424 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM424 was detected is described hereinabove with reference to Figs. 2-8.

[6638] GAM424 gene, herein designated GAM GENE, and GAM424 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6639] GAM424 gene, herein designated GAM GENE, encodes a GAM424 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM424 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM424 precursor RNA is designated SEQ ID:396, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:396 is located at position 3434864 relative to contig NT_009714.13, on chromosome 12.

[6640] GAM424 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[6641] SEQ ID:99360 detected in mouse EST Accession BG288438.1.

[6642] SEQ ID:99361 detected in mouse EST Accession BG288438.1.

[6643] GAM424 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6644] An enzyme complex designated DICER COMPLEX, dices

the GAM424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM424 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM424 RNA is designated SEQ ID:2072, and is provided hereinbelow with reference to the sequence listing part.

[6645] GAM424 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM424 target RNA, herein designated GAM TARGET RNA. GAM424 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6646] GAM424 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM424 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM424

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM424 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM424 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6647] The complementary binding of GAM424 RNA, herein designated GAM RNA, to target binding sites on GAM424 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM424 target RNA, herein designated GAM TARGET RNA, into GAM424 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6648] It is appreciated that GAM424 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM424 target genes. The mRNA of each one of this plurality of GAM424 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM424 RNA, herein designated GAM RNA, and which when bound by GAM424 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM424 target proteins.

[6649] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM424 gene, herein designated GAM GENE, on one or more GAM424 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6650] It is yet further appreciated that specific functions, and accordingly utilities, of GAM424 correlate with, and may be deduced from, the identity of the target genes which GAM424 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6651] Nucleotide sequences of the GAM424 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM424 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM424 are further described hereinbelow with reference to Table Table1.

[6652] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM424 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6653] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 425 (GAM425) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6654] GAM425 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM425 was detected is described hereinabove with reference to Figs. 2-8.

[6655] GAM425 gene, herein designated GAM GENE, and GAM425 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6656] GAM425 gene, herein designated GAM GENE, encodes a GAM425 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM425 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM425 precursor RNA is designated SEQ ID:397, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:397 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[6657] GAM425 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6658] An enzyme complex designated DICER COMPLEX, dices the GAM425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM425 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM425 RNA is designated SEQ ID:2073, and is provided hereinbelow with reference to the sequence listing part.

[6659] GAM425 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM425 target RNA, herein designated GAM TARGET RNA.

GAM425 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6660] GAM425 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM425 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM425 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM425 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM425 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6661] The complementary binding of GAM425 RNA, herein designated GAM RNA, to target binding sites on GAM425 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM425 target RNA, herein designated GAM TARGET RNA, into GAM425 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6662] It is appreciated that GAM425 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM425 target genes. The mRNA of each one of this plurality of GAM425 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM425 RNA, herein designated GAM RNA, and which when bound by GAM425 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM425 target proteins.

[6663] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM425 gene, herein designated GAM GENE, on one or more GAM425 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6664] It is yet further appreciated that specific functions, and accordingly utilities, of GAM425 correlate with, and may be deduced from, the identity of the target genes which GAM425 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6665] Nucleotide sequences of the GAM425 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM425 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM425 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM425 are further described hereinbelow with reference to Table Table1.

[6666] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM425 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6667] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 426 (GAM426) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6668] GAM426 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM426 was detected is described hereinabove with reference to Figs. 2-8.

[6669] GAM426 gene, herein designated GAM GENE, and GAM426 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6670] GAM426 gene, herein designated GAM GENE, encodes a GAM426 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM426 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM426 precursor RNA is designated SEQ ID:398, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:398 is located at position 1698742 relative to contig NT_028309.8, on chromosome 11.

[6671] GAM426 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6672] An enzyme complex designated DICER COMPLEX, dices the GAM426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM426 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM426 RNA is designated SEQ ID:2074, and is provided hereinbelow with reference to the sequence listing part.

[6673] GAM426 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM426 target RNA, herein designated GAM TARGET RNA. GAM426 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6674] GAM426 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM426 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM426 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM426 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM426 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6675] The complementary binding of GAM426 RNA, herein designated GAM RNA, to target binding sites on GAM426 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM426 target RNA, herein designated GAM TARGET RNA, into GAM426 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6676] It is appreciated that GAM426 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM426 target genes. The mRNA of each one of this plu-

rality of GAM426 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM426 RNA, herein designated GAM RNA, and which when bound by GAM426 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM426 target proteins.

[6677] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM426 gene, herein designated GAM GENE, on one or more GAM426 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6678] It is yet further appreciated that specific functions, and accordingly utilities, of GAM426 correlate with, and may be deduced from, the identity of the target genes which GAM426 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6679] Nucleotide sequences of the GAM426 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM426 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM426 are further described hereinbelow with reference to Table Table1.

[6680] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM426 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6681] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 427 (GAM427) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[6682] GAM427 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM427 was detected is described hereinabove with reference to Figs. 2-8.

[6683] GAM427 gene, herein designated GAM GENE, and GAM427 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6684] GAM427 gene, herein designated GAM GENE, encodes a GAM427 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM427 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM427 precursor RNA is designated SEQ ID:399, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:399 is located at position 11259454 relative to contig NT_007592.11, on chromosome 6.

[6685] GAM427 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6686] An enzyme complex designated DICER COMPLEX, dices the GAM427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM427 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM427 RNA is designated SEQ ID:2075, and is provided hereinbelow with reference to the sequence listing part.

[6687] GAM427 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM427 target RNA, herein designated GAM TARGET RNA. GAM427 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6688] GAM427 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM427 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM427 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM427 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM427 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6689] The complementary binding of GAM427 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM427 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM427 target RNA, herein designated GAM TARGET RNA, into GAM427 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6690] It is appreciated that GAM427 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM427 target genes. The mRNA of each one of this plurality of GAM427 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM427 RNA, herein designated GAM RNA, and which when bound by GAM427 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM427 target proteins.

[6691] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM427 gene, herein designated GAM GENE, on one or more GAM427 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6692] It is yet further appreciated that specific functions, and accordingly utilities, of GAM427 correlate with, and may be deduced from, the identity of the target genes which GAM427 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6693] Nucleotide sequences of the GAM427 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM427 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM427 are further described hereinbelow with reference to Table Table1.

[6694] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM427 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6695] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 428 (GAM428) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6696] GAM428 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM428 was detected is described hereinabove with reference to Figs. 2-8.

[6697] GAM428 gene, herein designated GAM GENE, and GAM428 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6698] GAM428 gene, herein designated GAM GENE, encodes a GAM428 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM428 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM428 precursor RNA is designated SEQ ID:400, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:400 is located at position 4784859 relative to contig NT_028392.4, on chromosome 20.

[6699] GAM428 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6700] An enzyme complex designated DICER COMPLEX, dices the GAM428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM428 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM428 RNA is designated SEQ ID:2076, and is provided hereinbelow with reference to the sequence listing part.

[6701] GAM428 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM428 target RNA, herein designated GAM TARGET RNA. GAM428 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6702] GAM428 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM428 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM428 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM428 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM428 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6703] The complementary binding of GAM428 RNA, herein designated GAM RNA, to target binding sites on GAM428 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM428 target RNA, herein designated GAM TARGET RNA, into GAM428 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6704] It is appreciated that GAM428 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM428 target genes. The mRNA of each one of this plurality of GAM428 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM428 RNA,

herein designated GAM RNA, and which when bound by GAM428 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM428 target proteins.

[6705] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM428 gene, herein designated GAM GENE, on one or more GAM428 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6706] It is yet further appreciated that specific functions, and accordingly utilities, of GAM428 correlate with, and may be deduced from, the identity of the target genes which

GAM428 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6707] Nucleotide sequences of the GAM428 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM428 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM428 are further described hereinbelow with reference to Table Table1.

[6708] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM428 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6709] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 429 (GAM429) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6710] GAM429 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM429 was detected is described hereinabove with reference to Figs. 2-8.

[6711] GAM429 gene, herein designated GAM GENE, and GAM429 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6712] GAM429 gene, herein designated GAM GENE, encodes a GAM429 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM429 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM429 precursor RNA is designated SEQ ID:401, and is provided hereinbelow with reference to the sequence listing part.

[6713] GAM429 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[6714] An enzyme complex designated DICER COMPLEX, dices the GAM429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM429 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM429 RNA is designated SEQ ID:2077, and is provided hereinbelow with reference to the sequence listing part.

[6715] GAM429 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM429 target RNA, herein designated GAM TARGET RNA. GAM429 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6716] GAM429 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM429 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM429 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM429 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM429 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6717] The complementary binding of GAM429 RNA, herein designated GAM RNA, to target binding sites on GAM429 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM429 target RNA, herein designated GAM TARGET RNA, into GAM429 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6718] It is appreciated that GAM429 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM429 target genes. The mRNA of each one of this plurality of GAM429 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM429 RNA, herein designated GAM RNA, and which when bound by GAM429 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM429 target proteins.

[6719] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM429 gene, herein designated GAM GENE, on one or more GAM429 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6720] It is yet further appreciated that specific functions, and accordingly utilities, of GAM429 correlate with, and may be deduced from, the identity of the target genes which GAM429 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6721] Nucleotide sequences of the GAM429 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM429 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM429 are further described hereinbelow with reference to Table Table1.

[6722] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM429 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6723] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 430 (GAM430) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6724] GAM430 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM430 was detected is described hereinabove with reference to Figs. 2-8.

[6725] GAM430 gene, herein designated GAM GENE, and GAM430 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6726] GAM430 gene, herein designated GAM GENE, encodes a GAM430 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM430 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM430 precursor RNA is designated SEQ ID:402, and is provided hereinbelow with reference to the sequence listing part.

[6727] GAM430 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6728] An enzyme complex designated DICER COMPLEX, dices the GAM430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM430 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM430 RNA is designated SEQ ID:2078, and is provided hereinbelow with reference to the sequence listing part.

[6729] GAM430 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM430 target RNA, herein designated GAM TARGET RNA.

GAM430 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6730] GAM430 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM430 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM430 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM430 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM430 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6731] The complementary binding of GAM430 RNA, herein designated GAM RNA, to target binding sites on GAM430 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM430 target RNA, herein designated GAM TARGET RNA, into GAM430 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6732] It is appreciated that GAM430 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM430 target genes. The mRNA of each one of this plurality of GAM430 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM430 RNA, herein designated GAM RNA, and which when bound by GAM430 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM430 target proteins.

[6733] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM430 gene, herein designated GAM GENE, on one or more GAM430 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6734] It is yet further appreciated that specific functions, and accordingly utilities, of GAM430 correlate with, and may be deduced from, the identity of the target genes which GAM430 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6735] Nucleotide sequences of the GAM430 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM430 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM430 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM430 are further described hereinbelow with reference to Table Table1.

[6736] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM430 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6737] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 431 (GAM431) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6738] GAM431 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM431 was detected is described hereinabove with reference to Figs. 2-8.

[6739] GAM431 gene, herein designated GAM GENE, and GAM431 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6740] GAM431 gene, herein designated GAM GENE, encodes a GAM431 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM431 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM431 precursor RNA is designated SEQ ID:403, and is provided hereinbelow with reference to the sequence listing part.

[6741] GAM431 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6742] An enzyme complex designated DICER COMPLEX, dices the GAM431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM431 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM431 RNA is designated SEQ ID:2079, and is provided hereinbelow with reference to the sequence listing part.

[6743] GAM431 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM431 target RNA, herein designated GAM TARGET RNA. GAM431 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6744] GAM431 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM431 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM431 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM431 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM431 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6745] The complementary binding of GAM431 RNA, herein designated GAM RNA, to target binding sites on GAM431 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM431 target RNA, herein designated GAM TARGET RNA, into GAM431 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6746] It is appreciated that GAM431 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM431 target genes. The mRNA of each one of this plurality of GAM431 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM431 RNA, herein designated GAM RNA, and which when bound by GAM431 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM431 target proteins.

[6747] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM431 gene, herein designated GAM GENE, on one or more GAM431 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6748] It is yet further appreciated that specific functions, and accordingly utilities, of GAM431 correlate with, and may

be deduced from, the identity of the target genes which GAM431 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6749] Nucleotide sequences of the GAM431 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM431 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM431 are further described hereinbelow with reference to Table Table1.

[6750] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM431 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6751] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 432 (GAM432) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6752] GAM432 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM432 was detected is described hereinabove with reference to Figs. 2-8.

[6753] GAM432 gene, herein designated GAM GENE, and GAM432 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6754] GAM432 gene, herein designated GAM GENE, encodes a GAM432 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM432 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM432 precursor RNA is designated SEQ ID:404, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:404 is located at position 7652379 relative to contig NT_010393.11, on chromosome 16.

[6755] GAM432 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6756] An enzyme complex designated DICER COMPLEX, dices the GAM432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM432 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM432 RNA is designated SEQ ID:2080, and is provided hereinbelow with reference to the sequence listing part.

[6757] GAM432 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM432 target RNA, herein designated GAM TARGET RNA.
GAM432 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6758] GAM432 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM432 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM432 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM432 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM432 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6759] The complementary binding of GAM432 RNA, herein designated GAM RNA, to target binding sites on GAM432 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM432 target RNA, herein designated GAM TARGET RNA, into GAM432 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6760] It is appreciated that GAM432 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM432 target genes. The mRNA of each one of this plurality of GAM432 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM432 RNA, herein designated GAM RNA, and which when bound by GAM432 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM432 target proteins.

[6761] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM432 gene, herein designated GAM GENE, on one or more GAM432 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6762] It is yet further appreciated that specific functions, and accordingly utilities, of GAM432 correlate with, and may be deduced from, the identity of the target genes which GAM432 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6763] Nucleotide sequences of the GAM432 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM432 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM432 are further described hereinbelow with reference to Table Table1.

[6764] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM432 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6765] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 433 (GAM433) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6766] GAM433 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM433 was detected is described hereinabove with reference to Figs. 2-8.

[6767] GAM433 gene, herein designated GAM GENE, and GAM433 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6768] GAM433 gene, herein designated GAM GENE, encodes a GAM433 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM433 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM433 precursor RNA is desig-

nated SEQ ID:405, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:405 is located at position 2630442 relative to contig NT_030059.8, on chromosome 10.

[6769] GAM433 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6770] An enzyme complex designated DICER COMPLEX, dices the GAM433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM433 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM433 RNA is designated SEQ ID:2081, and is provided hereinbelow with reference to the sequence listing part.

[6771] GAM433 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM433 target RNA, herein designated GAM TARGET RNA. GAM433 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6772] GAM433 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM433 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM433 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM433 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM433 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6773] The complementary binding of GAM433 RNA, herein designated GAM RNA, to target binding sites on GAM433 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM433 target RNA, herein designated GAM TARGET RNA, into GAM433 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6774] It is appreciated that GAM433 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM433 target genes. The mRNA of each one of this plurality of GAM433 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM433 RNA, herein designated GAM RNA, and which when bound by GAM433 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM433 target proteins.

[6775] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM433 gene, herein designated GAM GENE, on one or more GAM433 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6776] It is yet further appreciated that specific functions, and accordingly utilities, of GAM433 correlate with, and may be deduced from, the identity of the target genes which GAM433 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6777] Nucleotide sequences of the GAM433 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM433 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM433 are further described hereinbelow with reference to Table Table1.

[6778] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM433 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6779] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 434 (GAM434) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6780] GAM434 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM434 was detected is described hereinabove with reference to Figs. 2-8.

[6781] GAM434 gene, herein designated GAM GENE, and GAM434 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6782] GAM434 gene, herein designated GAM GENE, encodes a GAM434 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM434 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM434 precursor RNA is designated SEQ ID:406, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:406 is located at position 6633498 relative to contig NT_030828.7, on chromosome 15.

[6783] GAM434 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[6784] An enzyme complex designated DICER COMPLEX, dices the GAM434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM434 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM434 RNA is designated SEQ ID:2082, and is provided hereinbelow with reference to the sequence listing part.

[6785] GAM434 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM434 target RNA, herein designated GAM TARGET RNA. GAM434 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6786] GAM434 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM434 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM434 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM434 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM434 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6787] The complementary binding of GAM434 RNA, herein designated GAM RNA, to target binding sites on GAM434 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM434 target RNA, herein designated GAM TARGET RNA, into GAM434 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6788] It is appreciated that GAM434 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM434 target genes. The mRNA of each one of this plurality of GAM434 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM434 RNA, herein designated GAM RNA, and which when bound by GAM434 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM434 target proteins.

[6789] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM434 gene, herein designated GAM GENE, on one or more GAM434 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6790] It is yet further appreciated that specific functions, and accordingly utilities, of GAM434 correlate with, and may be deduced from, the identity of the target genes which GAM434 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6791] Nucleotide sequences of the GAM434 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM434 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM434 are further described hereinbelow with reference to Table Table1.

[6792] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM434 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6793] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 435 (GAM435) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6794] GAM435 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM435 was detected is described hereinabove with reference to Figs. 2-8.

[6795] GAM435 gene, herein designated GAM GENE, and GAM435 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6796] GAM435 gene, herein designated GAM GENE, encodes a GAM435 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM435 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM435 precursor RNA is designated SEQ ID:407, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:407 is located at position 2349674 relative to con-

tig NT_021907.13, on chromosome 1.

[6797] GAM435 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6798] An enzyme complex designated DICER COMPLEX, dices the GAM435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM435 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM435 RNA is designated SEQ ID:2083, and is provided hereinbelow with reference to the sequence listing part.

[6799] GAM435 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM435 target RNA, herein designated GAM TARGET RNA.

GAM435 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6800] GAM435 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM435 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM435 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM435 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM435 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6801] The complementary binding of GAM435 RNA, herein designated GAM RNA, to target binding sites on GAM435 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM435 target RNA, herein designated GAM TARGET RNA, into GAM435 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6802] It is appreciated that GAM435 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM435 target genes. The mRNA of each one of this plurality of GAM435 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM435 RNA, herein designated GAM RNA, and which when bound by GAM435 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM435 target proteins.

[6803] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM435 gene, herein designated GAM GENE, on one or more GAM435 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6804] It is yet further appreciated that specific functions, and accordingly utilities, of GAM435 correlate with, and may be deduced from, the identity of the target genes which GAM435 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6805] Nucleotide sequences of the GAM435 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM435 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM435 are further described hereinbelow with reference to Table Table1.

[6806] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM435 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6807] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 436 (GAM436) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6808] GAM436 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM436 was detected is described hereinabove with reference to Figs. 2-8.

[6809] GAM436 gene, herein designated GAM GENE, and GAM436 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6810] GAM436 gene, herein designated GAM GENE, encodes a GAM436 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM436 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM436 precursor RNA is designated SEQ ID:408, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:408 is located at position 2281900 relative to contig NT_024797.11, on chromosome 16.

[6811] GAM436 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[6812] SEQ ID:98494 detected in mouse EST Accession BF134656.1.

[6813] SEQ ID:98495 detected in mouse EST Accession BI149599.1.

[6814] GAM436 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6815] An enzyme complex designated DICER COMPLEX, dices the GAM436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM436 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM436 RNA is designated SEQ ID:2084, and is provided hereinbelow with reference to the sequence listing part.

[6816] GAM436 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM436 target RNA, herein designated GAM TARGET RNA. GAM436 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6817] GAM436 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM436 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM436 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM436 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM436 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6818] The complementary binding of GAM436 RNA, herein designated GAM RNA, to target binding sites on GAM436 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM436 target RNA, herein designated GAM TARGET RNA, into GAM436 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6819] It is appreciated that GAM436 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM436 target genes. The mRNA of each one of this plurality of GAM436 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM436 RNA, herein designated GAM RNA, and which when bound by GAM436 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM436 target proteins.

[6820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM436 gene, herein designated GAM GENE, on one or more GAM436 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6821] It is yet further appreciated that specific functions, and accordingly utilities, of GAM436 correlate with, and may be deduced from, the identity of the target genes which GAM436 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6822] Nucleotide sequences of the GAM436 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM436 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM436 are further described hereinbelow with reference to Table Table1.

[6823] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM436 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6824] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 437 (GAM437) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6825] GAM437 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM437 was detected is described hereinabove with reference to Figs. 2-8.

[6826] GAM437 gene, herein designated GAM GENE, and GAM437 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6827] GAM437 gene, herein designated GAM GENE, encodes a GAM437 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM437 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM437 precursor RNA is designated SEQ ID:409, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:409 is located at position 6294462 relative to contig NT_024981.11, on chromosome 18.

[6828] GAM437 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6829] An enzyme complex designated DICER COMPLEX, dices the GAM437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM437 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM437 RNA is designated SEQ ID:2085, and is provided hereinbelow with reference to the sequence listing part.

[6830] GAM437 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM437 target RNA, herein designated GAM TARGET RNA. GAM437 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6831] GAM437 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM437 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM437 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM437 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM437 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6832] The complementary binding of GAM437 RNA, herein designated GAM RNA, to target binding sites on GAM437 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM437 target RNA, herein designated GAM TARGET RNA, into GAM437 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6833] It is appreciated that GAM437 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM437 target genes. The mRNA of each one of this plurality of GAM437 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM437 RNA, herein designated GAM RNA, and which when bound by GAM437 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM437 target proteins.

[6834] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM437 gene, herein designated GAM GENE, on one or more GAM437 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6835] It is yet further appreciated that specific functions, and accordingly utilities, of GAM437 correlate with, and may

be deduced from, the identity of the target genes which GAM437 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6836] Nucleotide sequences of the GAM437 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM437 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM437 are further described hereinbelow with reference to Table Table1.

[6837] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM437 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6838] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 438 (GAM438) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6839] GAM438 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM438 was detected is described hereinabove with reference to Figs. 2-8.

[6840] GAM438 gene, herein designated GAM GENE, and GAM438 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6841] GAM438 gene, herein designated GAM GENE, encodes a GAM438 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM438 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM438 precursor RNA is designated SEQ ID:410, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:410 is located at position 4851368 relative to contig NT_022517.13, on chromosome 3.

[6842] GAM438 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6843] An enzyme complex designated DICER COMPLEX, dices the GAM438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM438 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM438 RNA is designated SEQ ID:2086, and is provided hereinbelow with reference to the sequence listing part.

[6844] GAM438 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM438 target RNA, herein designated GAM TARGET RNA. GAM438 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6845] GAM438 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM438 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM438 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM438 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM438 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6846] The complementary binding of GAM438 RNA, herein designated GAM RNA, to target binding sites on GAM438 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM438 target RNA, herein designated GAM TARGET RNA, into GAM438 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6847] It is appreciated that GAM438 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM438 target genes. The mRNA of each one of this plurality of GAM438 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM438 RNA, herein designated GAM RNA, and which when bound by GAM438 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM438 target proteins.

[6848] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM438 gene, herein designated GAM GENE, on one or more GAM438 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6849] It is yet further appreciated that specific functions, and accordingly utilities, of GAM438 correlate with, and may be deduced from, the identity of the target genes which GAM438 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6850] Nucleotide sequences of the GAM438 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM438 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM438 are further described hereinbelow with reference to Table Table1.

[6851] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM438 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6852] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 439 (GAM439) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6853] GAM439 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM439 was detected is described hereinabove with reference to Figs. 2-8.

[6854] GAM439 gene, herein designated GAM GENE, and GAM439 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6855] GAM439 gene, herein designated GAM GENE, encodes a GAM439 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM439 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM439 precursor RNA is desig-

nated SEQ ID:411, and is provided hereinbelow with reference to the sequence listing part.

[6856] GAM439 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[6857] SEQ ID:99508 detected in mouse EST Accession AW229351.1.

[6858] SEQ ID:99509 detected in mouse EST Accession BI413638.1.

[6859] SEQ ID:99510 detected in mouse EST Accession BG242453.1.

[6860] SEQ ID:99511 detected in mouse EST Accession BE862202.1.

[6861] GAM439 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[6862] An enzyme complex designated DICER COMPLEX, dices the GAM439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM439 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM439 RNA is designated SEQ ID:2087, and is provided hereinbelow with reference to the sequence listing part.

[6863] GAM439 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM439 target RNA, herein designated GAM TARGET RNA.
GAM439 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6864] GAM439 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM439 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM439 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM439 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM439 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6865] The complementary binding of GAM439 RNA, herein designated GAM RNA, to target binding sites on GAM439 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM439 target RNA, herein desig-

nated GAM TARGET RNA, into GAM439 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6866] It is appreciated that GAM439 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM439 target genes. The mRNA of each one of this plurality of GAM439 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM439 RNA, herein designated GAM RNA, and which when bound by GAM439 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM439 target proteins.

[6867] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM439 gene, herein designated GAM GENE, on one or more GAM439 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6868] It is yet further appreciated that specific functions, and accordingly utilities, of GAM439 correlate with, and may be deduced from, the identity of the target genes which GAM439 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6869] Nucleotide sequences of the GAM439 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM439 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM439 are further described hereinbelow with reference to Table Table1.

[6870] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM439 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[6871] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 440 (GAM440) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6872] GAM440 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM440 was detected is described hereinabove with reference to Figs. 2-8.

[6873] GAM440 gene, herein designated GAM GENE, and GAM440 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6874] GAM440 gene, herein designated GAM GENE, encodes a GAM440 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM440 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM440 precursor RNA is designated SEQ ID:412, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:412 is located at position 35050176 relative to contig NT_026437.9, on chromosome 14.

[6875] GAM440 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6876] An enzyme complex designated DICER COMPLEX, dices the GAM440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM440 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM440 RNA is designated SEQ ID:2088, and is provided hereinbelow with reference to the sequence listing part.

[6877] GAM440 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM440 target RNA, herein designated GAM TARGET RNA. GAM440 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6878] GAM440 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM440 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM440 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM440 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM440

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6879] The complementary binding of GAM440 RNA, herein designated GAM RNA, to target binding sites on GAM440 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM440 target RNA, herein designated GAM TARGET RNA, into GAM440 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6880] It is appreciated that GAM440 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM440 target genes. The mRNA of each one of this plurality of GAM440 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM440 RNA, herein designated GAM RNA, and which when bound by GAM440 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM440 target proteins.

[6881] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM440 gene, herein designated GAM GENE, on one or more GAM440 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6882] It is yet further appreciated that specific functions, and accordingly utilities, of GAM440 correlate with, and may be deduced from, the identity of the target genes which GAM440 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6883] Nucleotide sequences of the GAM440 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM440 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM440 are further described hereinbelow with reference to Table Table1.

[6884] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM440 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6885] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 441 (GAM441) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6886] GAM441 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM441 was detected is described hereinabove with reference to Figs. 2-8.

[6887] GAM441 gene, herein designated GAM GENE, and GAM441 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[6888] GAM441 gene, herein designated GAM GENE, encodes a GAM441 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM441 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM441 precursor RNA is designated SEQ ID:413, and is provided hereinbelow with reference to the sequence listing part.

[6889] GAM441 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6890] An enzyme complex designated DICER COMPLEX, dices the GAM441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM441 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM441 RNA is designated SEQ ID:2089, and is provided hereinbelow with reference to the sequence listing part.

[6891] GAM441 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM441 target RNA, herein designated GAM TARGET RNA. GAM441 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6892] GAM441 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM441 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM441 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM441 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM441 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6893] The complementary binding of GAM441 RNA, herein designated GAM RNA, to target binding sites on GAM441 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM441 target RNA, herein designated GAM TARGET RNA, into GAM441 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6894] It is appreciated that GAM441 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM441 target genes. The mRNA of each one of this plurality of GAM441 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM441 RNA, herein designated GAM RNA, and which when bound by GAM441 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM441 target proteins.

[6895] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM441 gene, herein designated GAM GENE, on one or more GAM441 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[6896] It is yet further appreciated that specific functions, and accordingly utilities, of GAM441 correlate with, and may be deduced from, the identity of the target genes which GAM441 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6897] Nucleotide sequences of the GAM441 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM441 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM441 are further described hereinbelow with reference to Table Table1.

[6898] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM441 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6899] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 442 (GAM442) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[6900] GAM442 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM442 was detected is described hereinabove with reference to Figs. 2-8.

[6901] GAM442 gene, herein designated GAM GENE, and GAM442 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6902] GAM442 gene, herein designated GAM GENE, encodes a GAM442 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM442 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM442 precursor RNA is designated SEQ ID:414, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:414 is located at position 5393908 relative to contig NT_006431.11, on chromosome 5.

[6903] GAM442 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of

SEQ ID:99284, which mouse homolog is detected in mouse EST accession BE654373.1.

[6904] GAM442 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6905] An enzyme complex designated DICER COMPLEX, dices the GAM442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM442 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM442 RNA is designated SEQ ID:2090, and is provided hereinbelow with reference to the sequence listing part.

[6906] GAM442 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM442 target RNA, herein designated GAM TARGET RNA. GAM442 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6907] GAM442 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM442 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM442 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM442 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM442

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6908] The complementary binding of GAM442 RNA, herein designated GAM RNA, to target binding sites on GAM442 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM442 target RNA, herein designated GAM TARGET RNA, into GAM442 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6909] It is appreciated that GAM442 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM442 target genes. The mRNA of each one of this plurality of GAM442 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM442 RNA, herein designated GAM RNA, and which when bound by GAM442 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM442 target proteins.

[6910] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM442 gene, herein designated GAM GENE, on one or more GAM442 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6911] It is yet further appreciated that specific functions, and accordingly utilities, of GAM442 correlate with, and may be deduced from, the identity of the target genes which GAM442 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6912] Nucleotide sequences of the GAM442 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM442 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM442 are further described hereinbelow with reference to Table Table1.

[6913] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM442 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6914] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 443 (GAM443) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6915] GAM443 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM443 was detected is described hereinabove with reference to Figs. 2-8.

[6916] GAM443 gene, herein designated GAM GENE, and GAM443 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[6917] GAM443 gene, herein designated GAM GENE, encodes a GAM443 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM443 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM443 precursor RNA is designated SEQ ID:415, and is provided hereinbelow with reference to the sequence listing part.

[6918] GAM443 has 12 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[6919] SEQ ID:97996 detected in mouse EST Accession BF146992.1.

[6920] SEQ ID:97997 detected in mouse EST Accession AI264984.1.

[6921] SEQ ID:97998 detected in mouse EST Accession AI156313.1.

[6922] SEQ ID:97999 detected in mouse EST Accession BG970816.1.

[6923] SEQ ID:98000 detected in mouse EST Accession BI153175.1.

[6924] SEQ ID:98001 detected in mouse EST Accession BG864461.1.

[6925] SEQ ID:98002 detected in mouse EST Accession AA144398.1.

[6926] SEQ ID:98003 detected in mouse EST Accession AW230495.1.

[6927] SEQ ID:98004 detected in mouse EST Accession BF144364.1.

[6928] SEQ ID:98005 detected in mouse EST Accession BG974532.1.

[6929] SEQ ID:98006 detected in mouse EST Accession BG870381.1.

[6930] SEQ ID:98007 detected in mouse EST Accession BG973293.1.

[6931] GAM443 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6932] An enzyme complex designated DICER COMPLEX, dices the GAM443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM443 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM443 RNA is designated SEQ ID:2091, and is provided hereinbelow with reference to the sequence listing part.

[6933] GAM443 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM443 target RNA, herein designated GAM TARGET RNA. GAM443 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6934] GAM443 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM443 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM443 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM443 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM443 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6935] The complementary binding of GAM443 RNA, herein designated GAM RNA, to target binding sites on GAM443 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM443 target RNA, herein designated GAM TARGET RNA, into GAM443 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6936] It is appreciated that GAM443 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM443 target genes. The mRNA of each one of this plurality of GAM443 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM443 RNA, herein designated GAM RNA, and which when bound by GAM443 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM443 target proteins.

[6937] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM443 gene, herein designated GAM GENE, on one or more GAM443 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6938] It is yet further appreciated that specific functions, and accordingly utilities, of GAM443 correlate with, and may be deduced from, the identity of the target genes which GAM443 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6939] Nucleotide sequences of the GAM443 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM443 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM443 are further described hereinbelow with reference to Table Table1.

[6940] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM443 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6941] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 444 (GAM444) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6942] GAM444 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM444 was detected is described hereinabove with reference to Figs. 2-8.

[6943] GAM444 gene, herein designated GAM GENE, and GAM444 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6944] GAM444 gene, herein designated GAM GENE, encodes a GAM444 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM444 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM444 precursor RNA is designated SEQ ID:416, and is provided hereinbelow with refer-

ence to the sequence listing part.

[6945] GAM444 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6946] An enzyme complex designated DICER COMPLEX, dices the GAM444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM444 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM444 RNA is designated SEQ ID:2092, and is provided hereinbelow with reference to the sequence listing part.

[6947] GAM444 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM444 target RNA, herein designated GAM TARGET RNA.

GAM444 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6948] GAM444 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM444 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM444 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM444 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM444 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6949] The complementary binding of GAM444 RNA, herein designated GAM RNA, to target binding sites on GAM444 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM444 target RNA, herein designated GAM TARGET RNA, into GAM444 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6950] It is appreciated that GAM444 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM444 target genes. The mRNA of each one of this plurality of GAM444 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM444 RNA, herein designated GAM RNA, and which when bound by GAM444 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM444 target proteins.

[6951] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM444 gene, herein designated GAM GENE, on one or more GAM444 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6952] It is yet further appreciated that specific functions, and accordingly utilities, of GAM444 correlate with, and may be deduced from, the identity of the target genes which GAM444 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6953] Nucleotide sequences of the GAM444 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM444 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM444 are further described hereinbelow with reference to Table Table1.

[6954] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM444 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6955] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 445 (GAM445) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6956] GAM445 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM445 was detected is described hereinabove with reference to Figs. 2-8.

[6957] GAM445 gene, herein designated GAM GENE, and GAM445 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6958] GAM445 gene, herein designated GAM GENE, encodes a GAM445 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM445 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM445 precursor RNA is designated SEQ ID:417, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:417 is located at position 268439 relative to contig NT_010692.9, on chromosome 17.

[6959] GAM445 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6960] An enzyme complex designated DICER COMPLEX, dices the GAM445 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM445 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM445 RNA is designated SEQ ID:2093, and is provided hereinbelow with reference to the sequence listing part.

[6961] GAM445 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM445 target RNA, herein designated GAM TARGET RNA. GAM445 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6962] GAM445 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM445 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM445 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM445 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM445 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6963] The complementary binding of GAM445 RNA, herein designated GAM RNA, to target binding sites on GAM445 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM445 target RNA, herein designated GAM TARGET RNA, into GAM445 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6964] It is appreciated that GAM445 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM445 target genes. The mRNA of each one of this plurality of GAM445 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM445 RNA, herein designated GAM RNA, and which when bound by GAM445 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM445 target proteins.

[6965] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM445 gene, herein designated GAM GENE, on one or more GAM445 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6966] It is yet further appreciated that specific functions, and accordingly utilities, of GAM445 correlate with, and may be deduced from, the identity of the target genes which GAM445 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6967] Nucleotide sequences of the GAM445 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM445 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM445 are further described hereinbelow with reference to Table Table1.

[6968] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM445 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6969] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

446 (GAM446) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6970] GAM446 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM446 was detected is described hereinabove with reference to Figs. 2-8.

[6971] GAM446 gene, herein designated GAM GENE, and GAM446 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6972] GAM446 gene, herein designated GAM GENE, encodes a GAM446 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM446 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM446 precursor RNA is designated SEQ ID:418, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:418 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[6973] GAM446 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM446 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6974] An enzyme complex designated DICER COMPLEX, dices the GAM446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM446 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM446 RNA is designated SEQ ID:2094, and is provided hereinbelow with reference to the sequence listing part.

[6975] GAM446 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM446 target RNA, herein designated GAM TARGET RNA. GAM446 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6976] GAM446 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM446 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM446 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM446 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM446 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[6977] The complementary binding of GAM446 RNA, herein designated GAM RNA, to target binding sites on GAM446 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM446 target RNA, herein designated GAM TARGET RNA, into GAM446 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6978] It is appreciated that GAM446 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM446 target genes. The mRNA of each one of this plurality of GAM446 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM446 RNA, herein designated GAM RNA, and which when bound by GAM446 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM446 target proteins.

[6979] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM446 gene, herein designated GAM GENE, on one or

more GAM446 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6980] It is yet further appreciated that specific functions, and accordingly utilities, of GAM446 correlate with, and may be deduced from, the identity of the target genes which GAM446 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6981] Nucleotide sequences of the GAM446 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM446 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM446 are further de-

scribed hereinbelow with reference to Table Table1.

[6982] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM446 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[6983] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 447 (GAM447) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[6984] GAM447 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM447 was detected is described hereinabove with reference to Figs. 2-8.

[6985] GAM447 gene, herein designated GAM GENE, and GAM447 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[6986] GAM447 gene, herein designated GAM GENE, encodes a GAM447 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM447 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM447 precursor RNA is designated SEQ ID:419, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:419 is located at position 1235063 relative to contig NT_009526.11, on chromosome 12.

[6987] GAM447 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[6988] SEQ ID:100040 detected in mouse EST Accession BI965972.1.

[6989] SEQ ID:100041 detected in mouse EST Accession AI326210.1.

[6990] SEQ ID:100042 detected in mouse EST Accession BI965652.1.

[6991] GAM447 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[6992] An enzyme complex designated DICER COMPLEX, dices the GAM447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM447 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM447 RNA is designated SEQ ID:2095, and is provided hereinbelow with reference to the sequence listing part.

[6993] GAM447 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM447 target RNA, herein designated GAM TARGET RNA. GAM447 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[6994] GAM447 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM447 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM447 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM447 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM447 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[6995] The complementary binding of GAM447 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM447 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM447 target RNA, herein designated GAM TARGET RNA, into GAM447 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[6996] It is appreciated that GAM447 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM447 target genes. The mRNA of each one of this plurality of GAM447 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM447 RNA, herein designated GAM RNA, and which when bound by GAM447 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM447 target proteins.

[6997] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM447 gene, herein designated GAM GENE, on one or more GAM447 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[6998] It is yet further appreciated that specific functions, and accordingly utilities, of GAM447 correlate with, and may be deduced from, the identity of the target genes which GAM447 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[6999] Nucleotide sequences of the GAM447 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM447 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM447 are further described hereinbelow with reference to Table Table1.

[7000] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM447 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7001] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 448 (GAM448) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7002] GAM448 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM448 was detected is described hereinabove with reference to Figs. 2-8.

[7003] GAM448 gene, herein designated GAM GENE, and GAM448 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7004] GAM448 gene, herein designated GAM GENE, encodes a GAM448 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM448 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM448 precursor RNA is designated SEQ ID:420, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:420 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[7005] GAM448 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7006] An enzyme complex designated DICER COMPLEX, dices the GAM448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM448 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM448 RNA is designated SEQ ID:2096, and is provided hereinbelow with reference to the sequence listing part.

[7007] GAM448 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM448 target RNA, herein designated GAM TARGET RNA. GAM448 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7008] GAM448 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM448 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM448 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM448 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM448 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7009] The complementary binding of GAM448 RNA, herein designated GAM RNA, to target binding sites on GAM448 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM448 target RNA, herein designated GAM TARGET RNA, into GAM448 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7010] It is appreciated that GAM448 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM448 target genes. The mRNA of each one of this plurality of GAM448 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM448 RNA,

herein designated GAM RNA, and which when bound by GAM448 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM448 target proteins.

[7011] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM448 gene, herein designated GAM GENE, on one or more GAM448 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7012] It is yet further appreciated that specific functions, and accordingly utilities, of GAM448 correlate with, and may be deduced from, the identity of the target genes which

GAM448 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7013] Nucleotide sequences of the GAM448 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM448 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM448 are further described hereinbelow with reference to Table Table1.

[7014] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM448 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7015] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 449 (GAM449) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7016] GAM449 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM449 was detected is described hereinabove with reference to Figs. 2-8.

[7017] GAM449 gene, herein designated GAM GENE, and GAM449 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7018] GAM449 gene, herein designated GAM GENE, encodes a GAM449 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM449 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM449 precursor RNA is designated SEQ ID:421, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:421 is located at position 7678826 relative to contig NT_004852.13, on chromosome 1.

[7019] GAM449 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7020] An enzyme complex designated DICER COMPLEX, dices the GAM449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM449 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM449 RNA is designated SEQ ID:2097, and is provided hereinbelow with reference to the sequence listing part.

[7021] GAM449 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM449 target RNA, herein designated GAM TARGET RNA. GAM449 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7022] GAM449 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM449 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM449 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM449 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM449 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7023] The complementary binding of GAM449 RNA, herein designated GAM RNA, to target binding sites on GAM449 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM449 target RNA, herein designated GAM TARGET RNA, into GAM449 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7024] It is appreciated that GAM449 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM449 target genes. The mRNA of each one of this plurality of GAM449 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM449 RNA, herein designated GAM RNA, and which when bound by GAM449 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM449 target proteins.

[7025] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM449 gene, herein designated GAM GENE, on one or more GAM449 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7026] It is yet further appreciated that specific functions, and accordingly utilities, of GAM449 correlate with, and may be deduced from, the identity of the target genes which GAM449 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7027] Nucleotide sequences of the GAM449 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM449 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM449 are further described hereinbelow with reference to Table Table1.

[7028] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM449 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7029] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 450 (GAM450) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7030] GAM450 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM450 was detected is described hereinabove with reference to Figs. 2-8.

[7031] GAM450 gene, herein designated GAM GENE, and GAM450 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7032] GAM450 gene, herein designated GAM GENE, encodes a GAM450 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM450 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM450 precursor RNA is designated SEQ ID:422, and is provided hereinbelow with refer-

ence to the sequence listing part.

[7033] GAM450 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7034] An enzyme complex designated DICER COMPLEX, dices the GAM450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM450 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM450 RNA is designated SEQ ID:2098, and is provided hereinbelow with reference to the sequence listing part.

[7035] GAM450 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM450 target RNA, herein designated GAM TARGET RNA.

GAM450 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7036] GAM450 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM450 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM450 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM450 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM450 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7037] The complementary binding of GAM450 RNA, herein designated GAM RNA, to target binding sites on GAM450 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM450 target RNA, herein designated GAM TARGET RNA, into GAM450 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7038] It is appreciated that GAM450 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM450 target genes. The mRNA of each one of this plurality of GAM450 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM450 RNA, herein designated GAM RNA, and which when bound by GAM450 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM450 target proteins.

[7039] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM450 gene, herein designated GAM GENE, on one or more GAM450 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7040] It is yet further appreciated that specific functions, and accordingly utilities, of GAM450 correlate with, and may be deduced from, the identity of the target genes which GAM450 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7041] Nucleotide sequences of the GAM450 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM450 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM450 are further described hereinbelow with reference to Table Table1.

[7042] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM450 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7043] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 451 (GAM451) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7044] GAM451 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM451 was detected is described hereinabove with reference to Figs. 2-8.

[7045] GAM451 gene, herein designated GAM GENE, and GAM451 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7046] GAM451 gene, herein designated GAM GENE, encodes a GAM451 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM451 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM451 precursor RNA is designated SEQ ID:423, and is provided hereinbelow with reference to the sequence listing part.

[7047] GAM451 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[7048] SEQ ID:99300 detected in mouse EST Accession BI965972.1.

[7049] SEQ ID:99301 detected in mouse EST Accession AI326210.1.

[7050] SEQ ID:99302 detected in mouse EST Accession BI965652.1.

[7051] GAM451 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7052] An enzyme complex designated DICER COMPLEX, dices the GAM451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM451 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM451 RNA is designated SEQ ID:2099, and is provided hereinbelow with reference to the sequence listing part.

[7053] GAM451 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM451 target RNA, herein designated GAM TARGET RNA. GAM451 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7054] GAM451 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM451 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM451 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM451 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM451 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7055] The complementary binding of GAM451 RNA, herein designated GAM RNA, to target binding sites on GAM451 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM451 target RNA, herein designated GAM TARGET RNA, into GAM451 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7056] It is appreciated that GAM451 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM451 target genes. The mRNA of each one of this plurality of GAM451 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM451 RNA, herein designated GAM RNA, and which when bound by GAM451 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM451 target proteins.

[7057] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM451 gene, herein designated GAM GENE, on one or more GAM451 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7058] It is yet further appreciated that specific functions, and accordingly utilities, of GAM451 correlate with, and may be deduced from, the identity of the target genes which GAM451 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7059] Nucleotide sequences of the GAM451 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM451 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM451 are further described hereinbelow with reference to Table Table1.

[7060] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM451 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7061] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 452 (GAM452) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7062] GAM452 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM452 was detected is described hereinabove with reference to Figs. 2-8.

[7063] GAM452 gene, herein designated GAM GENE, and GAM452 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7064] GAM452 gene, herein designated GAM GENE, encodes a GAM452 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM452 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM452 precursor RNA is designated SEQ ID:424, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:424 is located at position 2349689 relative to contig NT_021907.13, on chromosome 1.

[7065] GAM452 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7066] An enzyme complex designated DICER COMPLEX, dices the GAM452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM452 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM452 RNA is designated SEQ ID:2100, and is provided hereinbelow with reference to the sequence listing part.

[7067] GAM452 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM452 target RNA, herein designated GAM TARGET RNA. GAM452 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7068] GAM452 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM452 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM452 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM452 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM452 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7069] The complementary binding of GAM452 RNA, herein designated GAM RNA, to target binding sites on GAM452 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM452 target RNA, herein designated GAM TARGET RNA, into GAM452 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7070] It is appreciated that GAM452 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM452 target genes. The mRNA of each one of this plurality of GAM452 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM452 RNA, herein designated GAM RNA, and which when bound by GAM452 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM452 target proteins.

[7071] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM452 gene, herein designated GAM GENE, on one or more GAM452 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7072] It is yet further appreciated that specific functions, and accordingly utilities, of GAM452 correlate with, and may

be deduced from, the identity of the target genes which GAM452 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7073] Nucleotide sequences of the GAM452 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM452 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM452 are further described hereinbelow with reference to Table Table1.

[7074] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM452 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7075] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 453 (GAM453) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7076] GAM453 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM453 was detected is described hereinabove with reference to Figs. 2-8.

[7077] GAM453 gene, herein designated GAM GENE, and GAM453 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7078] GAM453 gene, herein designated GAM GENE, encodes a GAM453 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM453 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM453 precursor RNA is designated SEQ ID:425, and is provided hereinbelow with reference to the sequence listing part.

[7079] GAM453 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[7080] An enzyme complex designated DICER COMPLEX, dices the GAM453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM453 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM453 RNA is designated SEQ ID:2101, and is provided hereinbelow with reference to the sequence listing part.

[7081] GAM453 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM453 target RNA, herein designated GAM TARGET RNA.
GAM453 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7082] GAM453 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM453 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM453 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM453 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM453 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7083] The complementary binding of GAM453 RNA, herein designated GAM RNA, to target binding sites on GAM453 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM453 target RNA, herein desig-

nated GAM TARGET RNA, into GAM453 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7084] It is appreciated that GAM453 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM453 target genes. The mRNA of each one of this plurality of GAM453 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM453 RNA, herein designated GAM RNA, and which when bound by GAM453 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM453 target proteins.

[7085] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM453 gene, herein designated GAM GENE, on one or more GAM453 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7086] It is yet further appreciated that specific functions, and accordingly utilities, of GAM453 correlate with, and may be deduced from, the identity of the target genes which GAM453 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7087] Nucleotide sequences of the GAM453 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM453 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM453 are further described hereinbelow with reference to Table Table1.

[7088] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM453 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[7089] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 454 (GAM454) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7090] GAM454 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM454 was detected is described hereinabove with reference to Figs. 2-8.

[7091] GAM454 gene, herein designated GAM GENE, and GAM454 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7092] GAM454 gene, herein designated GAM GENE, encodes a GAM454 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM454 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM454 precursor RNA is designated SEQ ID:426, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:426 is located at position 65702783 relative to contig NT_026437.9, on chromosome 14.

[7093] GAM454 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7094] An enzyme complex designated DICER COMPLEX, dices the GAM454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM454 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM454 RNA is designated SEQ ID:2102, and is provided hereinbelow with reference to the sequence listing part.

[7095] GAM454 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM454 target RNA, herein designated GAM TARGET RNA. GAM454 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7096] GAM454 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM454 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM454 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM454 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM454

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7097] The complementary binding of GAM454 RNA, herein designated GAM RNA, to target binding sites on GAM454 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM454 target RNA, herein designated GAM TARGET RNA, into GAM454 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7098] It is appreciated that GAM454 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM454 target genes. The mRNA of each one of this plurality of GAM454 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM454 RNA, herein designated GAM RNA, and which when bound by GAM454 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM454 target proteins.

[7099] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM454 gene, herein designated GAM GENE, on one or more GAM454 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7100] It is yet further appreciated that specific functions, and accordingly utilities, of GAM454 correlate with, and may be deduced from, the identity of the target genes which GAM454 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7101] Nucleotide sequences of the GAM454 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM454 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM454 are further described hereinbelow with reference to Table Table1.

[7102] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM454 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7103] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 455 (GAM455) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7104] GAM455 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM455 was detected is described hereinabove with reference to Figs. 2-8.

[7105] GAM455 gene, herein designated GAM GENE, and GAM455 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[7106] GAM455 gene, herein designated GAM GENE, encodes a GAM455 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM455 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM455 precursor RNA is designated SEQ ID:427, and is provided hereinbelow with reference to the sequence listing part.

[7107] GAM455 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7108] An enzyme complex designated DICER COMPLEX, dices the GAM455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM455 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM455 RNA is designated SEQ ID:2103, and is provided hereinbelow with reference to the sequence listing part.

[7109] GAM455 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM455 target RNA, herein designated GAM TARGET RNA. GAM455 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7110] GAM455 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM455 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM455 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM455 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM455 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7111] The complementary binding of GAM455 RNA, herein designated GAM RNA, to target binding sites on GAM455 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM455 target RNA, herein designated GAM TARGET RNA, into GAM455 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7112] It is appreciated that GAM455 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM455 target genes. The mRNA of each one of this plurality of GAM455 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM455 RNA, herein designated GAM RNA, and which when bound by GAM455 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM455 target proteins.

[7113] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM455 gene, herein designated GAM GENE, on one or more GAM455 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[7114] It is yet further appreciated that specific functions, and accordingly utilities, of GAM455 correlate with, and may be deduced from, the identity of the target genes which GAM455 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7115] Nucleotide sequences of the GAM455 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM455 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM455 are further described hereinbelow with reference to Table Table1.

[7116] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM455 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7117] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 456 (GAM456) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[7118] GAM456 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM456 was detected is described hereinabove with reference to Figs. 2-8.

[7119] GAM456 gene, herein designated GAM GENE, and GAM456 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7120] GAM456 gene, herein designated GAM GENE, encodes a GAM456 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM456 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM456 precursor RNA is designated SEQ ID:428, and is provided hereinbelow with reference to the sequence listing part.

[7121] GAM456 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7122] An enzyme complex designated DICER COMPLEX, dices the GAM456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM456 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM456 RNA is designated SEQ ID:2104, and is provided hereinbelow with reference to the sequence listing part.

[7123] GAM456 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM456 target RNA, herein designated GAM TARGET RNA.
GAM456 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[7124] GAM456 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM456 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM456 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM456 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM456 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7125] The complementary binding of GAM456 RNA, herein designated GAM RNA, to target binding sites on GAM456 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM456 target RNA, herein designated GAM TARGET RNA, into GAM456 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7126] It is appreciated that GAM456 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM456 target genes. The mRNA of each one of this plurality of GAM456 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM456 RNA, herein designated GAM RNA, and which when bound by GAM456 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM456 target proteins.

[7127] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM456 gene, herein designated GAM GENE, on one or more GAM456 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7128] It is yet further appreciated that specific functions, and accordingly utilities, of GAM456 correlate with, and may be deduced from, the identity of the target genes which GAM456 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7129] Nucleotide sequences of the GAM456 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM456 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM456 are further described hereinbelow with reference to Table Table1.

[7130] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM456 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7131] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 457 (GAM457) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7132] GAM457 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM457 was detected is described hereinabove with reference to Figs. 2-8.

[7133] GAM457 gene, herein designated GAM GENE, and GAM457 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7134] GAM457 gene, herein designated GAM GENE, encodes a GAM457 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM457 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM457 precursor RNA is designated SEQ ID:429, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:429 is located at position 903537 relative to contig NT_008818.13, on chromosome 10.

[7135] GAM457 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7136] An enzyme complex designated DICER COMPLEX, dices the GAM457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM457 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM457 RNA is designated SEQ ID:2105, and is provided hereinbelow with reference to the sequence listing part.

[7137] GAM457 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM457 target RNA, herein designated GAM TARGET RNA. GAM457 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7138] GAM457 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM457 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM457 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM457 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM457 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7139] The complementary binding of GAM457 RNA, herein designated GAM RNA, to target binding sites on GAM457 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM457 target RNA, herein designated GAM TARGET RNA, into GAM457 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7140] It is appreciated that GAM457 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM457 target genes. The mRNA of each one of this plurality of GAM457 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM457 RNA, herein designated GAM RNA, and which when bound by

GAM457 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM457 target proteins.

[7141] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM457 gene, herein designated GAM GENE, on one or more GAM457 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7142] It is yet further appreciated that specific functions, and accordingly utilities, of GAM457 correlate with, and may be deduced from, the identity of the target genes which GAM457 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[7143] Nucleotide sequences of the GAM457 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM457 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM457 are further described hereinbelow with reference to Table Table1.

[7144] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM457 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7145] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 458 (GAM458) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7146] GAM458 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM458 was detected is described hereinabove

with reference to Figs. 2-8.

[7147] GAM458 gene, herein designated GAM GENE, and GAM458 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7148] GAM458 gene, herein designated GAM GENE, encodes a GAM458 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM458 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM458 precursor RNA is designated SEQ ID:430, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:430 is located at position 7474368 relative to contig NT_005403.11, on chromosome 2.

[7149] GAM458 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[7150] An enzyme complex designated DICER COMPLEX, dices the GAM458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM458 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM458 RNA is designated SEQ ID:2106, and is provided hereinbelow with reference to the sequence listing part.

[7151] GAM458 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM458 target RNA, herein designated GAM TARGET RNA.
GAM458 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7152] GAM458 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM458 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM458 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM458 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM458 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7153] The complementary binding of GAM458 RNA, herein designated GAM RNA, to target binding sites on GAM458 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM458 target RNA, herein desig-

nated GAM TARGET RNA, into GAM458 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7154] It is appreciated that GAM458 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM458 target genes. The mRNA of each one of this plurality of GAM458 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM458 RNA, herein designated GAM RNA, and which when bound by GAM458 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM458 target proteins.

[7155] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM458 gene, herein designated GAM GENE, on one or more GAM458 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7156] It is yet further appreciated that specific functions, and accordingly utilities, of GAM458 correlate with, and may be deduced from, the identity of the target genes which GAM458 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7157] Nucleotide sequences of the GAM458 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM458 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM458 are further described hereinbelow with reference to Table Table1.

[7158] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM458 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[7159] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 459 (GAM459) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7160] GAM459 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM459 was detected is described hereinabove with reference to Figs. 2-8.

[7161] GAM459 gene, herein designated GAM GENE, and GAM459 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7162] GAM459 gene, herein designated GAM GENE, encodes a GAM459 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM459 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM459 precursor RNA is designated SEQ ID:431, and is provided hereinbelow with reference to the sequence listing part.

[7163] GAM459 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[7164] SEQ ID:100242 detected in mouse EST Accession BF786784.1.

[7165] SEQ ID:100243 detected in mouse EST Accession BG923933.1.

[7166] SEQ ID:100244 detected in mouse EST Accession BF385482.1.

[7167] SEQ ID:100245 detected in mouse EST Accession BI328034.1.

[7168] SEQ ID:100260 detected in mouse EST Accession BF234553.1.

[7169] SEQ ID:100283 detected in mouse EST Accession BI328620.1.

[7170] SEQ ID:100284 detected in mouse EST Accession BI219823.1.

[7171] GAM459 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7172] An enzyme complex designated DICER COMPLEX, dices

the GAM459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM459 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM459 RNA is designated SEQ ID:2107, and is provided hereinbelow with reference to the sequence listing part.

[7173] GAM459 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM459 target RNA, herein designated GAM TARGET RNA. GAM459 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7174] GAM459 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM459 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM459

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM459 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM459 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7175] The complementary binding of GAM459 RNA, herein designated GAM RNA, to target binding sites on GAM459 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM459 target RNA, herein designated GAM TARGET RNA, into GAM459 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7176] It is appreciated that GAM459 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM459 target genes. The mRNA of each one of this plurality of GAM459 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM459 RNA, herein designated GAM RNA, and which when bound by GAM459 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM459 target proteins.

[7177] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM459 gene, herein designated GAM GENE, on one or more GAM459 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7178] It is yet further appreciated that specific functions, and accordingly utilities, of GAM459 correlate with, and may be deduced from, the identity of the target genes which GAM459 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7179] Nucleotide sequences of the GAM459 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM459 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM459 are further described hereinbelow with reference to Table Table1.

[7180] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM459 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7181] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 460 (GAM460) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7182] GAM460 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM460 was detected is described hereinabove with reference to Figs. 2-8.

[7183] GAM460 gene, herein designated GAM GENE, and GAM460 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7184] GAM460 gene, herein designated GAM GENE, encodes a GAM460 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM460 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM460 precursor RNA is designated SEQ ID:432, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:432 is located at position 387404 relative to contig NT_022508.11, on chromosome 3.

[7185] GAM460 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7186] An enzyme complex designated DICER COMPLEX, dices the GAM460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM460 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM460 RNA is designated SEQ ID:2108, and is provided hereinbelow with reference to the sequence listing part.

[7187] GAM460 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM460 target RNA, herein designated GAM TARGET RNA.

GAM460 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7188] GAM460 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM460 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM460 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM460 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM460 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7189] The complementary binding of GAM460 RNA, herein designated GAM RNA, to target binding sites on GAM460 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM460 target RNA, herein designated GAM TARGET RNA, into GAM460 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7190] It is appreciated that GAM460 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM460 target genes. The mRNA of each one of this plurality of GAM460 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM460 RNA, herein designated GAM RNA, and which when bound by GAM460 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM460 target proteins.

[7191] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM460 gene, herein designated GAM GENE, on one or more GAM460 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7192] It is yet further appreciated that specific functions, and accordingly utilities, of GAM460 correlate with, and may be deduced from, the identity of the target genes which GAM460 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7193] Nucleotide sequences of the GAM460 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM460 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM460 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM460 are further described hereinbelow with reference to Table Table1.

[7194] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM460 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7195] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 461 (GAM461) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7196] GAM461 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM461 was detected is described hereinabove with reference to Figs. 2-8.

[7197] GAM461 gene, herein designated GAM GENE, and GAM461 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7198] GAM461 gene, herein designated GAM GENE, encodes a GAM461 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM461 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM461 precursor RNA is designated SEQ ID:433, and is provided hereinbelow with reference to the sequence listing part.

[7199] GAM461 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7200] An enzyme complex designated DICER COMPLEX, dices the GAM461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM461 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM461 RNA is designated SEQ ID:2109, and is provided hereinbelow with reference to the sequence listing part.

[7201] GAM461 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM461 target RNA, herein designated GAM TARGET RNA. GAM461 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7202] GAM461 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM461 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM461 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM461 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM461 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7203] The complementary binding of GAM461 RNA, herein designated GAM RNA, to target binding sites on GAM461 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM461 target RNA, herein designated GAM TARGET RNA, into GAM461 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7204] It is appreciated that GAM461 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM461 target genes. The mRNA of each one of this plurality of GAM461 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM461 RNA, herein designated GAM RNA, and which when bound by GAM461 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM461 target proteins.

[7205] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM461 gene, herein designated GAM GENE, on one or more GAM461 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7206] It is yet further appreciated that specific functions, and accordingly utilities, of GAM461 correlate with, and may

be deduced from, the identity of the target genes which GAM461 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7207] Nucleotide sequences of the GAM461 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM461 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM461 are further described hereinbelow with reference to Table Table1.

[7208] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM461 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7209] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 462 (GAM462) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7210] GAM462 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM462 was detected is described hereinabove with reference to Figs. 2-8.

[7211] GAM462 gene, herein designated GAM GENE, and GAM462 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7212] GAM462 gene, herein designated GAM GENE, encodes a GAM462 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM462 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM462 precursor RNA is designated SEQ ID:434, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:434 is located at position 4581035 relative to contig NT_008580.11, on chromosome 9.

[7213] GAM462 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7214] An enzyme complex designated DICER COMPLEX, dices the GAM462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM462 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM462 RNA is designated SEQ ID:2110, and is provided hereinbelow with reference to the sequence listing part.

[7215] GAM462 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM462 target RNA, herein designated GAM TARGET RNA. GAM462 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7216] GAM462 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM462 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM462 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM462 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM462 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7217] The complementary binding of GAM462 RNA, herein designated GAM RNA, to target binding sites on GAM462 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM462 target RNA, herein designated GAM TARGET RNA, into GAM462 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7218] It is appreciated that GAM462 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM462 target genes. The mRNA of each one of this plurality of GAM462 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM462 RNA, herein designated GAM RNA, and which when bound by GAM462 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM462 target proteins.

[7219] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM462 gene, herein designated GAM GENE, on one or more GAM462 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7220] It is yet further appreciated that specific functions, and accordingly utilities, of GAM462 correlate with, and may be deduced from, the identity of the target genes which GAM462 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7221] Nucleotide sequences of the GAM462 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM462 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM462 are further described hereinbelow with reference to Table Table1.

[7222] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM462 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7223] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 463 (GAM463) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7224] GAM463 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM463 was detected is described hereinabove with reference to Figs. 2-8.

[7225] GAM463 gene, herein designated GAM GENE, and GAM463 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7226] GAM463 gene, herein designated GAM GENE, encodes a GAM463 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM463 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM463 precursor RNA is desig-

nated SEQ ID:435, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:435 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[7227] GAM463 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7228] An enzyme complex designated DICER COMPLEX, dices the GAM463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM463 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM463 RNA is designated SEQ ID:2111, and is provided hereinbelow with reference to the sequence listing part.

[7229] GAM463 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM463 target RNA, herein designated GAM TARGET RNA. GAM463 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7230] GAM463 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM463 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM463 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM463 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM463 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7231] The complementary binding of GAM463 RNA, herein designated GAM RNA, to target binding sites on GAM463 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM463 target RNA, herein designated GAM TARGET RNA, into GAM463 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7232] It is appreciated that GAM463 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM463 target genes. The mRNA of each one of this plurality of GAM463 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM463 RNA, herein designated GAM RNA, and which when bound by GAM463 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM463 target proteins.

[7233] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM463 gene, herein designated GAM GENE, on one or more GAM463 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7234] It is yet further appreciated that specific functions, and accordingly utilities, of GAM463 correlate with, and may be deduced from, the identity of the target genes which GAM463 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7235] Nucleotide sequences of the GAM463 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM463 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM463 are further described hereinbelow with reference to Table Table1.

[7236] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM463 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7237] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 464 (GAM464) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7238] GAM464 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM464 was detected is described hereinabove with reference to Figs. 2-8.

[7239] GAM464 gene, herein designated GAM GENE, and GAM464 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7240] GAM464 gene, herein designated GAM GENE, encodes a GAM464 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM464 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM464 precursor RNA is designated SEQ ID:436, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:436 is located at position 1998674 relative to contig NT_011362.7, on chromosome 20.

[7241] GAM464 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[7242] An enzyme complex designated DICER COMPLEX, dices the GAM464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM464 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM464 RNA is designated SEQ ID:2112, and is provided hereinbelow with reference to the sequence listing part.

[7243] GAM464 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM464 target RNA, herein designated GAM TARGET RNA. GAM464 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7244] GAM464 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM464 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM464 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM464 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM464 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7245] The complementary binding of GAM464 RNA, herein designated GAM RNA, to target binding sites on GAM464 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM464 target RNA, herein designated GAM TARGET RNA, into GAM464 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7246] It is appreciated that GAM464 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM464 target genes. The mRNA of each one of this plurality of GAM464 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM464 RNA, herein designated GAM RNA, and which when bound by GAM464 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM464 target proteins.

[7247] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM464 gene, herein designated GAM GENE, on one or more GAM464 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7248] It is yet further appreciated that specific functions, and accordingly utilities, of GAM464 correlate with, and may be deduced from, the identity of the target genes which GAM464 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7249] Nucleotide sequences of the GAM464 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM464 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM464 are further described hereinbelow with reference to Table Table1.

[7250] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM464 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7251] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 465 (GAM465) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7252] GAM465 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM465 was detected is described hereinabove with reference to Figs. 2-8.

[7253] GAM465 gene, herein designated GAM GENE, and GAM465 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7254] GAM465 gene, herein designated GAM GENE, encodes a GAM465 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM465 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM465 precursor RNA is designated SEQ ID:437, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:437 is located at position 898080 relative to contig

NT_011044.11, on chromosome 18.

[7255] GAM465 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7256] An enzyme complex designated DICER COMPLEX, dices the GAM465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM465 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM465 RNA is designated SEQ ID:2113, and is provided hereinbelow with reference to the sequence listing part.

[7257] GAM465 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM465 target RNA, herein designated GAM TARGET RNA.

GAM465 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7258] GAM465 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM465 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM465 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM465 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM465 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7259] The complementary binding of GAM465 RNA, herein designated GAM RNA, to target binding sites on GAM465 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM465 target RNA, herein designated GAM TARGET RNA, into GAM465 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7260] It is appreciated that GAM465 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM465 target genes. The mRNA of each one of this plurality of GAM465 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM465 RNA, herein designated GAM RNA, and which when bound by GAM465 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM465 target proteins.

[7261] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM465 gene, herein designated GAM GENE, on one or more GAM465 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7262] It is yet further appreciated that specific functions, and accordingly utilities, of GAM465 correlate with, and may be deduced from, the identity of the target genes which GAM465 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7263] Nucleotide sequences of the GAM465 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM465 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM465 are further described hereinbelow with reference to Table Table1.

[7264] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM465 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7265] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 466 (GAM466) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7266] GAM466 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM466 was detected is described hereinabove with reference to Figs. 2-8.

[7267] GAM466 gene, herein designated GAM GENE, and GAM466 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7268] GAM466 gene, herein designated GAM GENE, encodes a GAM466 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM466 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM466 precursor RNA is designated SEQ ID:438, and is provided hereinbelow with reference to the sequence listing part.

[7269] GAM466 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7270] An enzyme complex designated DICER COMPLEX, dices the GAM466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM466 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM466 RNA is designated SEQ ID:2114, and is provided hereinbelow with reference to the sequence listing part.

[7271] GAM466 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM466 target RNA, herein designated GAM TARGET RNA. GAM466 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7272] GAM466 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM466 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM466 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM466 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM466 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7273] The complementary binding of GAM466 RNA, herein designated GAM RNA, to target binding sites on GAM466 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM466 target RNA, herein designated GAM TARGET RNA, into GAM466 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7274] It is appreciated that GAM466 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM466 target genes. The mRNA of each one of this plu-

rality of GAM466 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM466 RNA, herein designated GAM RNA, and which when bound by GAM466 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM466 target proteins.

[7275] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM466 gene, herein designated GAM GENE, on one or more GAM466 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7276] It is yet further appreciated that specific functions, and accordingly utilities, of GAM466 correlate with, and may be deduced from, the identity of the target genes which GAM466 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7277] Nucleotide sequences of the GAM466 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM466 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM466 are further described hereinbelow with reference to Table Table1.

[7278] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM466 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7279] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 467 (GAM467) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[7280] GAM467 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM467 was detected is described hereinabove with reference to Figs. 2-8.

[7281] GAM467 gene, herein designated GAM GENE, and GAM467 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7282] GAM467 gene, herein designated GAM GENE, encodes a GAM467 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM467 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM467 precursor RNA is designated SEQ ID:439, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:439 is located at position 7678827 relative to contig NT_004852.13, on chromosome 1.

[7283] GAM467 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7284] An enzyme complex designated DICER COMPLEX, dices the GAM467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM467 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM467 RNA is designated SEQ ID:2115, and is provided hereinbelow with reference to the sequence listing part.

[7285] GAM467 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM467 target RNA, herein designated GAM TARGET RNA. GAM467 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7286] GAM467 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM467 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM467 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM467 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM467 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7287] The complementary binding of GAM467 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM467 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM467 target RNA, herein designated GAM TARGET RNA, into GAM467 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7288] It is appreciated that GAM467 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM467 target genes. The mRNA of each one of this plurality of GAM467 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM467 RNA, herein designated GAM RNA, and which when bound by GAM467 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM467 target proteins.

[7289] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM467 gene, herein designated GAM GENE, on one or more GAM467 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7290] It is yet further appreciated that specific functions, and accordingly utilities, of GAM467 correlate with, and may be deduced from, the identity of the target genes which GAM467 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7291] Nucleotide sequences of the GAM467 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM467 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM467 are further described hereinbelow with reference to Table Table1.

[7292] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM467 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7293] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 468 (GAM468) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7294] GAM468 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM468 was detected is described hereinabove with reference to Figs. 2-8.

[7295] GAM468 gene, herein designated GAM GENE, and GAM468 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7296] GAM468 gene, herein designated GAM GENE, encodes a GAM468 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM468 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM468 precursor RNA is designated SEQ ID:440, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:440 is located at position 159296 relative to contig NT_025664.12, on chromosome 3.

[7297] GAM468 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7298] An enzyme complex designated DICER COMPLEX, dices the GAM468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM468 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM468 RNA is designated SEQ ID:2116, and is provided hereinbelow with reference to the sequence listing part.

[7299] GAM468 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM468 target RNA, herein designated GAM TARGET RNA. GAM468 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7300] GAM468 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM468 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM468 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM468 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM468 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7301] The complementary binding of GAM468 RNA, herein designated GAM RNA, to target binding sites on GAM468 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM468 target RNA, herein designated GAM TARGET RNA, into GAM468 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7302] It is appreciated that GAM468 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM468 target genes. The mRNA of each one of this plurality of GAM468 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM468 RNA,

herein designated GAM RNA, and which when bound by GAM468 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM468 target proteins.

[7303] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM468 gene, herein designated GAM GENE, on one or more GAM468 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7304] It is yet further appreciated that specific functions, and accordingly utilities, of GAM468 correlate with, and may be deduced from, the identity of the target genes which

GAM468 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7305] Nucleotide sequences of the GAM468 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM468 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM468 are further described hereinbelow with reference to Table Table1.

[7306] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM468 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7307] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 469 (GAM469) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7308] GAM469 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM469 was detected is described hereinabove with reference to Figs. 2-8.

[7309] GAM469 gene, herein designated GAM GENE, and GAM469 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7310] GAM469 gene, herein designated GAM GENE, encodes a GAM469 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM469 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM469 precursor RNA is designated SEQ ID:441, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:441 is located at position 4532539 relative to contig NT_035212.2, on chromosome 12.

[7311] GAM469 has 10 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[7312] SEQ ID:99514 detected in mouse EST Accession AA981127.1.

[7313] SEQ ID:99515 detected in mouse EST Accession AA410034.1.

[7314] SEQ ID:99516 detected in mouse EST Accession BG073066.1.

[7315] SEQ ID:99517 detected in mouse EST Accession BE570198.1.

[7316] SEQ ID:99518 detected in mouse EST Accession BI686879.1.

[7317] SEQ ID:99519 detected in mouse EST Accession BF462203.1.

[7318] SEQ ID:99520 detected in mouse EST Accession BF318901.1.

[7319] SEQ ID:99521 detected in mouse EST Accession AW548168.1.

[7320] SEQ ID:99522 detected in mouse EST Accession BI150489.1.

[7321] SEQ ID:99523 detected in mouse EST Accession BF318900.1.

[7322] GAM469 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7323] An enzyme complex designated DICER COMPLEX, dices the GAM469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM469 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM469 RNA is designated SEQ ID:2117, and is provided hereinbelow with reference to the sequence listing part.

[7324] GAM469 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM469 target RNA, herein designated GAM TARGET RNA.
GAM469 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[7325] GAM469 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM469 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM469 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM469 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM469 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7326] The complementary binding of GAM469 RNA, herein designated GAM RNA, to target binding sites on GAM469 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM469 target RNA, herein designated GAM TARGET RNA, into GAM469 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7327] It is appreciated that GAM469 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM469 target genes. The mRNA of each one of this plurality of GAM469 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM469 RNA, herein designated GAM RNA, and which when bound by GAM469 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM469 target proteins.

[7328] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM469 gene, herein designated GAM GENE, on one or more GAM469 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7329] It is yet further appreciated that specific functions, and accordingly utilities, of GAM469 correlate with, and may be deduced from, the identity of the target genes which GAM469 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7330] Nucleotide sequences of the GAM469 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM469 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM469 are further described hereinbelow with reference to Table Table1.

[7331] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM469 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7332] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 470 (GAM470) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7333] GAM470 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM470 was detected is described hereinabove with reference to Figs. 2-8.

[7334] GAM470 gene, herein designated GAM GENE, and GAM470 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7335] GAM470 gene, herein designated GAM GENE, encodes a GAM470 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM470 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM470 precursor RNA is designated SEQ ID:442, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:442 is located at position 4242976 relative to contig NT_010692.9, on chromosome 17.

[7336] GAM470 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7337] An enzyme complex designated DICER COMPLEX, dices the GAM470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM470 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM470 RNA is designated SEQ ID:2118, and is provided hereinbelow with reference to the sequence listing part.

[7338] GAM470 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM470 target RNA, herein designated GAM TARGET RNA. GAM470 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7339] GAM470 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM470 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM470 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM470 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM470 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7340] The complementary binding of GAM470 RNA, herein designated GAM RNA, to target binding sites on GAM470 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM470 target RNA, herein designated GAM TARGET RNA, into GAM470 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7341] It is appreciated that GAM470 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM470 target genes. The mRNA of each one of this plurality of GAM470 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM470 RNA, herein designated GAM RNA, and which when bound by

GAM470 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM470 target proteins.

[7342] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM470 gene, herein designated GAM GENE, on one or more GAM470 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7343] It is yet further appreciated that specific functions, and accordingly utilities, of GAM470 correlate with, and may be deduced from, the identity of the target genes which GAM470 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[7344] Nucleotide sequences of the GAM470 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM470 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM470 are further described hereinbelow with reference to Table Table1.

[7345] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM470 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7346] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 471 (GAM471) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7347] GAM471 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM471 was detected is described hereinabove

with reference to Figs. 2-8.

[7348] GAM471 gene, herein designated GAM GENE, and GAM471 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7349] GAM471 gene, herein designated GAM GENE, encodes a GAM471 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM471 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM471 precursor RNA is designated SEQ ID:443, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:443 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[7350] GAM471 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[7351] An enzyme complex designated DICER COMPLEX, dices the GAM471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM471 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM471 RNA is designated SEQ ID:2119, and is provided hereinbelow with reference to the sequence listing part.

[7352] GAM471 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM471 target RNA, herein designated GAM TARGET RNA.
GAM471 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7353] GAM471 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM471 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM471 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM471 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM471 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7354] The complementary binding of GAM471 RNA, herein designated GAM RNA, to target binding sites on GAM471 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM471 target RNA, herein desig-

nated GAM TARGET RNA, into GAM471 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7355] It is appreciated that GAM471 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM471 target genes. The mRNA of each one of this plurality of GAM471 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM471 RNA, herein designated GAM RNA, and which when bound by GAM471 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM471 target proteins.

[7356] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM471 gene, herein designated GAM GENE, on one or more GAM471 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7357] It is yet further appreciated that specific functions, and accordingly utilities, of GAM471 correlate with, and may be deduced from, the identity of the target genes which GAM471 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7358] Nucleotide sequences of the GAM471 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM471 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM471 are further described hereinbelow with reference to Table Table1.

[7359] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM471 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[7360] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 472 (GAM472) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7361] GAM472 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM472 was detected is described hereinabove with reference to Figs. 2-8.

[7362] GAM472 gene, herein designated GAM GENE, and GAM472 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7363] GAM472 gene, herein designated GAM GENE, encodes a GAM472 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM472 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM472 precursor RNA is designated SEQ ID:444, and is provided hereinbelow with reference to the sequence listing part.

[7364] GAM472 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7365] An enzyme complex designated DICER COMPLEX, dices the GAM472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM472 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM472 RNA is designated SEQ ID:2120, and is provided hereinbelow with reference to the sequence listing part.

[7366] GAM472 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM472

target RNA, herein designated GAM TARGET RNA.

GAM472 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7367] GAM472 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM472 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM472 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM472 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM472 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7368] The complementary binding of GAM472 RNA, herein designated GAM RNA, to target binding sites on GAM472 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM472 target RNA, herein designated GAM TARGET RNA, into GAM472 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7369] It is appreciated that GAM472 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM472 target genes. The mRNA of each one of this plurality of GAM472 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM472 RNA, herein designated GAM RNA, and which when bound by GAM472 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM472 target proteins.

[7370] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM472 gene, herein designated GAM GENE, on one or more GAM472 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7371] It is yet further appreciated that specific functions, and accordingly utilities, of GAM472 correlate with, and may be deduced from, the identity of the target genes which GAM472 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7372] Nucleotide sequences of the GAM472 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM472 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM472 are further described hereinbelow with reference to Table Table1.

[7373] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM472 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7374] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 473 (GAM473) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7375] GAM473 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM473 was detected is described hereinabove with reference to Figs. 2-8.

[7376] GAM473 gene, herein designated GAM GENE, and GAM473 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7377] GAM473 gene, herein designated GAM GENE, encodes a

GAM473 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM473 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM473 precursor RNA is designated SEQ ID:445, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:445 is located at position 4107928 relative to contig NT_006576.11, on chromosome 5.

[7378] GAM473 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7379] An enzyme complex designated DICER COMPLEX, dices the GAM473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM473 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM473 RNA is designated SEQ ID:2121, and is provided hereinbelow with reference to the sequence listing part.

[7380] GAM473 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM473 target RNA, herein designated GAM TARGET RNA. GAM473 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7381] GAM473 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM473 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM473 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM473 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM473 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7382] The complementary binding of GAM473 RNA, herein designated GAM RNA, to target binding sites on GAM473 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM473 target RNA, herein designated GAM TARGET RNA, into GAM473 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7383] It is appreciated that GAM473 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM473 target genes. The mRNA of each one of this plurality of GAM473 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM473 RNA, herein designated GAM RNA, and which when bound by GAM473 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM473 target proteins.

[7384] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM473 gene, herein designated GAM GENE, on one or more GAM473 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[7385] It is yet further appreciated that specific functions, and accordingly utilities, of GAM473 correlate with, and may be deduced from, the identity of the target genes which GAM473 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7386] Nucleotide sequences of the GAM473 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM473 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM473 are further described hereinbelow with reference to Table Table1.

[7387] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM473 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7388] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 474 (GAM474) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[7389] GAM474 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM474 was detected is described hereinabove with reference to Figs. 2-8.

[7390] GAM474 gene, herein designated GAM GENE, and GAM474 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7391] GAM474 gene, herein designated GAM GENE, encodes a GAM474 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM474 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM474 precursor RNA is designated SEQ ID:446, and is provided hereinbelow with reference to the sequence listing part.

[7392] GAM474 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7393] An enzyme complex designated DICER COMPLEX, dices the GAM474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM474 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM474 RNA is designated SEQ ID:2122, and is provided hereinbelow with reference to the sequence listing part.

[7394] GAM474 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM474 target RNA, herein designated GAM TARGET RNA.
GAM474 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[7395] GAM474 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM474 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM474 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM474 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM474 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7396] The complementary binding of GAM474 RNA, herein designated GAM RNA, to target binding sites on GAM474 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM474 target RNA, herein designated GAM TARGET RNA, into GAM474 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7397] It is appreciated that GAM474 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM474 target genes. The mRNA of each one of this plurality of GAM474 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM474 RNA, herein designated GAM RNA, and which when bound by GAM474 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM474 target proteins.

[7398] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM474 gene, herein designated GAM GENE, on one or more GAM474 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7399] It is yet further appreciated that specific functions, and accordingly utilities, of GAM474 correlate with, and may be deduced from, the identity of the target genes which GAM474 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7400] Nucleotide sequences of the GAM474 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM474 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM474 are further described hereinbelow with reference to Table Table1.

[7401] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM474 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7402] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 475 (GAM475) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7403] GAM475 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM475 was detected is described hereinabove with reference to Figs. 2-8.

[7404] GAM475 gene, herein designated GAM GENE, and GAM475 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7405] GAM475 gene, herein designated GAM GENE, encodes a GAM475 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM475 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM475 precursor RNA is designated SEQ ID:447, and is provided hereinbelow with reference to the sequence listing part.

[7406] GAM475 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7407] An enzyme complex designated DICER COMPLEX, dices the GAM475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM475 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM475 RNA is designated SEQ ID:2123, and is provided

hereinbelow with reference to the sequence listing part.

[7408] GAM475 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM475 target RNA, herein designated GAM TARGET RNA.
GAM475 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7409] GAM475 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM475 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM475 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM475 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM475 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7410] The complementary binding of GAM475 RNA, herein designated GAM RNA, to target binding sites on GAM475 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM475 target RNA, herein designated GAM TARGET RNA, into GAM475 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7411] It is appreciated that GAM475 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM475 target genes. The mRNA of each one of this plurality of GAM475 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM475 RNA, herein designated GAM RNA, and which when bound by GAM475 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM475 tar-

get proteins.

[7412] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM475 gene, herein designated GAM GENE, on one or more GAM475 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7413] It is yet further appreciated that specific functions, and accordingly utilities, of GAM475 correlate with, and may be deduced from, the identity of the target genes which GAM475 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7414] Nucleotide sequences of the GAM475 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM475 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM475 are further described hereinbelow with reference to Table Table1.

[7415] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM475 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7416] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 476 (GAM476) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7417] GAM476 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM476 was detected is described hereinabove with reference to Figs. 2-8.

[7418] GAM476 gene, herein designated GAM GENE, and

GAM476 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7419] GAM476 gene, herein designated GAM GENE, encodes a GAM476 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM476 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM476 precursor RNA is designated SEQ ID:448, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:448 is located at position 15567257 relative to contig NT_007592.11, on chromosome 6.

[7420] GAM476 has 20 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[7421] SEQ ID:99778 detected in mouse EST Accession BF465841.1.

[7422] SEQ ID:99779 detected in mouse EST Accession AA798467.1.

[7423] SEQ ID:99780 detected in mouse EST Accession

AA798123.1.

[7424] SEQ ID:99781 detected in mouse EST Accession BG148023.1.

[7425] SEQ ID:99782 detected in mouse EST Accession BG147005.1.

[7426] SEQ ID:99783 detected in mouse EST Accession BE311050.1.

[7427] SEQ ID:99784 detected in mouse EST Accession BE625094.1.

[7428] SEQ ID:99785 detected in mouse EST Accession AI316639.1.

[7429] SEQ ID:99786 detected in mouse EST Accession BG803992.1.

[7430] SEQ ID:99787 detected in mouse EST Accession BI080618.1.

[7431] SEQ ID:99788 detected in mouse EST Accession BG914583.1.

[7432] SEQ ID:99789 detected in mouse EST Accession BI689042.1.

[7433] SEQ ID:99791 detected in mouse EST Accession BF784199.1.

[7434] SEQ ID:99794 detected in mouse EST Accession BG092976.1.

[7435] SEQ ID:99795 detected in mouse EST Accession AI194277.1.

[7436] SEQ ID:99796 detected in mouse EST Accession BI659175.1.

[7437] SEQ ID:99797 detected in mouse EST Accession BB067326.2.

[7438] SEQ ID:99798 detected in mouse EST Accession BG975946.1.

[7439] SEQ ID:99799 detected in mouse EST Accession BI696541.1.

[7440] SEQ ID:99800 detected in mouse EST Accession BF140373.1.

[7441] GAM476 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7442] An enzyme complex designated DICER COMPLEX, dices

the GAM476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM476 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM476 RNA is designated SEQ ID:2124, and is provided hereinbelow with reference to the sequence listing part.

[7443] GAM476 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM476 target RNA, herein designated GAM TARGET RNA. GAM476 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7444] GAM476 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM476 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM476

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM476 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM476 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7445] The complementary binding of GAM476 RNA, herein designated GAM RNA, to target binding sites on GAM476 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM476 target RNA, herein designated GAM TARGET RNA, into GAM476 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7446] It is appreciated that GAM476 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM476 target genes. The mRNA of each one of this plurality of GAM476 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM476 RNA, herein designated GAM RNA, and which when bound by GAM476 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM476 target proteins.

[7447] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM476 gene, herein designated GAM GENE, on one or more GAM476 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7448] It is yet further appreciated that specific functions, and accordingly utilities, of GAM476 correlate with, and may be deduced from, the identity of the target genes which GAM476 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7449] Nucleotide sequences of the GAM476 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM476 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM476 are further described hereinbelow with reference to Table Table1.

[7450] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM476 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7451] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 477 (GAM477) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7452] GAM477 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM477 was detected is described hereinabove with reference to Figs. 2-8.

[7453] GAM477 gene, herein designated GAM GENE, and GAM477 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7454] GAM477 gene, herein designated GAM GENE, encodes a GAM477 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM477 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM477 precursor RNA is designated SEQ ID:449, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:449 is located at position 4367480 relative to contig NT_007540.11, on chromosome 6.

[7455] GAM477 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7456] An enzyme complex designated DICER COMPLEX, dices the GAM477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM477 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM477 RNA is designated SEQ ID:2125, and is provided hereinbelow with reference to the sequence listing part.

[7457] GAM477 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM477 target RNA, herein designated GAM TARGET RNA.

GAM477 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7458] GAM477 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM477 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM477 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM477 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM477 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7459] The complementary binding of GAM477 RNA, herein designated GAM RNA, to target binding sites on GAM477 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM477 target RNA, herein designated GAM TARGET RNA, into GAM477 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7460] It is appreciated that GAM477 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM477 target genes. The mRNA of each one of this plurality of GAM477 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM477 RNA, herein designated GAM RNA, and which when bound by GAM477 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM477 target proteins.

[7461] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM477 gene, herein designated GAM GENE, on one or more GAM477 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7462] It is yet further appreciated that specific functions, and accordingly utilities, of GAM477 correlate with, and may be deduced from, the identity of the target genes which GAM477 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7463] Nucleotide sequences of the GAM477 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM477 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM477 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM477 are further described hereinbelow with reference to Table Table1.

[7464] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM477 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7465] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 478 (GAM478) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7466] GAM478 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM478 was detected is described hereinabove with reference to Figs. 2-8.

[7467] GAM478 gene, herein designated GAM GENE, and GAM478 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7468] GAM478 gene, herein designated GAM GENE, encodes a GAM478 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM478 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM478 precursor RNA is designated SEQ ID:450, and is provided hereinbelow with reference to the sequence listing part.

[7469] GAM478 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7470] An enzyme complex designated DICER COMPLEX, dices the GAM478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM478 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM478 RNA is designated SEQ ID:2126, and is provided hereinbelow with reference to the sequence listing part.

[7471] GAM478 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM478 target RNA, herein designated GAM TARGET RNA. GAM478 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7472] GAM478 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM478 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM478 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM478 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM478 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7473] The complementary binding of GAM478 RNA, herein designated GAM RNA, to target binding sites on GAM478 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM478 target RNA, herein designated GAM TARGET RNA, into GAM478 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7474] It is appreciated that GAM478 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM478 target genes. The mRNA of each one of this plurality of GAM478 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM478 RNA, herein designated GAM RNA, and which when bound by GAM478 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM478 target proteins.

[7475] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM478 gene, herein designated GAM GENE, on one or more GAM478 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7476] It is yet further appreciated that specific functions, and accordingly utilities, of GAM478 correlate with, and may

be deduced from, the identity of the target genes which GAM478 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7477] Nucleotide sequences of the GAM478 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM478 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM478 are further described hereinbelow with reference to Table Table1.

[7478] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM478 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7479] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 479 (GAM479) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7480] GAM479 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM479 was detected is described hereinabove with reference to Figs. 2-8.

[7481] GAM479 gene, herein designated GAM GENE, and GAM479 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7482] GAM479 gene, herein designated GAM GENE, encodes a GAM479 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM479 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM479 precursor RNA is designated SEQ ID:451, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:451 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[7483] GAM479 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7484] An enzyme complex designated DICER COMPLEX, dices the GAM479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM479 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM479 RNA is designated SEQ ID:2127, and is provided hereinbelow with reference to the sequence listing part.

[7485] GAM479 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM479 target RNA, herein designated GAM TARGET RNA. GAM479 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7486] GAM479 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM479 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM479 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM479 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM479 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7487] The complementary binding of GAM479 RNA, herein designated GAM RNA, to target binding sites on GAM479 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM479 target RNA, herein designated GAM TARGET RNA, into GAM479 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7488] It is appreciated that GAM479 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM479 target genes. The mRNA of each one of this plurality of GAM479 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM479 RNA, herein designated GAM RNA, and which when bound by GAM479 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM479 target proteins.

[7489] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM479 gene, herein designated GAM GENE, on one or more GAM479 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7490] It is yet further appreciated that specific functions, and accordingly utilities, of GAM479 correlate with, and may be deduced from, the identity of the target genes which GAM479 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7491] Nucleotide sequences of the GAM479 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM479 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM479 are further described hereinbelow with reference to Table Table1.

[7492] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM479 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7493] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 480 (GAM480) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7494] GAM480 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM480 was detected is described hereinabove with reference to Figs. 2-8.

[7495] GAM480 gene, herein designated GAM GENE, and GAM480 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7496] GAM480 gene, herein designated GAM GENE, encodes a GAM480 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM480 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM480 precursor RNA is desig-

nated SEQ ID:452, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:452 is located at position 1698742 relative to contig NT_028309.8, on chromosome 11.

[7497] GAM480 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7498] An enzyme complex designated DICER COMPLEX, dices the GAM480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM480 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM480 RNA is designated SEQ ID:2128, and is provided hereinbelow with reference to the sequence listing part.

[7499] GAM480 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM480 target RNA, herein designated GAM TARGET RNA. GAM480 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7500] GAM480 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM480 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM480 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM480 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM480 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7501] The complementary binding of GAM480 RNA, herein designated GAM RNA, to target binding sites on GAM480 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM480 target RNA, herein designated GAM TARGET RNA, into GAM480 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7502] It is appreciated that GAM480 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM480 target genes. The mRNA of each one of this plurality of GAM480 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM480 RNA, herein designated GAM RNA, and which when bound by GAM480 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM480 target proteins.

[7503] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM480 gene, herein designated GAM GENE, on one or more GAM480 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7504] It is yet further appreciated that specific functions, and accordingly utilities, of GAM480 correlate with, and may be deduced from, the identity of the target genes which GAM480 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7505] Nucleotide sequences of the GAM480 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM480 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM480 are further described hereinbelow with reference to Table Table1.

[7506] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM480 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7507] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 481 (GAM481) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7508] GAM481 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM481 was detected is described hereinabove with reference to Figs. 2-8.

[7509] GAM481 gene, herein designated GAM GENE, and GAM481 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7510] GAM481 gene, herein designated GAM GENE, encodes a GAM481 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM481 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM481 precursor RNA is designated SEQ ID:453, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:453 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[7511] GAM481 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[7512] An enzyme complex designated DICER COMPLEX, dices the GAM481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM481 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM481 RNA is designated SEQ ID:2129, and is provided hereinbelow with reference to the sequence listing part.

[7513] GAM481 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM481 target RNA, herein designated GAM TARGET RNA. GAM481 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7514] GAM481 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM481 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM481 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM481 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM481 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7515] The complementary binding of GAM481 RNA, herein designated GAM RNA, to target binding sites on GAM481 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM481 target RNA, herein designated GAM TARGET RNA, into GAM481 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7516] It is appreciated that GAM481 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM481 target genes. The mRNA of each one of this plurality of GAM481 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM481 RNA, herein designated GAM RNA, and which when bound by GAM481 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM481 target proteins.

[7517] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM481 gene, herein designated GAM GENE, on one or more GAM481 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7518] It is yet further appreciated that specific functions, and accordingly utilities, of GAM481 correlate with, and may be deduced from, the identity of the target genes which GAM481 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7519] Nucleotide sequences of the GAM481 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM481 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM481 are further described hereinbelow with reference to Table Table1.

[7520] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM481 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7521] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 482 (GAM482) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7522] GAM482 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM482 was detected is described hereinabove with reference to Figs. 2-8.

[7523] GAM482 gene, herein designated GAM GENE, and GAM482 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7524] GAM482 gene, herein designated GAM GENE, encodes a GAM482 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM482 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM482 precursor RNA is designated SEQ ID:454, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:454 is located at position 5750768 relative to con-

tig NT_010966.11, on chromosome 18.

[7525] GAM482 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7526] An enzyme complex designated DICER COMPLEX, dices the GAM482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM482 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM482 RNA is designated SEQ ID:2130, and is provided hereinbelow with reference to the sequence listing part.

[7527] GAM482 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM482 target RNA, herein designated GAM TARGET RNA.

GAM482 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7528] GAM482 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM482 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM482 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM482 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM482 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7529] The complementary binding of GAM482 RNA, herein designated GAM RNA, to target binding sites on GAM482 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM482 target RNA, herein designated GAM TARGET RNA, into GAM482 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7530] It is appreciated that GAM482 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM482 target genes. The mRNA of each one of this plurality of GAM482 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM482 RNA, herein designated GAM RNA, and which when bound by GAM482 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM482 target proteins.

[7531] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM482 gene, herein designated GAM GENE, on one or more GAM482 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7532] It is yet further appreciated that specific functions, and accordingly utilities, of GAM482 correlate with, and may be deduced from, the identity of the target genes which GAM482 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7533] Nucleotide sequences of the GAM482 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM482 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM482 are further described hereinbelow with reference to Table Table1.

[7534] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM482 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7535] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 483 (GAM483) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7536] GAM483 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM483 was detected is described hereinabove with reference to Figs. 2-8.

[7537] GAM483 gene, herein designated GAM GENE, and GAM483 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7538] GAM483 gene, herein designated GAM GENE, encodes a GAM483 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM483 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM483 precursor RNA is designated SEQ ID:455, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:455 is located at position 113544 relative to contig NT_033233.3, on chromosome 11.

[7539] GAM483 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7540] An enzyme complex designated DICER COMPLEX, dices the GAM483 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM483 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM483 RNA is designated SEQ ID:2131, and is provided hereinbelow with reference to the sequence listing part.

[7541] GAM483 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM483 target RNA, herein designated GAM TARGET RNA. GAM483 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7542] GAM483 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM483 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM483 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM483 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM483 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7543] The complementary binding of GAM483 RNA, herein designated GAM RNA, to target binding sites on GAM483 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM483 target RNA, herein designated GAM TARGET RNA, into GAM483 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7544] It is appreciated that GAM483 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM483 target genes. The mRNA of each one of this plurality of GAM483 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM483 RNA, herein designated GAM RNA, and which when bound by GAM483 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM483 target proteins.

[7545] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM483 gene, herein designated GAM GENE, on one or more GAM483 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7546] It is yet further appreciated that specific functions, and accordingly utilities, of GAM483 correlate with, and may be deduced from, the identity of the target genes which GAM483 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7547] Nucleotide sequences of the GAM483 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM483 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM483 are further described hereinbelow with reference to Table Table1.

[7548] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM483 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7549] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

484 (GAM484) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7550] GAM484 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM484 was detected is described hereinabove with reference to Figs. 2-8.

[7551] GAM484 gene, herein designated GAM GENE, and GAM484 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7552] GAM484 gene, herein designated GAM GENE, encodes a GAM484 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM484 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM484 precursor RNA is designated SEQ ID:456, and is provided hereinbelow with reference to the sequence listing part.

[7553] GAM484 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7554] An enzyme complex designated DICER COMPLEX, dices the GAM484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM484 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM484 RNA is designated SEQ ID:2132, and is provided hereinbelow with reference to the sequence listing part.

[7555] GAM484 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM484 target RNA, herein designated GAM TARGET RNA. GAM484 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7556] GAM484 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM484 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM484 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM484 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM484 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7557] The complementary binding of GAM484 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM484 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM484 target RNA, herein designated GAM TARGET RNA, into GAM484 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7558] It is appreciated that GAM484 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM484 target genes. The mRNA of each one of this plurality of GAM484 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM484 RNA, herein designated GAM RNA, and which when bound by GAM484 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM484 target proteins.

[7559] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM484 gene, herein designated GAM GENE, on one or more GAM484 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7560] It is yet further appreciated that specific functions, and accordingly utilities, of GAM484 correlate with, and may be deduced from, the identity of the target genes which GAM484 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7561] Nucleotide sequences of the GAM484 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM484 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM484 are further described hereinbelow with reference to Table Table1.

[7562] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM484 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7563] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 485 (GAM485) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7564] GAM485 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM485 was detected is described hereinabove with reference to Figs. 2-8.

[7565] GAM485 gene, herein designated GAM GENE, and GAM485 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7566] GAM485 gene, herein designated GAM GENE, encodes a GAM485 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM485 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM485 precursor RNA is designated SEQ ID:457, and is provided hereinbelow with reference to the sequence listing part.

[7567] GAM485 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7568] An enzyme complex designated DICER COMPLEX, dices the GAM485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM485 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM485 RNA is designated SEQ ID:2133, and is provided hereinbelow with reference to the sequence listing part.

[7569] GAM485 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM485 target RNA, herein designated GAM TARGET RNA. GAM485 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7570] GAM485 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM485 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM485 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM485 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM485 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7571] The complementary binding of GAM485 RNA, herein designated GAM RNA, to target binding sites on GAM485 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM485 target RNA, herein designated GAM TARGET RNA, into GAM485 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7572] It is appreciated that GAM485 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM485 target genes. The mRNA of each one of this plurality of GAM485 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM485 RNA, herein designated GAM RNA, and which when bound by GAM485 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM485 target proteins.

[7573] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM485 gene, herein designated GAM GENE, on one or more GAM485 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7574] It is yet further appreciated that specific functions, and accordingly utilities, of GAM485 correlate with, and may be deduced from, the identity of the target genes which GAM485 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7575] Nucleotide sequences of the GAM485 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM485 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM485 are further described hereinbelow with reference to Table Table1.

[7576] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM485 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7577] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 486 (GAM486) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7578] GAM486 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM486 was detected is described hereinabove with reference to Figs. 2-8.

[7579] GAM486 gene, herein designated GAM GENE, and GAM486 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7580] GAM486 gene, herein designated GAM GENE, encodes a GAM486 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM486 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM486 precursor RNA is designated SEQ ID:458, and is provided hereinbelow with reference to the sequence listing part.

[7581] GAM486 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7582] An enzyme complex designated DICER COMPLEX, dices

the GAM486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM486 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM486 RNA is designated SEQ ID:2134, and is provided hereinbelow with reference to the sequence listing part.

[7583] GAM486 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM486 target RNA, herein designated GAM TARGET RNA. GAM486 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7584] GAM486 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM486 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM486

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM486 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM486 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7585] The complementary binding of GAM486 RNA, herein designated GAM RNA, to target binding sites on GAM486 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM486 target RNA, herein designated GAM TARGET RNA, into GAM486 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7586] It is appreciated that GAM486 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM486 target genes. The mRNA of each one of this plurality of GAM486 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM486 RNA, herein designated GAM RNA, and which when bound by GAM486 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM486 target proteins.

[7587] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM486 gene, herein designated GAM GENE, on one or more GAM486 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7588] It is yet further appreciated that specific functions, and accordingly utilities, of GAM486 correlate with, and may be deduced from, the identity of the target genes which GAM486 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7589] Nucleotide sequences of the GAM486 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM486 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM486 are further described hereinbelow with reference to Table Table1.

[7590] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM486 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7591] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 487 (GAM487) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7592] GAM487 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM487 was detected is described hereinabove with reference to Figs. 2-8.

[7593] GAM487 gene, herein designated GAM GENE, and GAM487 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7594] GAM487 gene, herein designated GAM GENE, encodes a GAM487 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM487 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM487 precursor RNA is designated SEQ ID:459, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:459 is located at position 1258832 relative to contig NT_008583.13, on chromosome 10.

[7595] GAM487 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7596] An enzyme complex designated DICER COMPLEX, dices the GAM487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM487 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM487 RNA is designated SEQ ID:2135, and is provided hereinbelow with reference to the sequence listing part.

[7597] GAM487 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM487 target RNA, herein designated GAM TARGET RNA.

GAM487 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7598] GAM487 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM487 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM487 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM487 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM487 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7599] The complementary binding of GAM487 RNA, herein designated GAM RNA, to target binding sites on GAM487 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM487 target RNA, herein designated GAM TARGET RNA, into GAM487 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7600] It is appreciated that GAM487 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM487 target genes. The mRNA of each one of this plurality of GAM487 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM487 RNA, herein designated GAM RNA, and which when bound by GAM487 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM487 target proteins.

[7601] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM487 gene, herein designated GAM GENE, on one or more GAM487 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7602] It is yet further appreciated that specific functions, and accordingly utilities, of GAM487 correlate with, and may be deduced from, the identity of the target genes which GAM487 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7603] Nucleotide sequences of the GAM487 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM487 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM487 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM487 are further described hereinbelow with reference to Table Table1.

[7604] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM487 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7605] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 488 (GAM488) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7606] GAM488 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM488 was detected is described hereinabove with reference to Figs. 2-8.

[7607] GAM488 gene, herein designated GAM GENE, and GAM488 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7608] GAM488 gene, herein designated GAM GENE, encodes a GAM488 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM488 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM488 precursor RNA is designated SEQ ID:460, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:460 is located at position 1890847 relative to contig NT_016714.11, on chromosome 5.

[7609] GAM488 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7610] An enzyme complex designated DICER COMPLEX, dices the GAM488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM488 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM488 RNA is designated SEQ ID:2136, and is provided hereinbelow with reference to the sequence listing part.

[7611] GAM488 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM488 target RNA, herein designated GAM TARGET RNA. GAM488 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7612] GAM488 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM488 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM488 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM488 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM488 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7613] The complementary binding of GAM488 RNA, herein designated GAM RNA, to target binding sites on GAM488 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM488 target RNA, herein designated GAM TARGET RNA, into GAM488 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7614] It is appreciated that GAM488 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM488 target genes. The mRNA of each one of this plu-

rality of GAM488 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM488 RNA, herein designated GAM RNA, and which when bound by GAM488 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM488 target proteins.

[7615] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM488 gene, herein designated GAM GENE, on one or more GAM488 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7616] It is yet further appreciated that specific functions, and accordingly utilities, of GAM488 correlate with, and may be deduced from, the identity of the target genes which GAM488 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7617] Nucleotide sequences of the GAM488 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM488 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM488 are further described hereinbelow with reference to Table Table1.

[7618] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM488 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7619] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 489 (GAM489) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[7620] GAM489 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM489 was detected is described hereinabove with reference to Figs. 2-8.

[7621] GAM489 gene, herein designated GAM GENE, and GAM489 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7622] GAM489 gene, herein designated GAM GENE, encodes a GAM489 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM489 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM489 precursor RNA is designated SEQ ID:461, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:461 is located at position 1417543 relative to contig NT_034410.2, on chromosome 1.

[7623] GAM489 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7624] An enzyme complex designated DICER COMPLEX, dices the GAM489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM489 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM489 RNA is designated SEQ ID:2137, and is provided hereinbelow with reference to the sequence listing part.

[7625] GAM489 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM489 target RNA, herein designated GAM TARGET RNA. GAM489 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7626] GAM489 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM489 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM489 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM489 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM489 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7627] The complementary binding of GAM489 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM489 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM489 target RNA, herein designated GAM TARGET RNA, into GAM489 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7628] It is appreciated that GAM489 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM489 target genes. The mRNA of each one of this plurality of GAM489 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM489 RNA, herein designated GAM RNA, and which when bound by GAM489 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM489 target proteins.

[7629] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM489 gene, herein designated GAM GENE, on one or more GAM489 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7630] It is yet further appreciated that specific functions, and accordingly utilities, of GAM489 correlate with, and may be deduced from, the identity of the target genes which GAM489 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7631] Nucleotide sequences of the GAM489 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM489 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM489 are further described hereinbelow with reference to Table Table1.

[7632] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM489 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7633] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 490 (GAM490) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7634] GAM490 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM490 was detected is described hereinabove with reference to Figs. 2-8.

[7635] GAM490 gene, herein designated GAM GENE, and GAM490 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7636] GAM490 gene, herein designated GAM GENE, encodes a GAM490 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM490 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM490 precursor RNA is designated SEQ ID:462, and is provided hereinbelow with reference to the sequence listing part.

[7637] GAM490 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7638] An enzyme complex designated DICER COMPLEX, dices the GAM490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM490 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM490 RNA is designated SEQ ID:2138, and is provided hereinbelow with reference to the sequence listing part.

[7639] GAM490 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM490 target RNA, herein designated GAM TARGET RNA. GAM490 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7640] GAM490 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM490 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM490 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM490 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM490 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7641] The complementary binding of GAM490 RNA, herein designated GAM RNA, to target binding sites on GAM490 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM490 target RNA, herein designated GAM TARGET RNA, into GAM490 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7642] It is appreciated that GAM490 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM490 target genes. The mRNA of each one of this plurality of GAM490 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM490 RNA, herein designated GAM RNA, and which when bound by GAM490 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM490 target proteins.

[7643] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM490 gene, herein designated GAM GENE, on one or more GAM490 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7644] It is yet further appreciated that specific functions, and accordingly utilities, of GAM490 correlate with, and may be deduced from, the identity of the target genes which GAM490 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7645] Nucleotide sequences of the GAM490 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM490 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM490 are further described hereinbelow with reference to Table Table1.

[7646] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM490 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7647] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 491 (GAM491) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7648] GAM491 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM491 was detected is described hereinabove with reference to Figs. 2-8.

[7649] GAM491 gene, herein designated GAM GENE, and GAM491 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7650] GAM491 gene, herein designated GAM GENE, encodes a GAM491 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM491 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM491 precursor RNA is designated SEQ ID:463, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:463 is located at position 264499 relative to contig NT_029419.8, on chromosome 12.

[7651] GAM491 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[7652] An enzyme complex designated DICER COMPLEX, dices the GAM491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM491 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM491 RNA is designated SEQ ID:2139, and is provided hereinbelow with reference to the sequence listing part.

[7653] GAM491 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM491 target RNA, herein designated GAM TARGET RNA. GAM491 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7654] GAM491 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM491 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM491 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM491 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM491 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7655] The complementary binding of GAM491 RNA, herein designated GAM RNA, to target binding sites on GAM491 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM491 target RNA, herein designated GAM TARGET RNA, into GAM491 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7656] It is appreciated that GAM491 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM491 target genes. The mRNA of each one of this plurality of GAM491 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM491 RNA, herein designated GAM RNA, and which when bound by GAM491 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM491 target proteins.

[7657] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM491 gene, herein designated GAM GENE, on one or more GAM491 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7658] It is yet further appreciated that specific functions, and accordingly utilities, of GAM491 correlate with, and may be deduced from, the identity of the target genes which GAM491 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7659] Nucleotide sequences of the GAM491 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM491 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM491 are further described hereinbelow with reference to Table Table1.

[7660] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM491 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7661] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 492 (GAM492) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7662] GAM492 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM492 was detected is described hereinabove with reference to Figs. 2-8.

[7663] GAM492 gene, herein designated GAM GENE, and GAM492 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7664] GAM492 gene, herein designated GAM GENE, encodes a GAM492 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM492 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM492 precursor RNA is designated SEQ ID:464, and is provided hereinbelow with reference to the sequence listing part.

[7665] GAM492 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7666] An enzyme complex designated DICER COMPLEX, dices the GAM492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM492 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM492 RNA is designated SEQ ID:2140, and is provided hereinbelow with reference to the sequence listing part.

[7667] GAM492 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM492 target RNA, herein designated GAM TARGET RNA.

GAM492 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7668] GAM492 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM492 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM492 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM492 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM492 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7669] The complementary binding of GAM492 RNA, herein designated GAM RNA, to target binding sites on GAM492 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM492 target RNA, herein designated GAM TARGET RNA, into GAM492 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7670] It is appreciated that GAM492 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM492 target genes. The mRNA of each one of this plurality of GAM492 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM492 RNA, herein designated GAM RNA, and which when bound by GAM492 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM492 target proteins.

[7671] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM492 gene, herein designated GAM GENE, on one or more GAM492 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7672] It is yet further appreciated that specific functions, and accordingly utilities, of GAM492 correlate with, and may be deduced from, the identity of the target genes which GAM492 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7673] Nucleotide sequences of the GAM492 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM492 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM492 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM492 are further described hereinbelow with reference to Table Table1.

[7674] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM492 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7675] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 493 (GAM493) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7676] GAM493 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM493 was detected is described hereinabove with reference to Figs. 2-8.

[7677] GAM493 gene, herein designated GAM GENE, and GAM493 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7678] GAM493 gene, herein designated GAM GENE, encodes a GAM493 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM493 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM493 precursor RNA is designated SEQ ID:465, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:465 is located at position 1417543 relative to contig NT_034410.2, on chromosome 1.

[7679] GAM493 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7680] An enzyme complex designated DICER COMPLEX, dices the GAM493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM493 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM493 RNA is designated SEQ ID:2141, and is provided hereinbelow with reference to the sequence listing part.

[7681] GAM493 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM493 target RNA, herein designated GAM TARGET RNA. GAM493 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7682] GAM493 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM493 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM493 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM493 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM493 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7683] The complementary binding of GAM493 RNA, herein designated GAM RNA, to target binding sites on GAM493 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM493 target RNA, herein designated GAM TARGET RNA, into GAM493 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7684] It is appreciated that GAM493 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM493 target genes. The mRNA of each one of this plu-

rality of GAM493 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM493 RNA, herein designated GAM RNA, and which when bound by GAM493 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM493 target proteins.

[7685] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM493 gene, herein designated GAM GENE, on one or more GAM493 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7686] It is yet further appreciated that specific functions, and accordingly utilities, of GAM493 correlate with, and may be deduced from, the identity of the target genes which GAM493 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7687] Nucleotide sequences of the GAM493 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM493 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM493 are further described hereinbelow with reference to Table Table1.

[7688] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM493 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7689] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 494 (GAM494) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[7690] GAM494 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM494 was detected is described hereinabove with reference to Figs. 2-8.

[7691] GAM494 gene, herein designated GAM GENE, and GAM494 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7692] GAM494 gene, herein designated GAM GENE, encodes a GAM494 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM494 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM494 precursor RNA is designated SEQ ID:466, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:466 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[7693] GAM494 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7694] An enzyme complex designated DICER COMPLEX, dices the GAM494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM494 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM494 RNA is designated SEQ ID:2142, and is provided hereinbelow with reference to the sequence listing part.

[7695] GAM494 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM494 target RNA, herein designated GAM TARGET RNA. GAM494 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7696] GAM494 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM494 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM494 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM494 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM494 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7697] The complementary binding of GAM494 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM494 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM494 target RNA, herein designated GAM TARGET RNA, into GAM494 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7698] It is appreciated that GAM494 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM494 target genes. The mRNA of each one of this plurality of GAM494 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM494 RNA, herein designated GAM RNA, and which when bound by GAM494 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM494 target proteins.

[7699] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM494 gene, herein designated GAM GENE, on one or more GAM494 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7700] It is yet further appreciated that specific functions, and accordingly utilities, of GAM494 correlate with, and may be deduced from, the identity of the target genes which GAM494 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7701] Nucleotide sequences of the GAM494 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM494 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM494 are further described hereinbelow with reference to Table Table1.

[7702] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM494 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7703] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 495 (GAM495) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7704] GAM495 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM495 was detected is described hereinabove with reference to Figs. 2-8.

[7705] GAM495 gene, herein designated GAM GENE, and GAM495 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7706] GAM495 gene, herein designated GAM GENE, encodes a GAM495 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM495 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM495 precursor RNA is designated SEQ ID:467, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:467 is located at position 4851364 relative to contig NT_022517.13, on chromosome 3.

[7707] GAM495 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7708] An enzyme complex designated DICER COMPLEX, dices the GAM495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM495 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM495 RNA is designated SEQ ID:2143, and is provided hereinbelow with reference to the sequence listing part.

[7709] GAM495 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM495 target RNA, herein designated GAM TARGET RNA. GAM495 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7710] GAM495 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM495 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM495 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM495 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM495 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7711] The complementary binding of GAM495 RNA, herein designated GAM RNA, to target binding sites on GAM495 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM495 target RNA, herein designated GAM TARGET RNA, into GAM495 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7712] It is appreciated that GAM495 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM495 target genes. The mRNA of each one of this plurality of GAM495 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM495 RNA,

herein designated GAM RNA, and which when bound by GAM495 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM495 target proteins.

[7713] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM495 gene, herein designated GAM GENE, on one or more GAM495 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7714] It is yet further appreciated that specific functions, and accordingly utilities, of GAM495 correlate with, and may be deduced from, the identity of the target genes which

GAM495 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7715] Nucleotide sequences of the GAM495 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM495 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM495 are further described hereinbelow with reference to Table Table1.

[7716] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM495 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7717] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 496 (GAM496) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7718] GAM496 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM496 was detected is described hereinabove with reference to Figs. 2-8.

[7719] GAM496 gene, herein designated GAM GENE, and GAM496 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7720] GAM496 gene, herein designated GAM GENE, encodes a GAM496 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM496 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM496 precursor RNA is designated SEQ ID:468, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:468 is located at position 7678826 relative to contig NT_004852.13, on chromosome 1.

[7721] GAM496 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7722] An enzyme complex designated DICER COMPLEX, dices the GAM496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM496 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM496 RNA is designated SEQ ID:2144, and is provided hereinbelow with reference to the sequence listing part.

[7723] GAM496 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM496 target RNA, herein designated GAM TARGET RNA. GAM496 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7724] GAM496 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM496 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM496 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM496 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM496 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7725] The complementary binding of GAM496 RNA, herein designated GAM RNA, to target binding sites on GAM496 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM496 target RNA, herein designated GAM TARGET RNA, into GAM496 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7726] It is appreciated that GAM496 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM496 target genes. The mRNA of each one of this plurality of GAM496 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM496 RNA, herein designated GAM RNA, and which when bound by GAM496 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM496 target proteins.

[7727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM496 gene, herein designated GAM GENE, on one or more GAM496 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7728] It is yet further appreciated that specific functions, and accordingly utilities, of GAM496 correlate with, and may be deduced from, the identity of the target genes which GAM496 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7729] Nucleotide sequences of the GAM496 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM496 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM496 are further described hereinbelow with reference to Table Table1.

[7730] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM496 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7731] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 497 (GAM497) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7732] GAM497 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM497 was detected is described hereinabove with reference to Figs. 2-8.

[7733] GAM497 gene, herein designated GAM GENE, and GAM497 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7734] GAM497 gene, herein designated GAM GENE, encodes a GAM497 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM497 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM497 precursor RNA is designated SEQ ID:469, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:469 is located at position 9611278 relative to contig NT_005375.11, on chromosome 2.

[7735] GAM497 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7736] An enzyme complex designated DICER COMPLEX, dices the GAM497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM497 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM497 RNA is designated SEQ ID:2145, and is provided

hereinbelow with reference to the sequence listing part.

[7737] GAM497 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM497 target RNA, herein designated GAM TARGET RNA.
GAM497 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7738] GAM497 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM497 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM497 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM497 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM497 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7739] The complementary binding of GAM497 RNA, herein designated GAM RNA, to target binding sites on GAM497 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM497 target RNA, herein designated GAM TARGET RNA, into GAM497 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7740] It is appreciated that GAM497 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM497 target genes. The mRNA of each one of this plurality of GAM497 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM497 RNA, herein designated GAM RNA, and which when bound by GAM497 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM497 tar-

get proteins.

[7741] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM497 gene, herein designated GAM GENE, on one or more GAM497 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7742] It is yet further appreciated that specific functions, and accordingly utilities, of GAM497 correlate with, and may be deduced from, the identity of the target genes which GAM497 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7743] Nucleotide sequences of the GAM497 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM497 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM497 are further described hereinbelow with reference to Table Table1.

[7744] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM497 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7745] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 498 (GAM498) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7746] GAM498 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM498 was detected is described hereinabove with reference to Figs. 2-8.

[7747] GAM498 gene, herein designated GAM GENE, and

GAM498 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7748] GAM498 gene, herein designated GAM GENE, encodes a GAM498 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM498 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM498 precursor RNA is designated SEQ ID:470, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:470 is located at position 8666480 relative to contig NT_026437.9, on chromosome 14.

[7749] GAM498 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7750] An enzyme complex designated DICER COMPLEX, dices the GAM498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM498 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM498 RNA is designated SEQ ID:2146, and is provided hereinbelow with reference to the sequence listing part.

[7751] GAM498 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM498 target RNA, herein designated GAM TARGET RNA. GAM498 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7752] GAM498 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM498 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM498 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM498 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM498 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7753] The complementary binding of GAM498 RNA, herein designated GAM RNA, to target binding sites on GAM498 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM498 target RNA, herein designated GAM TARGET RNA, into GAM498 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[7754] It is appreciated that GAM498 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM498 target genes. The mRNA of each one of this plurality of GAM498 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM498 RNA, herein designated GAM RNA, and which when bound by GAM498 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM498 target proteins.

[7755] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM498 gene, herein designated GAM GENE, on one or more GAM498 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7756] It is yet further appreciated that specific functions, and accordingly utilities, of GAM498 correlate with, and may be deduced from, the identity of the target genes which GAM498 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7757] Nucleotide sequences of the GAM498 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM498 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM498 are further described hereinbelow with reference to Table Table1.

[7758] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM498 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7759] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 499 (GAM499) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7760] GAM499 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM499 was detected is described hereinabove with reference to Figs. 2-8.

[7761] GAM499 gene, herein designated GAM GENE, and GAM499 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7762] GAM499 gene, herein designated GAM GENE, encodes a GAM499 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM499 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM499 precursor RNA is designated SEQ ID:471, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:471 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[7763] GAM499 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7764] An enzyme complex designated DICER COMPLEX, dices the GAM499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM499 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM499 RNA is designated SEQ ID:2147, and is provided hereinbelow with reference to the sequence listing part.

[7765] GAM499 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM499

target RNA, herein designated GAM TARGET RNA.

GAM499 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7766] GAM499 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM499 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM499 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM499 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM499 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7767] The complementary binding of GAM499 RNA, herein designated GAM RNA, to target binding sites on GAM499 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM499 target RNA, herein designated GAM TARGET RNA, into GAM499 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7768] It is appreciated that GAM499 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM499 target genes. The mRNA of each one of this plurality of GAM499 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM499 RNA, herein designated GAM RNA, and which when bound by GAM499 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM499 target proteins.

[7769] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM499 gene, herein designated GAM GENE, on one or more GAM499 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7770] It is yet further appreciated that specific functions, and accordingly utilities, of GAM499 correlate with, and may be deduced from, the identity of the target genes which GAM499 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7771] Nucleotide sequences of the GAM499 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM499 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM499 are further described hereinbelow with reference to Table Table1.

[7772] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM499 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7773] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 500 (GAM500) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7774] GAM500 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM500 was detected is described hereinabove with reference to Figs. 2-8.

[7775] GAM500 gene, herein designated GAM GENE, and GAM500 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7776] GAM500 gene, herein designated GAM GENE, encodes a

GAM500 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM500 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM500 precursor RNA is designated SEQ ID:472, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:472 is located at position 31138663 relative to contig NT_026437.9, on chromosome 14.

[7777] GAM500 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7778] An enzyme complex designated DICER COMPLEX, dices the GAM500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM500 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM500 RNA is designated SEQ ID:2148, and is provided hereinbelow with reference to the sequence listing part.

[7779] GAM500 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM500 target RNA, herein designated GAM TARGET RNA. GAM500 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7780] GAM500 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM500 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM500 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM500 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM500 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7781] The complementary binding of GAM500 RNA, herein designated GAM RNA, to target binding sites on GAM500 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM500 target RNA, herein designated GAM TARGET RNA, into GAM500 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7782] It is appreciated that GAM500 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM500 target genes. The mRNA of each one of this plurality of GAM500 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM500 RNA, herein designated GAM RNA, and which when bound by GAM500 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM500 target proteins.

[7783] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM500 gene, herein designated GAM GENE, on one or more GAM500 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[7784] It is yet further appreciated that specific functions, and accordingly utilities, of GAM500 correlate with, and may be deduced from, the identity of the target genes which GAM500 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7785] Nucleotide sequences of the GAM500 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM500 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM500 are further described hereinbelow with reference to Table Table1.

[7786] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM500 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7787] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 501 (GAM501) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[7788] GAM501 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM501 was detected is described hereinabove with reference to Figs. 2-8.

[7789] GAM501 gene, herein designated GAM GENE, and GAM501 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7790] GAM501 gene, herein designated GAM GENE, encodes a GAM501 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM501 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM501 precursor RNA is designated SEQ ID:473, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:473 is located at position 5677198 relative to contig NT_028309.8, on chromosome 11.

[7791] GAM501 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences

of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[7792] SEQ ID:99299 detected in mouse EST Accession BI688569.1.

[7793] SEQ ID:99334 detected in mouse EST Accession BF021563.1.

[7794] GAM501 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7795] An enzyme complex designated DICER COMPLEX, dices the GAM501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM501 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM501 RNA is designated SEQ ID:2149, and is provided hereinbelow with reference to the sequence listing part.

[7796] GAM501 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM501 target RNA, herein designated GAM TARGET RNA. GAM501 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7797] GAM501 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM501 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM501 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM501 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM501 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7798] The complementary binding of GAM501 RNA, herein designated GAM RNA, to target binding sites on GAM501 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM501 target RNA, herein designated GAM TARGET RNA, into GAM501 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7799] It is appreciated that GAM501 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM501 target genes. The mRNA of each one of this plurality of GAM501 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM501 RNA,

herein designated GAM RNA, and which when bound by GAM501 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM501 target proteins.

[7800] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM501 gene, herein designated GAM GENE, on one or more GAM501 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7801] It is yet further appreciated that specific functions, and accordingly utilities, of GAM501 correlate with, and may be deduced from, the identity of the target genes which

GAM501 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7802] Nucleotide sequences of the GAM501 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM501 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM501 are further described hereinbelow with reference to Table Table1.

[7803] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM501 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7804] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 502 (GAM502) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7805] GAM502 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM502 was detected is described hereinabove with reference to Figs. 2-8.

[7806] GAM502 gene, herein designated GAM GENE, and GAM502 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7807] GAM502 gene, herein designated GAM GENE, encodes a GAM502 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM502 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM502 precursor RNA is designated SEQ ID:474, and is provided hereinbelow with reference to the sequence listing part.

[7808] GAM502 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[7809] An enzyme complex designated DICER COMPLEX, dices the GAM502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM502 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM502 RNA is designated SEQ ID:2150, and is provided hereinbelow with reference to the sequence listing part.

[7810] GAM502 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM502 target RNA, herein designated GAM TARGET RNA. GAM502 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7811] GAM502 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM502 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM502 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM502 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM502 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7812] The complementary binding of GAM502 RNA, herein designated GAM RNA, to target binding sites on GAM502 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM502 target RNA, herein designated GAM TARGET RNA, into GAM502 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7813] It is appreciated that GAM502 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM502 target genes. The mRNA of each one of this plurality of GAM502 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM502 RNA, herein designated GAM RNA, and which when bound by GAM502 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM502 target proteins.

[7814] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM502 gene, herein designated GAM GENE, on one or more GAM502 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7815] It is yet further appreciated that specific functions, and accordingly utilities, of GAM502 correlate with, and may be deduced from, the identity of the target genes which GAM502 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7816] Nucleotide sequences of the GAM502 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM502 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM502 are further described hereinbelow with reference to Table Table1.

[7817] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM502 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7818] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 503 (GAM503) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7819] GAM503 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM503 was detected is described hereinabove with reference to Figs. 2-8.

[7820] GAM503 gene, herein designated GAM GENE, and GAM503 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7821] GAM503 gene, herein designated GAM GENE, encodes a GAM503 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM503 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM503 precursor RNA is designated SEQ ID:475, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:475 is located at position 21721 relative to contig

NT_011523.8, on chromosome 22.

[7822] GAM503 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[7823] SEQ ID:99210 detected in mouse EST Accession BE691213.1.

[7824] SEQ ID:99211 detected in mouse EST Accession AI551238.1.

[7825] SEQ ID:99212 detected in mouse EST Accession AI481799.1.

[7826] SEQ ID:99213 detected in mouse EST Accession BE990520.1.

[7827] GAM503 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[7828] An enzyme complex designated DICER COMPLEX, dices the GAM503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM503 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM503 RNA is designated SEQ ID:2151, and is provided hereinbelow with reference to the sequence listing part.

[7829] GAM503 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM503 target RNA, herein designated GAM TARGET RNA. GAM503 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7830] GAM503 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM503 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM503 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM503 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM503 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7831] The complementary binding of GAM503 RNA, herein designated GAM RNA, to target binding sites on GAM503 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM503 target RNA, herein designated GAM TARGET RNA, into GAM503 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7832] It is appreciated that GAM503 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM503 target genes. The mRNA of each one of this plurality of GAM503 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM503 RNA, herein designated GAM RNA, and which when bound by GAM503 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM503 target proteins.

[7833] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM503 gene, herein designated GAM GENE, on one or more GAM503 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7834] It is yet further appreciated that specific functions, and accordingly utilities, of GAM503 correlate with, and may be deduced from, the identity of the target genes which GAM503 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7835] Nucleotide sequences of the GAM503 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM503 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM503 are further described hereinbelow with reference to Table Table1.

[7836] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM503 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7837] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 504 (GAM504) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7838] GAM504 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM504 was detected is described hereinabove with reference to Figs. 2-8.

[7839] GAM504 gene, herein designated GAM GENE, and GAM504 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7840] GAM504 gene, herein designated GAM GENE, encodes a GAM504 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM504 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM504 precursor RNA is designated SEQ ID:476, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:476 is located at position 2860733 relative to con-

tig NT_023081.8, on chromosome 5.

[7841] GAM504 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7842] An enzyme complex designated DICER COMPLEX, dices the GAM504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM504 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM504 RNA is designated SEQ ID:2152, and is provided hereinbelow with reference to the sequence listing part.

[7843] GAM504 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM504 target RNA, herein designated GAM TARGET RNA.

GAM504 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7844] GAM504 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM504 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM504 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM504 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM504 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7845] The complementary binding of GAM504 RNA, herein designated GAM RNA, to target binding sites on GAM504 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM504 target RNA, herein designated GAM TARGET RNA, into GAM504 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7846] It is appreciated that GAM504 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM504 target genes. The mRNA of each one of this plurality of GAM504 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM504 RNA, herein designated GAM RNA, and which when bound by GAM504 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM504 target proteins.

[7847] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM504 gene, herein designated GAM GENE, on one or more GAM504 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7848] It is yet further appreciated that specific functions, and accordingly utilities, of GAM504 correlate with, and may be deduced from, the identity of the target genes which GAM504 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7849] Nucleotide sequences of the GAM504 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM504 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM504 are further described hereinbelow with reference to Table Table1.

[7850] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM504 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7851] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 505 (GAM505) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7852] GAM505 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM505 was detected is described hereinabove with reference to Figs. 2-8.

[7853] GAM505 gene, herein designated GAM GENE, and GAM505 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7854] GAM505 gene, herein designated GAM GENE, encodes a GAM505 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM505 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM505 precursor RNA is designated SEQ ID:477, and is provided hereinbelow with reference to the sequence listing part.

[7855] GAM505 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7856] An enzyme complex designated DICER COMPLEX, dices the GAM505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM505 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM505 RNA is designated SEQ ID:2153, and is provided hereinbelow with reference to the sequence listing part.

[7857] GAM505 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM505 target RNA, herein designated GAM TARGET RNA. GAM505 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7858] GAM505 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM505 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM505 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM505 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM505 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7859] The complementary binding of GAM505 RNA, herein designated GAM RNA, to target binding sites on GAM505 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM505 target RNA, herein designated GAM TARGET RNA, into GAM505 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7860] It is appreciated that GAM505 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM505 target genes. The mRNA of each one of this plu-

rality of GAM505 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM505 RNA, herein designated GAM RNA, and which when bound by GAM505 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM505 target proteins.

[7861] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM505 gene, herein designated GAM GENE, on one or more GAM505 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7862] It is yet further appreciated that specific functions, and accordingly utilities, of GAM505 correlate with, and may be deduced from, the identity of the target genes which GAM505 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7863] Nucleotide sequences of the GAM505 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM505 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM505 are further described hereinbelow with reference to Table Table1.

[7864] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM505 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7865] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 506 (GAM506) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[7866] GAM506 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM506 was detected is described hereinabove with reference to Figs. 2-8.

[7867] GAM506 gene, herein designated GAM GENE, and GAM506 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7868] GAM506 gene, herein designated GAM GENE, encodes a GAM506 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM506 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM506 precursor RNA is designated SEQ ID:478, and is provided hereinbelow with reference to the sequence listing part.

[7869] GAM506 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7870] An enzyme complex designated DICER COMPLEX, dices the GAM506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM506 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM506 RNA is designated SEQ ID:2154, and is provided hereinbelow with reference to the sequence listing part.

[7871] GAM506 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM506 target RNA, herein designated GAM TARGET RNA.
GAM506 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7872] GAM506 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM506 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM506 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM506 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM506 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7873] The complementary binding of GAM506 RNA, herein designated GAM RNA, to target binding sites on GAM506 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM506 target RNA, herein designated GAM TARGET RNA, into GAM506 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7874] It is appreciated that GAM506 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM506 target genes. The mRNA of each one of this plurality of GAM506 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM506 RNA, herein designated GAM RNA, and which when bound by GAM506 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM506 target proteins.

[7875] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM506 gene, herein designated GAM GENE, on one or more GAM506 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7876] It is yet further appreciated that specific functions, and accordingly utilities, of GAM506 correlate with, and may be deduced from, the identity of the target genes which GAM506 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7877] Nucleotide sequences of the GAM506 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM506 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM506 are further described hereinbelow with reference to Table Table1.

[7878] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM506 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7879] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 507 (GAM507) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7880] GAM507 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM507 was detected is described hereinabove with reference to Figs. 2-8.

[7881] GAM507 gene, herein designated GAM GENE, and GAM507 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7882] GAM507 gene, herein designated GAM GENE, encodes a GAM507 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM507 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM507 precursor RNA is desig-

nated SEQ ID:479, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:479 is located at position 24722503 relative to contig NT_026437.9, on chromosome 14.

[7883] GAM507 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7884] An enzyme complex designated DICER COMPLEX, dices the GAM507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM507 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM507 RNA is designated SEQ ID:2155, and is provided hereinbelow with reference to the sequence listing part.

[7885] GAM507 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM507 target RNA, herein designated GAM TARGET RNA. GAM507 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7886] GAM507 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM507 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM507 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM507 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM507 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7887] The complementary binding of GAM507 RNA, herein designated GAM RNA, to target binding sites on GAM507 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM507 target RNA, herein designated GAM TARGET RNA, into GAM507 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7888] It is appreciated that GAM507 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM507 target genes. The mRNA of each one of this plurality of GAM507 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM507 RNA, herein designated GAM RNA, and which when bound by GAM507 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM507 target proteins.

[7889] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM507 gene, herein designated GAM GENE, on one or more GAM507 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7890] It is yet further appreciated that specific functions, and accordingly utilities, of GAM507 correlate with, and may be deduced from, the identity of the target genes which GAM507 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7891] Nucleotide sequences of the GAM507 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM507 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM507 are further described hereinbelow with reference to Table Table1.

[7892] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM507 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7893] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 508 (GAM508) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7894] GAM508 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM508 was detected is described hereinabove with reference to Figs. 2-8.

[7895] GAM508 gene, herein designated GAM GENE, and GAM508 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7896] GAM508 gene, herein designated GAM GENE, encodes a GAM508 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM508 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM508 precursor RNA is designated SEQ ID:480, and is provided hereinbelow with reference to the sequence listing part.

[7897] GAM508 has 18 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[7898] SEQ ID:100330 detected in mouse EST Accession W70733.1.

[7899] SEQ ID:100331 detected in mouse EST Accession AI326799.1.

[7900] SEQ ID:100332 detected in mouse EST Accession AV302612.2.

[7901] SEQ ID:100333 detected in mouse EST Accession BG918878.1.

[7902] SEQ ID:100334 detected in mouse EST Accession BB364160.2.

[7903] SEQ ID:100335 detected in mouse EST Accession BB737041.1.

[7904] SEQ ID:100336 detected in mouse EST Accession BB680489.1.

[7905] SEQ ID:100337 detected in mouse EST Accession AI430109.1.

[7906] SEQ ID:100338 detected in mouse EST Accession BG069615.1.

[7907] SEQ ID:100339 detected in mouse EST Accession BE197523.1.

[7908] SEQ ID:100340 detected in mouse EST Accession BB740707.1.

[7909] SEQ ID:100341 detected in mouse EST Accession AI604799.1.

[7910] SEQ ID:100342 detected in mouse EST Accession AI604818.1.

[7911] SEQ ID:100343 detected in mouse EST Accession AV137141.1.

[7912] SEQ ID:100344 detected in mouse EST Accession

BB466785.1.

[7913] SEQ ID:100345 detected in mouse EST Accession BI686102.1.

[7914] SEQ ID:100346 detected in mouse EST Accession BI686187.1.

[7915] SEQ ID:100347 detected in mouse EST Accession BB095267.1.

[7916] GAM508 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7917] An enzyme complex designated DICER COMPLEX, dices the GAM508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM508 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM508 RNA is designated SEQ ID:2156, and is provided hereinbelow with reference to the sequence listing part.

[7918] GAM508 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM508 target RNA, herein designated GAM TARGET RNA. GAM508 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7919] GAM508 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM508 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM508 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM508 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM508 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7920] The complementary binding of GAM508 RNA, herein designated GAM RNA, to target binding sites on GAM508 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM508 target RNA, herein designated GAM TARGET RNA, into GAM508 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7921] It is appreciated that GAM508 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM508 target genes. The mRNA of each one of this plurality of GAM508 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM508 RNA, herein designated GAM RNA, and which when bound by GAM508 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM508 target proteins.

[7922] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM508 gene, herein designated GAM GENE, on one or more GAM508 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7923] It is yet further appreciated that specific functions, and accordingly utilities, of GAM508 correlate with, and may

be deduced from, the identity of the target genes which GAM508 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7924] Nucleotide sequences of the GAM508 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM508 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM508 are further described hereinbelow with reference to Table Table1.

[7925] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM508 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7926] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 509 (GAM509) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7927] GAM509 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM509 was detected is described hereinabove with reference to Figs. 2-8.

[7928] GAM509 gene, herein designated GAM GENE, and GAM509 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7929] GAM509 gene, herein designated GAM GENE, encodes a GAM509 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM509 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM509 precursor RNA is designated SEQ ID:481, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:481 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[7930] GAM509 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7931] An enzyme complex designated DICER COMPLEX, dices the GAM509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM509 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM509 RNA is designated SEQ ID:2157, and is provided hereinbelow with reference to the sequence listing part.

[7932] GAM509 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM509 target RNA, herein designated GAM TARGET RNA.
GAM509 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7933] GAM509 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM509 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM509 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM509 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM509 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7934] The complementary binding of GAM509 RNA, herein designated GAM RNA, to target binding sites on GAM509 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM509 target RNA, herein designated GAM TARGET RNA, into GAM509 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7935] It is appreciated that GAM509 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM509 target genes. The mRNA of each one of this plurality of GAM509 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM509 RNA, herein designated GAM RNA, and which when bound by GAM509 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM509 target proteins.

[7936] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM509 gene, herein designated GAM GENE, on one or more GAM509 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7937] It is yet further appreciated that specific functions, and accordingly utilities, of GAM509 correlate with, and may be deduced from, the identity of the target genes which GAM509 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7938] Nucleotide sequences of the GAM509 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM509 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM509 are further described hereinbelow with reference to Table Table1.

[7939] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM509 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7940] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 510 (GAM510) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7941] GAM510 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM510 was detected is described hereinabove with reference to Figs. 2-8.

[7942] GAM510 gene, herein designated GAM GENE, and GAM510 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7943] GAM510 gene, herein designated GAM GENE, encodes a GAM510 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM510 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM510 precursor RNA is desig-

nated SEQ ID:482, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:482 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[7944] GAM510 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7945] An enzyme complex designated DICER COMPLEX, dices the GAM510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM510 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM510 RNA is designated SEQ ID:2158, and is provided hereinbelow with reference to the sequence listing part.

[7946] GAM510 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM510 target RNA, herein designated GAM TARGET RNA. GAM510 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7947] GAM510 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM510 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM510 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM510 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM510 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7948] The complementary binding of GAM510 RNA, herein designated GAM RNA, to target binding sites on GAM510 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM510 target RNA, herein designated GAM TARGET RNA, into GAM510 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7949] It is appreciated that GAM510 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM510 target genes. The mRNA of each one of this plurality of GAM510 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM510 RNA, herein designated GAM RNA, and which when bound by GAM510 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM510 target proteins.

[7950] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM510 gene, herein designated GAM GENE, on one or more GAM510 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7951] It is yet further appreciated that specific functions, and accordingly utilities, of GAM510 correlate with, and may be deduced from, the identity of the target genes which GAM510 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7952] Nucleotide sequences of the GAM510 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM510 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM510 are further described hereinbelow with reference to Table Table1.

[7953] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM510 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7954] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 511 (GAM511) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7955] GAM511 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM511 was detected is described hereinabove with reference to Figs. 2-8.

[7956] GAM511 gene, herein designated GAM GENE, and GAM511 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7957] GAM511 gene, herein designated GAM GENE, encodes a GAM511 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM511 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM511 precursor RNA is designated SEQ ID:483, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:483 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[7958] GAM511 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[7959] An enzyme complex designated DICER COMPLEX, dices the GAM511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM511 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM511 RNA is designated SEQ ID:2159, and is provided hereinbelow with reference to the sequence listing part.

[7960] GAM511 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM511 target RNA, herein designated GAM TARGET RNA. GAM511 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7961] GAM511 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM511 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM511 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM511 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM511 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7962] The complementary binding of GAM511 RNA, herein designated GAM RNA, to target binding sites on GAM511 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM511 target RNA, herein designated GAM TARGET RNA, into GAM511 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7963] It is appreciated that GAM511 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM511 target genes. The mRNA of each one of this plurality of GAM511 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM511 RNA, herein designated GAM RNA, and which when bound by GAM511 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM511 target proteins.

[7964] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM511 gene, herein designated GAM GENE, on one or more GAM511 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7965] It is yet further appreciated that specific functions, and accordingly utilities, of GAM511 correlate with, and may be deduced from, the identity of the target genes which GAM511 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7966] Nucleotide sequences of the GAM511 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM511 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM511 are further described hereinbelow with reference to Table Table1.

[7967] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM511 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7968] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 512 (GAM512) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7969] GAM512 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM512 was detected is described hereinabove with reference to Figs. 2-8.

[7970] GAM512 gene, herein designated GAM GENE, and GAM512 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7971] GAM512 gene, herein designated GAM GENE, encodes a GAM512 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM512 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM512 precursor RNA is designated SEQ ID:484, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:484 is located at position 4887990 relative to con-

tig NT_011520.8, on chromosome 22.

[7972] GAM512 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7973] An enzyme complex designated DICER COMPLEX, dices the GAM512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM512 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM512 RNA is designated SEQ ID:2160, and is provided hereinbelow with reference to the sequence listing part.

[7974] GAM512 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM512 target RNA, herein designated GAM TARGET RNA.

GAM512 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7975] GAM512 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM512 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM512 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM512 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM512 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7976] The complementary binding of GAM512 RNA, herein designated GAM RNA, to target binding sites on GAM512 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM512 target RNA, herein designated GAM TARGET RNA, into GAM512 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7977] It is appreciated that GAM512 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM512 target genes. The mRNA of each one of this plurality of GAM512 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM512 RNA, herein designated GAM RNA, and which when bound by GAM512 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM512 target proteins.

[7978] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM512 gene, herein designated GAM GENE, on one or more GAM512 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7979] It is yet further appreciated that specific functions, and accordingly utilities, of GAM512 correlate with, and may be deduced from, the identity of the target genes which GAM512 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7980] Nucleotide sequences of the GAM512 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM512 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM512 are further described hereinbelow with reference to Table Table1.

[7981] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM512 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7982] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 513 (GAM513) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[7983] GAM513 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM513 was detected is described hereinabove with reference to Figs. 2-8.

[7984] GAM513 gene, herein designated GAM GENE, and GAM513 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7985] GAM513 gene, herein designated GAM GENE, encodes a GAM513 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM513 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM513 precursor RNA is designated SEQ ID:485, and is provided hereinbelow with reference to the sequence listing part.

[7986] GAM513 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[7987] An enzyme complex designated DICER COMPLEX, dices the GAM513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM513 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM513 RNA is designated SEQ ID:2161, and is provided hereinbelow with reference to the sequence listing part.

[7988] GAM513 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM513 target RNA, herein designated GAM TARGET RNA. GAM513 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[7989] GAM513 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM513 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM513 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM513 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM513 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[7990] The complementary binding of GAM513 RNA, herein designated GAM RNA, to target binding sites on GAM513 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM513 target RNA, herein designated GAM TARGET RNA, into GAM513 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[7991] It is appreciated that GAM513 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM513 target genes. The mRNA of each one of this plu-

rality of GAM513 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM513 RNA, herein designated GAM RNA, and which when bound by GAM513 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM513 target proteins.

[7992] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM513 gene, herein designated GAM GENE, on one or more GAM513 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[7993] It is yet further appreciated that specific functions, and accordingly utilities, of GAM513 correlate with, and may be deduced from, the identity of the target genes which GAM513 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[7994] Nucleotide sequences of the GAM513 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM513 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM513 are further described hereinbelow with reference to Table Table1.

[7995] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM513 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[7996] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 514 (GAM514) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[7997] GAM514 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM514 was detected is described hereinabove with reference to Figs. 2-8.

[7998] GAM514 gene, herein designated GAM GENE, and GAM514 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[7999] GAM514 gene, herein designated GAM GENE, encodes a GAM514 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM514 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM514 precursor RNA is designated SEQ ID:486, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:486 is located at position 1333603 relative to contig NT_016714.11, on chromosome 5.

[8000] GAM514 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8001] An enzyme complex designated DICER COMPLEX, dices the GAM514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM514 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM514 RNA is designated SEQ ID:2162, and is provided hereinbelow with reference to the sequence listing part.

[8002] GAM514 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM514 target RNA, herein designated GAM TARGET RNA. GAM514 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8003] GAM514 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM514 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM514 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM514 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM514 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8004] The complementary binding of GAM514 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM514 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM514 target RNA, herein designated GAM TARGET RNA, into GAM514 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8005] It is appreciated that GAM514 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM514 target genes. The mRNA of each one of this plurality of GAM514 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM514 RNA, herein designated GAM RNA, and which when bound by GAM514 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM514 target proteins.

[8006] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM514 gene, herein designated GAM GENE, on one or more GAM514 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8007] It is yet further appreciated that specific functions, and accordingly utilities, of GAM514 correlate with, and may be deduced from, the identity of the target genes which GAM514 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8008] Nucleotide sequences of the GAM514 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM514 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM514 are further described hereinbelow with reference to Table Table1.

[8009] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM514 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8010] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 515 (GAM515) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8011] GAM515 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM515 was detected is described hereinabove with reference to Figs. 2-8.

[8012] GAM515 gene, herein designated GAM GENE, and GAM515 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8013] GAM515 gene, herein designated GAM GENE, encodes a GAM515 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM515 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM515 precursor RNA is designated SEQ ID:487, and is provided hereinbelow with reference to the sequence listing part.

[8014] GAM515 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8015] An enzyme complex designated DICER COMPLEX, dices the GAM515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM515 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM515 RNA is designated SEQ ID:2163, and is provided hereinbelow with reference to the sequence listing part.

[8016] GAM515 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM515 target RNA, herein designated GAM TARGET RNA. GAM515 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8017] GAM515 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM515 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM515 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM515 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM515 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8018] The complementary binding of GAM515 RNA, herein designated GAM RNA, to target binding sites on GAM515 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM515 target RNA, herein designated GAM TARGET RNA, into GAM515 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8019] It is appreciated that GAM515 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM515 target genes. The mRNA of each one of this plurality of GAM515 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM515 RNA, herein designated GAM RNA, and which when bound by GAM515 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM515 target proteins.

[8020] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM515 gene, herein designated GAM GENE, on one or more GAM515 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8021] It is yet further appreciated that specific functions, and accordingly utilities, of GAM515 correlate with, and may be deduced from, the identity of the target genes which GAM515 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8022] Nucleotide sequences of the GAM515 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM515 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM515 are further described hereinbelow with reference to Table Table1.

[8023] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM515 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8024] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 516 (GAM516) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8025] GAM516 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM516 was detected is described hereinabove with reference to Figs. 2-8.

[8026] GAM516 gene, herein designated GAM GENE, and GAM516 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8027] GAM516 gene, herein designated GAM GENE, encodes a GAM516 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM516 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM516 precursor RNA is designated SEQ ID:488, and is provided hereinbelow with reference to the sequence listing part.

[8028] GAM516 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8029] An enzyme complex designated DICER COMPLEX, dices

the GAM516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM516 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM516 RNA is designated SEQ ID:2164, and is provided hereinbelow with reference to the sequence listing part.

[8030] GAM516 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM516 target RNA, herein designated GAM TARGET RNA. GAM516 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8031] GAM516 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM516 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM516

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM516 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM516 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8032] The complementary binding of GAM516 RNA, herein designated GAM RNA, to target binding sites on GAM516 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM516 target RNA, herein designated GAM TARGET RNA, into GAM516 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8033] It is appreciated that GAM516 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM516 target genes. The mRNA of each one of this plurality of GAM516 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM516 RNA, herein designated GAM RNA, and which when bound by GAM516 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM516 target proteins.

[8034] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM516 gene, herein designated GAM GENE, on one or more GAM516 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8035] It is yet further appreciated that specific functions, and accordingly utilities, of GAM516 correlate with, and may be deduced from, the identity of the target genes which GAM516 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8036] Nucleotide sequences of the GAM516 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM516 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM516 are further described hereinbelow with reference to Table Table1.

[8037] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM516 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8038] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 517 (GAM517) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8039] GAM517 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM517 was detected is described hereinabove with reference to Figs. 2-8.

[8040] GAM517 gene, herein designated GAM GENE, and GAM517 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8041] GAM517 gene, herein designated GAM GENE, encodes a GAM517 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM517 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM517 precursor RNA is designated SEQ ID:489, and is provided hereinbelow with reference to the sequence listing part.

[8042] GAM517 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8043] An enzyme complex designated DICER COMPLEX, dices the GAM517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM517 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM517 RNA is designated SEQ ID:2165, and is provided hereinbelow with reference to the sequence listing part.

[8044] GAM517 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM517 target RNA, herein designated GAM TARGET RNA. GAM517 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8045] GAM517 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM517 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM517 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM517 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM517 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8046] The complementary binding of GAM517 RNA, herein designated GAM RNA, to target binding sites on GAM517 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM517 target RNA, herein designated GAM TARGET RNA, into GAM517 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8047] It is appreciated that GAM517 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM517 target genes. The mRNA of each one of this plurality of GAM517 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM517 RNA, herein designated GAM RNA, and which when bound by GAM517 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM517 target proteins.

[8048] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM517 gene, herein designated GAM GENE, on one or more GAM517 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8049] It is yet further appreciated that specific functions, and accordingly utilities, of GAM517 correlate with, and may be deduced from, the identity of the target genes which GAM517 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8050] Nucleotide sequences of the GAM517 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM517 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM517 are further described hereinbelow with reference to Table Table1.

[8051] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM517 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8052] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 518 (GAM518) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8053] GAM518 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM518 was detected is described hereinabove with reference to Figs. 2-8.

[8054] GAM518 gene, herein designated GAM GENE, and GAM518 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8055] GAM518 gene, herein designated GAM GENE, encodes a GAM518 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM518 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM518 precursor RNA is designated SEQ ID:490, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:490 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[8056] GAM518 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8057] An enzyme complex designated DICER COMPLEX, dices the GAM518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM518 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM518 RNA is designated SEQ ID:2166, and is provided hereinbelow with reference to the sequence listing part.

[8058] GAM518 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM518 target RNA, herein designated GAM TARGET RNA. GAM518 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8059] GAM518 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM518 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM518 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM518 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM518 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8060] The complementary binding of GAM518 RNA, herein designated GAM RNA, to target binding sites on GAM518 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM518 target RNA, herein designated GAM TARGET RNA, into GAM518 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8061] It is appreciated that GAM518 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM518 target genes. The mRNA of each one of this plurality of GAM518 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM518 RNA, herein designated GAM RNA, and which when bound by GAM518 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM518 target proteins.

[8062] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM518 gene, herein designated GAM GENE, on one or more GAM518 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8063] It is yet further appreciated that specific functions, and accordingly utilities, of GAM518 correlate with, and may

be deduced from, the identity of the target genes which GAM518 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8064] Nucleotide sequences of the GAM518 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM518 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM518 are further described hereinbelow with reference to Table Table1.

[8065] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM518 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8066] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 519 (GAM519) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8067] GAM519 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM519 was detected is described hereinabove with reference to Figs. 2-8.

[8068] GAM519 gene, herein designated GAM GENE, and GAM519 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8069] GAM519 gene, herein designated GAM GENE, encodes a GAM519 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM519 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM519 precursor RNA is designated SEQ ID:491, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:491 is located at position 1552136 relative to contig NT_010783.11, on chromosome 17.

[8070] GAM519 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8071] An enzyme complex designated DICER COMPLEX, dices the GAM519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM519 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM519 RNA is designated SEQ ID:2167, and is provided hereinbelow with reference to the sequence listing part.

[8072] GAM519 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM519 target RNA, herein designated GAM TARGET RNA. GAM519 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8073] GAM519 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM519 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM519 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM519 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM519 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8074] The complementary binding of GAM519 RNA, herein designated GAM RNA, to target binding sites on GAM519 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM519 target RNA, herein designated GAM TARGET RNA, into GAM519 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8075] It is appreciated that GAM519 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM519 target genes. The mRNA of each one of this plurality of GAM519 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM519 RNA, herein designated GAM RNA, and which when bound by GAM519 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM519 target proteins.

[8076] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM519 gene, herein designated GAM GENE, on one or more GAM519 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8077] It is yet further appreciated that specific functions, and accordingly utilities, of GAM519 correlate with, and may be deduced from, the identity of the target genes which GAM519 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8078] Nucleotide sequences of the GAM519 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM519 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM519 are further described hereinbelow with reference to Table Table1.

[8079] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM519 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8080] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 520 (GAM520) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8081] GAM520 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM520 was detected is described hereinabove with reference to Figs. 2-8.

[8082] GAM520 gene, herein designated GAM GENE, and GAM520 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8083] GAM520 gene, herein designated GAM GENE, encodes a GAM520 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM520 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM520 precursor RNA is desig-

nated SEQ ID:492, and is provided hereinbelow with reference to the sequence listing part.

[8084] GAM520 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8085] An enzyme complex designated DICER COMPLEX, dices the GAM520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM520 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM520 RNA is designated SEQ ID:2168, and is provided hereinbelow with reference to the sequence listing part.

[8086] GAM520 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM520 target RNA, herein designated GAM TARGET RNA. GAM520 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8087] GAM520 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM520 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM520 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM520 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM520

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8088] The complementary binding of GAM520 RNA, herein designated GAM RNA, to target binding sites on GAM520 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM520 target RNA, herein designated GAM TARGET RNA, into GAM520 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8089] It is appreciated that GAM520 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM520 target genes. The mRNA of each one of this plurality of GAM520 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM520 RNA, herein designated GAM RNA, and which when bound by GAM520 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM520 target proteins.

[8090] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM520 gene, herein designated GAM GENE, on one or more GAM520 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8091] It is yet further appreciated that specific functions, and accordingly utilities, of GAM520 correlate with, and may be deduced from, the identity of the target genes which GAM520 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8092] Nucleotide sequences of the GAM520 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM520 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM520 are further described hereinbelow with reference to Table Table1.

[8093] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM520 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8094] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 521 (GAM521) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8095] GAM521 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM521 was detected is described hereinabove with reference to Figs. 2-8.

[8096] GAM521 gene, herein designated GAM GENE, and GAM521 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[8097] GAM521 gene, herein designated GAM GENE, encodes a GAM521 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM521 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM521 precursor RNA is designated SEQ ID:493, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:493 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[8098] GAM521 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8099] An enzyme complex designated DICER COMPLEX, dices

the GAM521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM521 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM521 RNA is designated SEQ ID:2169, and is provided hereinbelow with reference to the sequence listing part.

[8100] GAM521 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM521 target RNA, herein designated GAM TARGET RNA. GAM521 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8101] GAM521 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM521 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM521

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM521 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM521 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8102] The complementary binding of GAM521 RNA, herein designated GAM RNA, to target binding sites on GAM521 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM521 target RNA, herein designated GAM TARGET RNA, into GAM521 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8103] It is appreciated that GAM521 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM521 target genes. The mRNA of each one of this plurality of GAM521 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM521 RNA, herein designated GAM RNA, and which when bound by GAM521 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM521 target proteins.

[8104] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM521 gene, herein designated GAM GENE, on one or more GAM521 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8105] It is yet further appreciated that specific functions, and accordingly utilities, of GAM521 correlate with, and may be deduced from, the identity of the target genes which GAM521 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8106] Nucleotide sequences of the GAM521 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM521 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM521 are further described hereinbelow with reference to Table Table1.

[8107] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM521 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8108] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 522 (GAM522) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8109] GAM522 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM522 was detected is described hereinabove with reference to Figs. 2-8.

[8110] GAM522 gene, herein designated GAM GENE, and GAM522 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8111] GAM522 gene, herein designated GAM GENE, encodes a GAM522 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM522 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM522 precursor RNA is designated SEQ ID:494, and is provided hereinbelow with reference to the sequence listing part.

[8112] GAM522 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8113] An enzyme complex designated DICER COMPLEX, dices the GAM522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM522 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM522 RNA is designated SEQ ID:2170, and is provided hereinbelow with reference to the sequence listing part.

[8114] GAM522 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM522 target RNA, herein designated GAM TARGET RNA. GAM522 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8115] GAM522 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM522 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM522 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM522 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM522 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8116] The complementary binding of GAM522 RNA, herein designated GAM RNA, to target binding sites on GAM522 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM522 target RNA, herein designated GAM TARGET RNA, into GAM522 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8117] It is appreciated that GAM522 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM522 target genes. The mRNA of each one of this plurality of GAM522 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM522 RNA, herein designated GAM RNA, and which when bound by GAM522 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM522 target proteins.

[8118] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM522 gene, herein designated GAM GENE, on one or more GAM522 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8119] It is yet further appreciated that specific functions, and accordingly utilities, of GAM522 correlate with, and may be deduced from, the identity of the target genes which GAM522 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8120] Nucleotide sequences of the GAM522 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM522 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM522 are further described hereinbelow with reference to Table Table1.

[8121] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM522 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8122] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 523 (GAM523) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8123] GAM523 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM523 was detected is described hereinabove with reference to Figs. 2-8.

[8124] GAM523 gene, herein designated GAM GENE, and GAM523 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8125] GAM523 gene, herein designated GAM GENE, encodes a GAM523 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM523 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM523 precursor RNA is designated SEQ ID:495, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:495 is located at position 4851355 relative to contig NT_022517.13, on chromosome 3.

[8126] GAM523 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8127] An enzyme complex designated DICER COMPLEX, dices the GAM523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM523 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM523 RNA is designated SEQ ID:2171, and is provided hereinbelow with reference to the sequence listing part.

[8128] GAM523 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM523 target RNA, herein designated GAM TARGET RNA. GAM523 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8129] GAM523 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM523 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM523 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM523 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM523 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8130] The complementary binding of GAM523 RNA, herein designated GAM RNA, to target binding sites on GAM523 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM523 target RNA, herein designated GAM TARGET RNA, into GAM523 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8131] It is appreciated that GAM523 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM523 target genes. The mRNA of each one of this plurality of GAM523 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM523 RNA, herein designated GAM RNA, and which when bound by GAM523 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM523 target proteins.

[8132] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM523 gene, herein designated GAM GENE, on one or more GAM523 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8133] It is yet further appreciated that specific functions, and accordingly utilities, of GAM523 correlate with, and may

be deduced from, the identity of the target genes which GAM523 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8134] Nucleotide sequences of the GAM523 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM523 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM523 are further described hereinbelow with reference to Table Table1.

[8135] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM523 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8136] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 524 (GAM524) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8137] GAM524 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM524 was detected is described hereinabove with reference to Figs. 2-8.

[8138] GAM524 gene, herein designated GAM GENE, and GAM524 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8139] GAM524 gene, herein designated GAM GENE, encodes a GAM524 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM524 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM524 precursor RNA is designated SEQ ID:496, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:496 is located at position 4279505 relative to contig NT_017568.11, on chromosome 9.

[8140] GAM524 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8141] An enzyme complex designated DICER COMPLEX, dices the GAM524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM524 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM524 RNA is designated SEQ ID:2172, and is provided hereinbelow with reference to the sequence listing part.

[8142] GAM524 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM524 target RNA, herein designated GAM TARGET RNA. GAM524 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8143] GAM524 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM524 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM524 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM524 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM524 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8144] The complementary binding of GAM524 RNA, herein designated GAM RNA, to target binding sites on GAM524 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM524 target RNA, herein designated GAM TARGET RNA, into GAM524 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8145] It is appreciated that GAM524 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM524 target genes. The mRNA of each one of this plurality of GAM524 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM524 RNA, herein designated GAM RNA, and which when bound by GAM524 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM524 target proteins.

[8146] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM524 gene, herein designated GAM GENE, on one or more GAM524 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8147] It is yet further appreciated that specific functions, and accordingly utilities, of GAM524 correlate with, and may be deduced from, the identity of the target genes which GAM524 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8148] Nucleotide sequences of the GAM524 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM524 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM524 are further described hereinbelow with reference to Table Table1.

[8149] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM524 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8150] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 525 (GAM525) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8151] GAM525 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM525 was detected is described hereinabove with reference to Figs. 2-8.

[8152] GAM525 gene, herein designated GAM GENE, and GAM525 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8153] GAM525 gene, herein designated GAM GENE, encodes a GAM525 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM525 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM525 precursor RNA is desig-

nated SEQ ID:497, and is provided hereinbelow with reference to the sequence listing part.

[8154] GAM525 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8155] An enzyme complex designated DICER COMPLEX, dices the GAM525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM525 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM525 RNA is designated SEQ ID:2173, and is provided hereinbelow with reference to the sequence listing part.

[8156] GAM525 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM525 target RNA, herein designated GAM TARGET RNA. GAM525 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8157] GAM525 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM525 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM525 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM525 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM525

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8158] The complementary binding of GAM525 RNA, herein designated GAM RNA, to target binding sites on GAM525 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM525 target RNA, herein designated GAM TARGET RNA, into GAM525 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8159] It is appreciated that GAM525 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM525 target genes. The mRNA of each one of this plurality of GAM525 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM525 RNA, herein designated GAM RNA, and which when bound by GAM525 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM525 target proteins.

[8160] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM525 gene, herein designated GAM GENE, on one or more GAM525 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8161] It is yet further appreciated that specific functions, and accordingly utilities, of GAM525 correlate with, and may be deduced from, the identity of the target genes which GAM525 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8162] Nucleotide sequences of the GAM525 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM525 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM525 are further described hereinbelow with reference to Table Table1.

[8163] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM525 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8164] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 526 (GAM526) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8165] GAM526 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM526 was detected is described hereinabove with reference to Figs. 2-8.

[8166] GAM526 gene, herein designated GAM GENE, and GAM526 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[8167] GAM526 gene, herein designated GAM GENE, encodes a GAM526 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM526 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM526 precursor RNA is designated SEQ ID:498, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:498 is located at position 19447472 relative to contig NT_007933.10, on chromosome 7.

[8168] GAM526 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8169] An enzyme complex designated DICER COMPLEX, dices

the GAM526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM526 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM526 RNA is designated SEQ ID:2174, and is provided hereinbelow with reference to the sequence listing part.

[8170] GAM526 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM526 target RNA, herein designated GAM TARGET RNA. GAM526 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8171] GAM526 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM526 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM526

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM526 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM526 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8172] The complementary binding of GAM526 RNA, herein designated GAM RNA, to target binding sites on GAM526 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM526 target RNA, herein designated GAM TARGET RNA, into GAM526 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8173] It is appreciated that GAM526 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM526 target genes. The mRNA of each one of this plurality of GAM526 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM526 RNA, herein designated GAM RNA, and which when bound by GAM526 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM526 target proteins.

[8174] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM526 gene, herein designated GAM GENE, on one or more GAM526 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8175] It is yet further appreciated that specific functions, and accordingly utilities, of GAM526 correlate with, and may be deduced from, the identity of the target genes which GAM526 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8176] Nucleotide sequences of the GAM526 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM526 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM526 are further described hereinbelow with reference to Table Table1.

[8177] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM526 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8178] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 527 (GAM527) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8179] GAM527 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM527 was detected is described hereinabove with reference to Figs. 2-8.

[8180] GAM527 gene, herein designated GAM GENE, and GAM527 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8181] GAM527 gene, herein designated GAM GENE, encodes a GAM527 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM527 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM527 precursor RNA is designated SEQ ID:499, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:499 is located at position 631083 relative to contig NT_026397.11, on chromosome 12.

[8182] GAM527 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8183] An enzyme complex designated DICER COMPLEX, dices the GAM527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM527 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM527 RNA is designated SEQ ID:2175, and is provided hereinbelow with reference to the sequence listing part.

[8184] GAM527 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM527 target RNA, herein designated GAM TARGET RNA. GAM527 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[8185] GAM527 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM527 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM527 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM527 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM527 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8186] The complementary binding of GAM527 RNA, herein designated GAM RNA, to target binding sites on GAM527 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM527 target RNA, herein designated GAM TARGET RNA, into GAM527 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8187] It is appreciated that GAM527 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM527 target genes. The mRNA of each one of this plurality of GAM527 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM527 RNA, herein designated GAM RNA, and which when bound by GAM527 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM527 target proteins.

[8188] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM527 gene, herein designated GAM GENE, on one or more GAM527 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8189] It is yet further appreciated that specific functions, and accordingly utilities, of GAM527 correlate with, and may be deduced from, the identity of the target genes which GAM527 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8190] Nucleotide sequences of the GAM527 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM527 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM527 are further described hereinbelow with reference to Table Table1.

[8191] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM527 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8192] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 528 (GAM528) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8193] GAM528 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM528 was detected is described hereinabove with reference to Figs. 2-8.

[8194] GAM528 gene, herein designated GAM GENE, and GAM528 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8195] GAM528 gene, herein designated GAM GENE, encodes a GAM528 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM528 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM528 precursor RNA is designated SEQ ID:500, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:500 is located at position 1421005 relative to contig NT_005927.13, on chromosome 3.

[8196] GAM528 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8197] An enzyme complex designated DICER COMPLEX, dices the GAM528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM528 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM528 RNA is designated SEQ ID:2176, and is provided hereinbelow with reference to the sequence listing part.

[8198] GAM528 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM528 target RNA, herein designated GAM TARGET RNA. GAM528 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8199] GAM528 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM528 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM528 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM528 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM528 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8200] The complementary binding of GAM528 RNA, herein designated GAM RNA, to target binding sites on GAM528 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM528 target RNA, herein designated GAM TARGET RNA, into GAM528 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8201] It is appreciated that GAM528 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM528 target genes. The mRNA of each one of this plurality of GAM528 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM528 RNA, herein designated GAM RNA, and which when bound by

GAM528 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM528 target proteins.

[8202] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM528 gene, herein designated GAM GENE, on one or more GAM528 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8203] It is yet further appreciated that specific functions, and accordingly utilities, of GAM528 correlate with, and may be deduced from, the identity of the target genes which GAM528 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[8204] Nucleotide sequences of the GAM528 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM528 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM528 are further described hereinbelow with reference to Table Table1.

[8205] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM528 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8206] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 529 (GAM529) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8207] GAM529 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM529 was detected is described hereinabove

with reference to Figs. 2-8.

[8208] GAM529 gene, herein designated GAM GENE, and GAM529 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8209] GAM529 gene, herein designated GAM GENE, encodes a GAM529 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM529 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM529 precursor RNA is designated SEQ ID:501, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:501 is located at position 1274566 relative to contig NT_010552.11, on chromosome 16.

[8210] GAM529 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[8211] An enzyme complex designated DICER COMPLEX, dices the GAM529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM529 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM529 RNA is designated SEQ ID:2177, and is provided hereinbelow with reference to the sequence listing part.

[8212] GAM529 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM529 target RNA, herein designated GAM TARGET RNA.
GAM529 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8213] GAM529 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM529 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM529 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM529 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM529 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8214] The complementary binding of GAM529 RNA, herein designated GAM RNA, to target binding sites on GAM529 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM529 target RNA, herein desig-

nated GAM TARGET RNA, into GAM529 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8215] It is appreciated that GAM529 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM529 target genes. The mRNA of each one of this plurality of GAM529 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM529 RNA, herein designated GAM RNA, and which when bound by GAM529 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM529 target proteins.

[8216] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM529 gene, herein designated GAM GENE, on one or more GAM529 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8217] It is yet further appreciated that specific functions, and accordingly utilities, of GAM529 correlate with, and may be deduced from, the identity of the target genes which GAM529 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8218] Nucleotide sequences of the GAM529 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM529 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM529 are further described hereinbelow with reference to Table Table1.

[8219] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM529 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[8220] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 530 (GAM530) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8221] GAM530 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM530 was detected is described hereinabove with reference to Figs. 2-8.

[8222] GAM530 gene, herein designated GAM GENE, and GAM530 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8223] GAM530 gene, herein designated GAM GENE, encodes a GAM530 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM530 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM530 precursor RNA is designated SEQ ID:502, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:502 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[8224] GAM530 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8225] An enzyme complex designated DICER COMPLEX, dices the GAM530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM530 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM530 RNA is designated SEQ ID:2178, and is provided hereinbelow with reference to the sequence listing part.

[8226] GAM530 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM530 target RNA, herein designated GAM TARGET RNA. GAM530 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8227] GAM530 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM530 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM530 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM530 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM530

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8228] The complementary binding of GAM530 RNA, herein designated GAM RNA, to target binding sites on GAM530 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM530 target RNA, herein designated GAM TARGET RNA, into GAM530 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8229] It is appreciated that GAM530 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM530 target genes. The mRNA of each one of this plurality of GAM530 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM530 RNA, herein designated GAM RNA, and which when bound by GAM530 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM530 target proteins.

[8230] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM530 gene, herein designated GAM GENE, on one or more GAM530 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8231] It is yet further appreciated that specific functions, and accordingly utilities, of GAM530 correlate with, and may be deduced from, the identity of the target genes which GAM530 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8232] Nucleotide sequences of the GAM530 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM530 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM530 are further described hereinbelow with reference to Table Table1.

[8233] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM530 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8234] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 531 (GAM531) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8235] GAM531 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM531 was detected is described hereinabove with reference to Figs. 2-8.

[8236] GAM531 gene, herein designated GAM GENE, and GAM531 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[8237] GAM531 gene, herein designated GAM GENE, encodes a GAM531 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM531 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM531 precursor RNA is designated SEQ ID:503, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:503 is located at position 4851356 relative to contig NT_022517.13, on chromosome 3.

[8238] GAM531 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8239] An enzyme complex designated DICER COMPLEX, dices

the GAM531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM531 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM531 RNA is designated SEQ ID:2179, and is provided hereinbelow with reference to the sequence listing part.

[8240] GAM531 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM531 target RNA, herein designated GAM TARGET RNA. GAM531 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8241] GAM531 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM531 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM531

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM531 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM531 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8242] The complementary binding of GAM531 RNA, herein designated GAM RNA, to target binding sites on GAM531 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM531 target RNA, herein designated GAM TARGET RNA, into GAM531 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8243] It is appreciated that GAM531 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM531 target genes. The mRNA of each one of this plurality of GAM531 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM531 RNA, herein designated GAM RNA, and which when bound by GAM531 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM531 target proteins.

[8244] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM531 gene, herein designated GAM GENE, on one or more GAM531 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8245] It is yet further appreciated that specific functions, and accordingly utilities, of GAM531 correlate with, and may be deduced from, the identity of the target genes which GAM531 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8246] Nucleotide sequences of the GAM531 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM531 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM531 are further described hereinbelow with reference to Table Table1.

[8247] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM531 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8248] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 532 (GAM532) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8249] GAM532 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM532 was detected is described hereinabove with reference to Figs. 2-8.

[8250] GAM532 gene, herein designated GAM GENE, and GAM532 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8251] GAM532 gene, herein designated GAM GENE, encodes a GAM532 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM532 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM532 precursor RNA is designated SEQ ID:504, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:504 is located at position 2401990 relative to contig NT_034563.2, on chromosome 3.

[8252] GAM532 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8253] An enzyme complex designated DICER COMPLEX, dices the GAM532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM532 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM532 RNA is designated SEQ ID:2180, and is provided hereinbelow with reference to the sequence listing part.

[8254] GAM532 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM532 target RNA, herein designated GAM TARGET RNA.

GAM532 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8255] GAM532 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM532 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM532 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM532 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM532 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8256] The complementary binding of GAM532 RNA, herein designated GAM RNA, to target binding sites on GAM532 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM532 target RNA, herein designated GAM TARGET RNA, into GAM532 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8257] It is appreciated that GAM532 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM532 target genes. The mRNA of each one of this plurality of GAM532 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM532 RNA, herein designated GAM RNA, and which when bound by GAM532 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM532 target proteins.

[8258] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM532 gene, herein designated GAM GENE, on one or more GAM532 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8259] It is yet further appreciated that specific functions, and accordingly utilities, of GAM532 correlate with, and may be deduced from, the identity of the target genes which GAM532 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8260] Nucleotide sequences of the GAM532 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM532 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM532 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM532 are further described hereinbelow with reference to Table Table1.

[8261] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM532 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8262] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 533 (GAM533) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8263] GAM533 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM533 was detected is described hereinabove with reference to Figs. 2-8.

[8264] GAM533 gene, herein designated GAM GENE, and GAM533 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8265] GAM533 gene, herein designated GAM GENE, encodes a GAM533 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM533 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM533 precursor RNA is designated SEQ ID:505, and is provided hereinbelow with reference to the sequence listing part.

[8266] GAM533 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8267] An enzyme complex designated DICER COMPLEX, dices the GAM533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM533 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM533 RNA is designated SEQ ID:2181, and is provided hereinbelow with reference to the sequence listing part.

[8268] GAM533 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM533 target RNA, herein designated GAM TARGET RNA. GAM533 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8269] GAM533 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM533 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM533 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM533 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM533 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8270] The complementary binding of GAM533 RNA, herein designated GAM RNA, to target binding sites on GAM533 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM533 target RNA, herein designated GAM TARGET RNA, into GAM533 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8271] It is appreciated that GAM533 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM533 target genes. The mRNA of each one of this plurality of GAM533 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM533 RNA, herein designated GAM RNA, and which when bound by GAM533 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM533 target proteins.

[8272] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM533 gene, herein designated GAM GENE, on one or more GAM533 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8273] It is yet further appreciated that specific functions, and accordingly utilities, of GAM533 correlate with, and may

be deduced from, the identity of the target genes which GAM533 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8274] Nucleotide sequences of the GAM533 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM533 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM533 are further described hereinbelow with reference to Table Table1.

[8275] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM533 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8276] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 534 (GAM534) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8277] GAM534 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM534 was detected is described hereinabove with reference to Figs. 2-8.

[8278] GAM534 gene, herein designated GAM GENE, and GAM534 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8279] GAM534 gene, herein designated GAM GENE, encodes a GAM534 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM534 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM534 precursor RNA is designated SEQ ID:506, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:506 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[8280] GAM534 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8281] An enzyme complex designated DICER COMPLEX, dices the GAM534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM534 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM534 RNA is designated SEQ ID:2182, and is provided hereinbelow with reference to the sequence listing part.

[8282] GAM534 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM534 target RNA, herein designated GAM TARGET RNA. GAM534 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8283] GAM534 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM534 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM534 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM534 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM534 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8284] The complementary binding of GAM534 RNA, herein designated GAM RNA, to target binding sites on GAM534 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM534 target RNA, herein designated GAM TARGET RNA, into GAM534 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8285] It is appreciated that GAM534 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM534 target genes. The mRNA of each one of this plurality of GAM534 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM534 RNA, herein designated GAM RNA, and which when bound by GAM534 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM534 target proteins.

[8286] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM534 gene, herein designated GAM GENE, on one or more GAM534 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8287] It is yet further appreciated that specific functions, and accordingly utilities, of GAM534 correlate with, and may be deduced from, the identity of the target genes which GAM534 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8288] Nucleotide sequences of the GAM534 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM534 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM534 are further described hereinbelow with reference to Table Table1.

[8289] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM534 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8290] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 535 (GAM535) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8291] GAM535 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM535 was detected is described hereinabove with reference to Figs. 2-8.

[8292] GAM535 gene, herein designated GAM GENE, and GAM535 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8293] GAM535 gene, herein designated GAM GENE, encodes a GAM535 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM535 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM535 precursor RNA is desig-

nated SEQ ID:507, and is provided hereinbelow with reference to the sequence listing part.

[8294] GAM535 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8295] An enzyme complex designated DICER COMPLEX, dices the GAM535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM535 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM535 RNA is designated SEQ ID:2183, and is provided hereinbelow with reference to the sequence listing part.

[8296] GAM535 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM535 target RNA, herein designated GAM TARGET RNA. GAM535 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8297] GAM535 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM535 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM535 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM535 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM535

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8298] The complementary binding of GAM535 RNA, herein designated GAM RNA, to target binding sites on GAM535 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM535 target RNA, herein designated GAM TARGET RNA, into GAM535 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8299] It is appreciated that GAM535 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM535 target genes. The mRNA of each one of this plurality of GAM535 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM535 RNA, herein designated GAM RNA, and which when bound by GAM535 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM535 target proteins.

[8300] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM535 gene, herein designated GAM GENE, on one or more GAM535 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8301] It is yet further appreciated that specific functions, and accordingly utilities, of GAM535 correlate with, and may be deduced from, the identity of the target genes which GAM535 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8302] Nucleotide sequences of the GAM535 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM535 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM535 are further described hereinbelow with reference to Table Table1.

[8303] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM535 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8304] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 536 (GAM536) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8305] GAM536 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM536 was detected is described hereinabove with reference to Figs. 2-8.

[8306] GAM536 gene, herein designated GAM GENE, and GAM536 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[8307] GAM536 gene, herein designated GAM GENE, encodes a GAM536 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM536 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM536 precursor RNA is designated SEQ ID:508, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:508 is located at position 2907544 relative to contig NT_015805.11, on chromosome 2.

[8308] GAM536 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8309] An enzyme complex designated DICER COMPLEX, dices

the GAM536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM536 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM536 RNA is designated SEQ ID:2184, and is provided hereinbelow with reference to the sequence listing part.

[8310] GAM536 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM536 target RNA, herein designated GAM TARGET RNA. GAM536 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8311] GAM536 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM536 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM536

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM536 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM536 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8312] The complementary binding of GAM536 RNA, herein designated GAM RNA, to target binding sites on GAM536 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM536 target RNA, herein designated GAM TARGET RNA, into GAM536 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8313] It is appreciated that GAM536 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM536 target genes. The mRNA of each one of this plurality of GAM536 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM536 RNA, herein designated GAM RNA, and which when bound by GAM536 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM536 target proteins.

[8314] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM536 gene, herein designated GAM GENE, on one or more GAM536 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8315] It is yet further appreciated that specific functions, and accordingly utilities, of GAM536 correlate with, and may be deduced from, the identity of the target genes which GAM536 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8316] Nucleotide sequences of the GAM536 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM536 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM536 are further described hereinbelow with reference to Table Table1.

[8317] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM536 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8318] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 537 (GAM537) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8319] GAM537 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM537 was detected is described hereinabove with reference to Figs. 2-8.

[8320] GAM537 gene, herein designated GAM GENE, and GAM537 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8321] GAM537 gene, herein designated GAM GENE, encodes a GAM537 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM537 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM537 precursor RNA is designated SEQ ID:509, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:509 is located at position 2934173 relative to contig NT_009458.12, on chromosome 12.

[8322] GAM537 has 2 highly conserved, expressed mouse ho-

mologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[8323] SEQ ID:97984 detected in mouse EST Accession AA692083.1.

[8324] SEQ ID:97993 detected in mouse EST Accession BI202421.1.

[8325] GAM537 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8326] An enzyme complex designated DICER COMPLEX, dices the GAM537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM537 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM537 RNA is designated SEQ ID:2185, and is provided hereinbelow with reference to the sequence listing part.

[8327] GAM537 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM537 target RNA, herein designated GAM TARGET RNA. GAM537 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8328] GAM537 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM537 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM537 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM537 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM537 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8329] The complementary binding of GAM537 RNA, herein designated GAM RNA, to target binding sites on GAM537 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM537 target RNA, herein designated GAM TARGET RNA, into GAM537 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8330] It is appreciated that GAM537 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM537 target genes. The mRNA of each one of this plurality of GAM537 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM537 RNA, herein designated GAM RNA, and which when bound by GAM537 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM537 target proteins.

[8331] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM537 gene, herein designated GAM GENE, on one or more GAM537 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8332] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM537 correlate with, and may be deduced from, the identity of the target genes which GAM537 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8333] Nucleotide sequences of the GAM537 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM537 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM537 are further described hereinbelow with reference to Table Table1.

[8334] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM537 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8335] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 538 (GAM538) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8336] GAM538 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM538 was detected is described hereinabove with reference to Figs. 2-8.

[8337] GAM538 gene, herein designated GAM GENE, and GAM538 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8338] GAM538 gene, herein designated GAM GENE, encodes a GAM538 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM538 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM538 precursor RNA is designated SEQ ID:510, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:510 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[8339] GAM538 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8340] An enzyme complex designated DICER COMPLEX, dices the GAM538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM538 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM538 RNA is designated SEQ ID:2186, and is provided hereinbelow with reference to the sequence listing part.

[8341] GAM538 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM538 target RNA, herein designated GAM TARGET RNA. GAM538 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[8342] GAM538 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM538 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM538 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM538 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM538 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8343] The complementary binding of GAM538 RNA, herein designated GAM RNA, to target binding sites on GAM538 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM538 target RNA, herein designated GAM TARGET RNA, into GAM538 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8344] It is appreciated that GAM538 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM538 target genes. The mRNA of each one of this plurality of GAM538 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM538 RNA, herein designated GAM RNA, and which when bound by GAM538 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM538 target proteins.

[8345] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM538 gene, herein designated GAM GENE, on one or more GAM538 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8346] It is yet further appreciated that specific functions, and accordingly utilities, of GAM538 correlate with, and may be deduced from, the identity of the target genes which GAM538 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8347] Nucleotide sequences of the GAM538 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM538 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM538 are further described hereinbelow with reference to Table Table1.

[8348] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM538 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8349] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 539 (GAM539) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8350] GAM539 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM539 was detected is described hereinabove with reference to Figs. 2-8.

[8351] GAM539 gene, herein designated GAM GENE, and GAM539 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8352] GAM539 gene, herein designated GAM GENE, encodes a GAM539 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM539 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM539 precursor RNA is designated SEQ ID:512, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:512 is located at position 1698742 relative to contig NT_028309.8, on chromosome 11.

[8353] GAM539 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8354] An enzyme complex designated DICER COMPLEX, dices the GAM539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM539 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM539 RNA is designated SEQ ID:2188, and is provided hereinbelow with reference to the sequence listing part.

[8355] GAM539 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM539 target RNA, herein designated GAM TARGET RNA. GAM539 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8356] GAM539 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM539 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM539 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM539 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM539 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8357] The complementary binding of GAM539 RNA, herein designated GAM RNA, to target binding sites on GAM539 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM539 target RNA, herein designated GAM TARGET RNA, into GAM539 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8358] It is appreciated that GAM539 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM539 target genes. The mRNA of each one of this plurality of GAM539 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM539 RNA, herein designated GAM RNA, and which when bound by

GAM539 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM539 target proteins.

[8359] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM539 gene, herein designated GAM GENE, on one or more GAM539 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8360] It is yet further appreciated that specific functions, and accordingly utilities, of GAM539 correlate with, and may be deduced from, the identity of the target genes which GAM539 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[8361] Nucleotide sequences of the GAM539 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM539 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM539 are further described hereinbelow with reference to Table Table1.

[8362] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM539 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8363] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 540 (GAM540) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8364] GAM540 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM540 was detected is described hereinabove

with reference to Figs. 2-8.

[8365] GAM540 gene, herein designated GAM GENE, and GAM540 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8366] GAM540 gene, herein designated GAM GENE, encodes a GAM540 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM540 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM540 precursor RNA is designated SEQ ID:513, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:513 is located at position 3434864 relative to contig NT_009714.13, on chromosome 12.

[8367] GAM540 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99839, which mouse homolog is detected in mouse EST accession BG288438.1.

[8368] GAM540 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8369] An enzyme complex designated DICER COMPLEX, dices the GAM540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM540 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM540 RNA is designated SEQ ID:2189, and is provided hereinbelow with reference to the sequence listing part.

[8370] GAM540 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM540 target RNA, herein designated GAM TARGET RNA. GAM540 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8371] GAM540 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM540 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM540 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM540 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM540 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8372] The complementary binding of GAM540 RNA, herein designated GAM RNA, to target binding sites on GAM540 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM540 target RNA, herein designated GAM TARGET RNA, into GAM540 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8373] It is appreciated that GAM540 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM540 target genes. The mRNA of each one of this plurality of GAM540 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM540 RNA, herein designated GAM RNA, and which when bound by GAM540 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM540 target proteins.

[8374] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM540 gene, herein designated GAM GENE, on one or more GAM540 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8375] It is yet further appreciated that specific functions, and accordingly utilities, of GAM540 correlate with, and may be deduced from, the identity of the target genes which GAM540 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8376] Nucleotide sequences of the GAM540 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM540 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM540 are further described hereinbelow with reference to Table Table1.

[8377] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM540 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8378] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 541 (GAM541) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8379] GAM541 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM541 was detected is described hereinabove with reference to Figs. 2-8.

[8380] GAM541 gene, herein designated GAM GENE, and GAM541 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8381] GAM541 gene, herein designated GAM GENE, encodes a GAM541 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM541 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM541 precursor RNA is designated SEQ ID:514, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:514 is located at position 1469616 relative to contig NT_008251.11, on chromosome 8.

[8382] GAM541 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8383] An enzyme complex designated DICER COMPLEX, dices the GAM541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM541 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM541 RNA is designated SEQ ID:2190, and is provided hereinbelow with reference to the sequence listing part.

[8384] GAM541 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM541 target RNA, herein designated GAM TARGET RNA. GAM541 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8385] GAM541 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM541 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM541 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM541 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM541 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8386] The complementary binding of GAM541 RNA, herein designated GAM RNA, to target binding sites on GAM541 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM541 target RNA, herein designated GAM TARGET RNA, into GAM541 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8387] It is appreciated that GAM541 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM541 target genes. The mRNA of each one of this plurality of GAM541 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM541 RNA, herein designated GAM RNA, and which when bound by GAM541 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM541 target proteins.

[8388] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM541 gene, herein designated GAM GENE, on one or more GAM541 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8389] It is yet further appreciated that specific functions, and accordingly utilities, of GAM541 correlate with, and may

be deduced from, the identity of the target genes which GAM541 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8390] Nucleotide sequences of the GAM541 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM541 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM541 are further described hereinbelow with reference to Table Table1.

[8391] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM541 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8392] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 542 (GAM542) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8393] GAM542 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM542 was detected is described hereinabove with reference to Figs. 2-8.

[8394] GAM542 gene, herein designated GAM GENE, and GAM542 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8395] GAM542 gene, herein designated GAM GENE, encodes a GAM542 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM542 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM542 precursor RNA is designated SEQ ID:515, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:515 is located at position 2515950 relative to contig NT_008023.13, on chromosome 8.

[8396] GAM542 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8397] An enzyme complex designated DICER COMPLEX, dices the GAM542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM542 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM542 RNA is designated SEQ ID:2191, and is provided hereinbelow with reference to the sequence listing part.

[8398] GAM542 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM542 target RNA, herein designated GAM TARGET RNA. GAM542 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8399] GAM542 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM542 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM542 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM542 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM542 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8400] The complementary binding of GAM542 RNA, herein designated GAM RNA, to target binding sites on GAM542 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM542 target RNA, herein designated GAM TARGET RNA, into GAM542 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8401] It is appreciated that GAM542 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM542 target genes. The mRNA of each one of this plurality of GAM542 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM542 RNA, herein designated GAM RNA, and which when bound by GAM542 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM542 target proteins.

[8402] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM542 gene, herein designated GAM GENE, on one or more GAM542 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8403] It is yet further appreciated that specific functions, and accordingly utilities, of GAM542 correlate with, and may be deduced from, the identity of the target genes which GAM542 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8404] Nucleotide sequences of the GAM542 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM542 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM542 are further described hereinbelow with reference to Table Table1.

[8405] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM542 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8406] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 543 (GAM543) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8407] GAM543 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM543 was detected is described hereinabove with reference to Figs. 2-8.

[8408] GAM543 gene, herein designated GAM GENE, and GAM543 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8409] GAM543 gene, herein designated GAM GENE, encodes a GAM543 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM543 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM543 precursor RNA is desig-

nated SEQ ID:516, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:516 is located at position 1332912 relative to contig NT_005120.11, on chromosome 2.

[8410] GAM543 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8411] An enzyme complex designated DICER COMPLEX, dices the GAM543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM543 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM543 RNA is designated SEQ ID:2192, and is provided hereinbelow with reference to the sequence listing part.

[8412] GAM543 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM543 target RNA, herein designated GAM TARGET RNA. GAM543 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8413] GAM543 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM543 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM543 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM543 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM543 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8414] The complementary binding of GAM543 RNA, herein designated GAM RNA, to target binding sites on GAM543 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM543 target RNA, herein designated GAM TARGET RNA, into GAM543 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8415] It is appreciated that GAM543 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM543 target genes. The mRNA of each one of this plurality of GAM543 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM543 RNA, herein designated GAM RNA, and which when bound by GAM543 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM543 target proteins.

[8416] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM543 gene, herein designated GAM GENE, on one or more GAM543 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8417] It is yet further appreciated that specific functions, and accordingly utilities, of GAM543 correlate with, and may be deduced from, the identity of the target genes which GAM543 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8418] Nucleotide sequences of the GAM543 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM543 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM543 are further described hereinbelow with reference to Table Table1.

[8419] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM543 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8420] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 544 (GAM544) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8421] GAM544 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM544 was detected is described hereinabove with reference to Figs. 2-8.

[8422] GAM544 gene, herein designated GAM GENE, and GAM544 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8423] GAM544 gene, herein designated GAM GENE, encodes a GAM544 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM544 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM544 precursor RNA is designated SEQ ID:517, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:517 is located at position 4918962 relative to contig NT_011255.11, on chromosome 19.

[8424] GAM544 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[8425] An enzyme complex designated DICER COMPLEX, dices the GAM544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM544 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM544 RNA is designated SEQ ID:2193, and is provided hereinbelow with reference to the sequence listing part.

[8426] GAM544 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM544 target RNA, herein designated GAM TARGET RNA. GAM544 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8427] GAM544 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM544 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM544 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM544 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM544 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8428] The complementary binding of GAM544 RNA, herein designated GAM RNA, to target binding sites on GAM544 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM544 target RNA, herein designated GAM TARGET RNA, into GAM544 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8429] It is appreciated that GAM544 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM544 target genes. The mRNA of each one of this plurality of GAM544 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM544 RNA, herein designated GAM RNA, and which when bound by GAM544 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM544 target proteins.

[8430] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM544 gene, herein designated GAM GENE, on one or more GAM544 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8431] It is yet further appreciated that specific functions, and accordingly utilities, of GAM544 correlate with, and may be deduced from, the identity of the target genes which GAM544 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8432] Nucleotide sequences of the GAM544 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM544 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM544 are further described hereinbelow with reference to Table Table1.

[8433] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM544 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8434] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 545 (GAM545) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8435] GAM545 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM545 was detected is described hereinabove with reference to Figs. 2-8.

[8436] GAM545 gene, herein designated GAM GENE, and GAM545 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8437] GAM545 gene, herein designated GAM GENE, encodes a GAM545 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM545 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM545 precursor RNA is designated SEQ ID:518, and is provided hereinbelow with reference to the sequence listing part.

[8438] GAM545 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8439] An enzyme complex designated DICER COMPLEX, dices the GAM545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM545 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM545 RNA is designated SEQ ID:2194, and is provided hereinbelow with reference to the sequence listing part.

[8440] GAM545 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM545 target RNA, herein designated GAM TARGET RNA.

GAM545 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8441] GAM545 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM545 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM545 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM545 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM545 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8442] The complementary binding of GAM545 RNA, herein designated GAM RNA, to target binding sites on GAM545 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM545 target RNA, herein designated GAM TARGET RNA, into GAM545 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8443] It is appreciated that GAM545 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM545 target genes. The mRNA of each one of this plurality of GAM545 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM545 RNA, herein designated GAM RNA, and which when bound by GAM545 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM545 target proteins.

[8444] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM545 gene, herein designated GAM GENE, on one or more GAM545 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8445] It is yet further appreciated that specific functions, and accordingly utilities, of GAM545 correlate with, and may be deduced from, the identity of the target genes which GAM545 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8446] Nucleotide sequences of the GAM545 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM545 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM545 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM545 are further described hereinbelow with reference to Table Table1.

[8447] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM545 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8448] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 546 (GAM546) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8449] GAM546 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM546 was detected is described hereinabove with reference to Figs. 2-8.

[8450] GAM546 gene, herein designated GAM GENE, and GAM546 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8451] GAM546 gene, herein designated GAM GENE, encodes a GAM546 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM546 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM546 precursor RNA is designated SEQ ID:519, and is provided hereinbelow with reference to the sequence listing part.

[8452] GAM546 has 228 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[8453] SEQ ID:100449 detected in mouse EST Accession AW913459.1.

[8454] SEQ ID:100450 detected in mouse EST Accession BI648116.1.

[8455] SEQ ID:100451 detected in mouse EST Accession BF166214.1.

[8456] SEQ ID:100452 detected in mouse EST Accession BI155866.1.

[8457] SEQ ID:100453 detected in mouse EST Accession BG864659.1.

[8458] SEQ ID:100454 detected in mouse EST Accession

BI688026.1.

[8459] SEQ ID:100455 detected in mouse EST Accession BI556954.1.

[8460] SEQ ID:100456 detected in mouse EST Accession AA250314.1.

[8461] SEQ ID:100457 detected in mouse EST Accession BI526366.1.

[8462] SEQ ID:100458 detected in mouse EST Accession BG969713.1.

[8463] SEQ ID:100459 detected in mouse EST Accession BF536160.1.

[8464] SEQ ID:100460 detected in mouse EST Accession BI108596.1.

[8465] SEQ ID:100461 detected in mouse EST Accession BI554516.1.

[8466] SEQ ID:100462 detected in mouse EST Accession BI083058.1.

[8467] SEQ ID:100463 detected in mouse EST Accession BF384644.1.

[8468] SEQ ID:100464 detected in mouse EST Accession AI227285.1.

[8469] SEQ ID:100465 detected in mouse EST Accession BI696253.1.

[8470] SEQ ID:100466 detected in mouse EST Accession BE370187.1.

[8471] SEQ ID:100467 detected in mouse EST Accession AA638819.1.

[8472] SEQ ID:100468 detected in mouse EST Accession AA611289.1.

[8473] SEQ ID:100469 detected in mouse EST Accession BI248557.1.

[8474] SEQ ID:100470 detected in mouse EST Accession AA403518.1.

[8475] SEQ ID:100471 detected in mouse EST Accession AA815762.1.

[8476] SEQ ID:100472 detected in mouse EST Accession BG974012.1.

[8477] SEQ ID:100473 detected in mouse EST Accession BE306702.1.

[8478] SEQ ID:100474 detected in mouse EST Accession BI650761.1.

[8479] SEQ ID:100475 detected in mouse EST Accession BI651219.1.

[8480] SEQ ID:100476 detected in mouse EST Accession BI697622.1.

[8481] SEQ ID:100477 detected in mouse EST Accession

BI904025.1.

[8482] SEQ ID:100478 detected in mouse EST Accession BI414123.1.

[8483] SEQ ID:100479 detected in mouse EST Accession BI150262.1.

[8484] SEQ ID:100480 detected in mouse EST Accession BI079082.1.

[8485] SEQ ID:100481 detected in mouse EST Accession AU067077.1.

[8486] SEQ ID:100482 detected in mouse EST Accession BF468331.1.

[8487] SEQ ID:100483 detected in mouse EST Accession BI652832.1.

[8488] SEQ ID:100484 detected in mouse EST Accession BI455581.1.

[8489] SEQ ID:100485 detected in mouse EST Accession BE572744.1.

[8490] SEQ ID:100486 detected in mouse EST Accession BI684651.1.

[8491] SEQ ID:100487 detected in mouse EST Accession BI686779.1.

[8492] SEQ ID:100488 detected in mouse EST Accession BI649123.1.

[8493] SEQ ID:100489 detected in mouse EST Accession BI079941.1.

[8494] SEQ ID:100490 detected in mouse EST Accession BI649619.1.

[8495] SEQ ID:100491 detected in mouse EST Accession BI731285.1.

[8496] SEQ ID:100492 detected in mouse EST Accession BI149752.1.

[8497] SEQ ID:100493 detected in mouse EST Accession BI652797.1.

[8498] SEQ ID:100494 detected in mouse EST Accession BI653709.1.

[8499] SEQ ID:100495 detected in mouse EST Accession BI556674.1.

[8500] SEQ ID:100496 detected in mouse EST Accession BF533635.1.

[8501] SEQ ID:100497 detected in mouse EST Accession BG962828.1.

[8502] SEQ ID:100498 detected in mouse EST Accession BI100403.1.

[8503] SEQ ID:100499 detected in mouse EST Accession BI651872.1.

[8504] SEQ ID:100500 detected in mouse EST Accession

BG966122.1.

[8505] SEQ ID:100501 detected in mouse EST Accession BE371887.1.

[8506] SEQ ID:100502 detected in mouse EST Accession BI855552.1.

[8507] SEQ ID:100503 detected in mouse EST Accession BI687130.1.

[8508] SEQ ID:100504 detected in mouse EST Accession AU080184.1.

[8509] SEQ ID:100505 detected in mouse EST Accession BI248473.1.

[8510] SEQ ID:100506 detected in mouse EST Accession AA637374.1.

[8511] SEQ ID:100507 detected in mouse EST Accession BI648506.1.

[8512] SEQ ID:100508 detected in mouse EST Accession BI696623.1.

[8513] SEQ ID:100509 detected in mouse EST Accession BI855233.1.

[8514] SEQ ID:100510 detected in mouse EST Accession AI119644.1.

[8515] SEQ ID:100511 detected in mouse EST Accession AI226439.1.

[8516] SEQ ID:100512 detected in mouse EST Accession BE307875.1.

[8517] SEQ ID:100513 detected in mouse EST Accession AI607048.1.

[8518] SEQ ID:100514 detected in mouse EST Accession BI903751.1.

[8519] SEQ ID:100515 detected in mouse EST Accession AA869680.1.

[8520] SEQ ID:100516 detected in mouse EST Accession AI386056.1.

[8521] SEQ ID:100517 detected in mouse EST Accession BI647022.1.

[8522] SEQ ID:100518 detected in mouse EST Accession BG246688.1.

[8523] SEQ ID:100519 detected in mouse EST Accession BG242577.1.

[8524] SEQ ID:100520 detected in mouse EST Accession AI746726.1.

[8525] SEQ ID:100521 detected in mouse EST Accession BG963049.1.

[8526] SEQ ID:100522 detected in mouse EST Accession BF134640.1.

[8527] SEQ ID:100523 detected in mouse EST Accession

BI080836.1.

[8528] SEQ ID:100524 detected in mouse EST Accession BI409278.1.

[8529] SEQ ID:100525 detected in mouse EST Accession BG969184.1.

[8530] SEQ ID:100526 detected in mouse EST Accession BF161341.1.

[8531] SEQ ID:100527 detected in mouse EST Accession BF144600.1.

[8532] SEQ ID:100528 detected in mouse EST Accession BI407807.1.

[8533] SEQ ID:100529 detected in mouse EST Accession BF181669.1.

[8534] SEQ ID:100530 detected in mouse EST Accession BF138410.1.

[8535] SEQ ID:100531 detected in mouse EST Accession BF143135.1.

[8536] SEQ ID:100532 detected in mouse EST Accession BF165753.1.

[8537] SEQ ID:100533 detected in mouse EST Accession BF301595.1.

[8538] SEQ ID:100534 detected in mouse EST Accession BG342815.1.

[8539] SEQ ID:100535 detected in mouse EST Accession BI157479.1.

[8540] SEQ ID:100536 detected in mouse EST Accession BI219105.1.

[8541] SEQ ID:100537 detected in mouse EST Accession BE571962.1.

[8542] SEQ ID:100538 detected in mouse EST Accession BI414120.1.

[8543] SEQ ID:100539 detected in mouse EST Accession AI226114.1.

[8544] SEQ ID:100567 detected in mouse EST Accession BI689047.1.

[8545] SEQ ID:100568 detected in mouse EST Accession BI648693.1.

[8546] SEQ ID:100569 detected in mouse EST Accession BI556211.1.

[8547] SEQ ID:100570 detected in mouse EST Accession BI905549.1.

[8548] SEQ ID:100571 detected in mouse EST Accession BI082994.1.

[8549] SEQ ID:100572 detected in mouse EST Accession BG970065.1.

[8550] SEQ ID:100573 detected in mouse EST Accession

AI304142.1.

[8551] SEQ ID:100574 detected in mouse EST Accession BG975135.1.

[8552] SEQ ID:100575 detected in mouse EST Accession BG964088.1.

[8553] SEQ ID:100576 detected in mouse EST Accession BI646007.1.

[8554] SEQ ID:100577 detected in mouse EST Accession BI557333.1.

[8555] SEQ ID:100578 detected in mouse EST Accession BI456089.1.

[8556] SEQ ID:100579 detected in mouse EST Accession BI655689.1.

[8557] SEQ ID:100580 detected in mouse EST Accession AW044908.1.

[8558] SEQ ID:100581 detected in mouse EST Accession AI151757.1.

[8559] SEQ ID:100582 detected in mouse EST Accession BI686313.1.

[8560] SEQ ID:100583 detected in mouse EST Accession BI661402.1.

[8561] SEQ ID:100584 detected in mouse EST Accession AW107043.1.

[8562] SEQ ID:100585 detected in mouse EST Accession BI105501.1.

[8563] SEQ ID:100586 detected in mouse EST Accession BI903517.1.

[8564] SEQ ID:100587 detected in mouse EST Accession BI851754.1.

[8565] SEQ ID:100588 detected in mouse EST Accession BF181514.1.

[8566] SEQ ID:100589 detected in mouse EST Accession BF166637.1.

[8567] SEQ ID:100590 detected in mouse EST Accession BF133877.1.

[8568] SEQ ID:100591 detected in mouse EST Accession BF138201.1.

[8569] SEQ ID:100592 detected in mouse EST Accession BF162465.1.

[8570] SEQ ID:100593 detected in mouse EST Accession BF608015.1.

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[8572] SEQ ID:100595 detected in mouse EST Accession BF162705.1.

[8573] SEQ ID:100596 detected in mouse EST Accession

AI529809.1.

[8574] SEQ ID:100597 detected in mouse EST Accession BF162736.1.

[8575] SEQ ID:100598 detected in mouse EST Accession BF584299.1.

[8576] SEQ ID:100599 detected in mouse EST Accession BI416279.1.

[8577] SEQ ID:100600 detected in mouse EST Accession BF160954.1.

[8578] SEQ ID:100601 detected in mouse EST Accession BI456180.1.

[8579] SEQ ID:100602 detected in mouse EST Accession BF579586.1.

[8580] SEQ ID:100603 detected in mouse EST Accession BG243978.1.

[8581] SEQ ID:100604 detected in mouse EST Accession BF160575.1.

[8582] SEQ ID:100350 detected in mouse EST Accession AL363657.1.

[8583] SEQ ID:100351 detected in mouse EST Accession AA432821.1.

[8584] SEQ ID:100352 detected in mouse EST Accession AA511590.1.

[8585] SEQ ID:100353 detected in mouse EST Accession AA734342.1.

[8586] SEQ ID:100354 detected in mouse EST Accession AA636168.1.

[8587] SEQ ID:100355 detected in mouse EST Accession BF540407.1.

[8588] SEQ ID:100356 detected in mouse EST Accession AA268751.1.

[8589] SEQ ID:100357 detected in mouse EST Accession BG974023.1.

[8590] SEQ ID:100358 detected in mouse EST Accession BE192578.1.

[8591] SEQ ID:100359 detected in mouse EST Accession AI265080.1.

[8592] SEQ ID:100360 detected in mouse EST Accession AA412839.1.

[8593] SEQ ID:100361 detected in mouse EST Accession BE289979.1.

[8594] SEQ ID:100362 detected in mouse EST Accession AA474507.1.

[8595] SEQ ID:100363 detected in mouse EST Accession BE651810.1.

[8596] SEQ ID:100364 detected in mouse EST Accession

AA432713.1.

[8597] SEQ ID:100365 detected in mouse EST Accession AA498626.1.

[8598] SEQ ID:100366 detected in mouse EST Accession AA840078.1.

[8599] SEQ ID:100367 detected in mouse EST Accession BE288955.1.

[8600] SEQ ID:100368 detected in mouse EST Accession AA122835.1.

[8601] SEQ ID:100369 detected in mouse EST Accession BG086288.1.

[8602] SEQ ID:100370 detected in mouse EST Accession AW260598.1.

[8603] SEQ ID:100371 detected in mouse EST Accession AL022775.1.

[8604] SEQ ID:100372 detected in mouse EST Accession BE625412.1.

[8605] SEQ ID:100373 detected in mouse EST Accession BI249607.1.

[8606] SEQ ID:100374 detected in mouse EST Accession AA473842.1.

[8607] SEQ ID:100375 detected in mouse EST Accession AA589303.1.

[8608] SEQ ID:100376 detected in mouse EST Accession D77123.1.

[8609] SEQ ID:100377 detected in mouse EST Accession AW012462.1.

[8610] SEQ ID:100378 detected in mouse EST Accession BF320334.1.

[8611] SEQ ID:100379 detected in mouse EST Accession AA397159.1.

[8612] SEQ ID:100380 detected in mouse EST Accession BF150779.1.

[8613] SEQ ID:100381 detected in mouse EST Accession BE369186.1.

[8614] SEQ ID:100382 detected in mouse EST Accession AA154704.1.

[8615] SEQ ID:100383 detected in mouse EST Accession AA509423.1.

[8616] SEQ ID:100384 detected in mouse EST Accession AI529740.1.

[8617] SEQ ID:100385 detected in mouse EST Accession BE534948.1.

[8618] SEQ ID:100386 detected in mouse EST Accession AA562691.1.

[8619] SEQ ID:100387 detected in mouse EST Accession

BI987359.1.

[8620] SEQ ID:100388 detected in mouse EST Accession BI990647.1.

[8621] SEQ ID:100389 detected in mouse EST Accession BI990897.1.

[8622] SEQ ID:100390 detected in mouse EST Accession BI989999.1.

[8623] SEQ ID:100391 detected in mouse EST Accession BI987017.1.

[8624] SEQ ID:100392 detected in mouse EST Accession BI990809.1.

[8625] SEQ ID:100393 detected in mouse EST Accession BG803876.1.

[8626] SEQ ID:100394 detected in mouse EST Accession BI987029.1.

[8627] SEQ ID:100395 detected in mouse EST Accession BI988202.1.

[8628] SEQ ID:100396 detected in mouse EST Accession BI990132.1.

[8629] SEQ ID:100397 detected in mouse EST Accession BI988456.1.

[8630] SEQ ID:100398 detected in mouse EST Accession BG808381.1.

[8631] SEQ ID:100399 detected in mouse EST Accession BI985312.1.

[8632] SEQ ID:100400 detected in mouse EST Accession BI990340.1.

[8633] SEQ ID:100401 detected in mouse EST Accession BG803934.1.

[8634] SEQ ID:100402 detected in mouse EST Accession BG804147.1.

[8635] SEQ ID:100403 detected in mouse EST Accession AA571235.1.

[8636] SEQ ID:100404 detected in mouse EST Accession AI786884.1.

[8637] SEQ ID:100405 detected in mouse EST Accession AA517105.1.

[8638] SEQ ID:100406 detected in mouse EST Accession BE554088.1.

[8639] SEQ ID:100407 detected in mouse EST Accession BI651993.1.

[8640] SEQ ID:100408 detected in mouse EST Accession AA815698.1.

[8641] SEQ ID:100409 detected in mouse EST Accession BE553274.1.

[8642] SEQ ID:100410 detected in mouse EST Accession

AW322927.1.

[8643] SEQ ID:100411 detected in mouse EST Accession AA162860.1.

[8644] SEQ ID:100412 detected in mouse EST Accession AW762618.1.

[8645] SEQ ID:100413 detected in mouse EST Accession BF181745.1.

[8646] SEQ ID:100414 detected in mouse EST Accession BI077479.1.

[8647] SEQ ID:100415 detected in mouse EST Accession BE288640.1.

[8648] SEQ ID:100416 detected in mouse EST Accession AA667198.1.

[8649] SEQ ID:100417 detected in mouse EST Accession BE135699.1.

[8650] SEQ ID:100418 detected in mouse EST Accession AA638218.1.

[8651] SEQ ID:100419 detected in mouse EST Accession BG964164.1.

[8652] SEQ ID:100420 detected in mouse EST Accession BE288428.1.

[8653] SEQ ID:100421 detected in mouse EST Accession BE305613.1.

[8654] SEQ ID:100422 detected in mouse EST Accession BE369722.1.

[8655] SEQ ID:100423 detected in mouse EST Accession AW323540.1.

[8656] SEQ ID:100424 detected in mouse EST Accession BE915336.1.

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[8658] SEQ ID:100426 detected in mouse EST Accession AA655164.1.

[8659] SEQ ID:100427 detected in mouse EST Accession AA870952.1.

[8660] SEQ ID:100428 detected in mouse EST Accession BE290274.1.

[8661] SEQ ID:100429 detected in mouse EST Accession AA146026.1.

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[8663] SEQ ID:100431 detected in mouse EST Accession BI414626.1.

[8664] SEQ ID:100432 detected in mouse EST Accession BI112605.1.

[8665] SEQ ID:100433 detected in mouse EST Accession

BF785644.1.

[8666] SEQ ID:100434 detected in mouse EST Accession BI108092.1.

[8667] SEQ ID:100435 detected in mouse EST Accession AI746628.1.

[8668] SEQ ID:100436 detected in mouse EST Accession AW740738.1.

[8669] SEQ ID:100437 detected in mouse EST Accession BI647923.1.

[8670] SEQ ID:100438 detected in mouse EST Accession BI852612.1.

[8671] SEQ ID:100439 detected in mouse EST Accession AA116663.1.

[8672] SEQ ID:100440 detected in mouse EST Accession BF143771.1.

[8673] SEQ ID:100441 detected in mouse EST Accession BG294522.1.

[8674] SEQ ID:100442 detected in mouse EST Accession BI111952.1.

[8675] SEQ ID:100443 detected in mouse EST Accession BG963533.1.

[8676] SEQ ID:100444 detected in mouse EST Accession AA619432.1.

[8677] SEQ ID:100445 detected in mouse EST Accession BG976552.1.

[8678] SEQ ID:100446 detected in mouse EST Accession BG246946.1.

[8679] SEQ ID:100447 detected in mouse EST Accession AA139611.1.

[8680] SEQ ID:100448 detected in mouse EST Accession BE912204.1.

[8681] GAM546 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8682] An enzyme complex designated DICER COMPLEX, dices the GAM546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM546 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM546 RNA is designated SEQ ID:2195, and is provided hereinbelow with reference to the sequence listing part.

[8683] GAM546 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM546 target RNA, herein designated GAM TARGET RNA. GAM546 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8684] GAM546 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM546 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM546 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM546 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM546 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8685] The complementary binding of GAM546 RNA, herein designated GAM RNA, to target binding sites on GAM546 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM546 target RNA, herein designated GAM TARGET RNA, into GAM546 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8686] It is appreciated that GAM546 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM546 target genes. The mRNA of each one of this plurality of GAM546 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM546 RNA, herein designated GAM RNA, and which when bound by GAM546 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM546 target proteins.

[8687] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM546 gene, herein designated GAM GENE, on one or more GAM546 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8688] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM546 correlate with, and may be deduced from, the identity of the target genes which GAM546 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8689] Nucleotide sequences of the GAM546 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM546 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM546 are further described hereinbelow with reference to Table Table1.

[8690] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM546 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8691] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 547 (GAM547) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8692] GAM547 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM547 was detected is described hereinabove with reference to Figs. 2-8.

[8693] GAM547 gene, herein designated GAM GENE, and GAM547 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8694] GAM547 gene, herein designated GAM GENE, encodes a GAM547 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM547 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM547 precursor RNA is designated SEQ ID:520, and is provided hereinbelow with reference to the sequence listing part.

[8695] GAM547 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8696] An enzyme complex designated DICER COMPLEX, dices the GAM547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM547 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM547 RNA is designated SEQ ID:2196, and is provided hereinbelow with reference to the sequence listing part.

[8697] GAM547 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM547 target RNA, herein designated GAM TARGET RNA. GAM547 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8698] GAM547 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM547 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM547 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM547 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM547 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8699] The complementary binding of GAM547 RNA, herein designated GAM RNA, to target binding sites on GAM547 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM547 target RNA, herein designated GAM TARGET RNA, into GAM547 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8700] It is appreciated that GAM547 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM547 target genes. The mRNA of each one of this plurality of GAM547 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM547 RNA, herein designated GAM RNA, and which when bound by GAM547 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM547 target proteins.

[8701] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM547 gene, herein designated GAM GENE, on one or more GAM547 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8702] It is yet further appreciated that specific functions, and accordingly utilities, of GAM547 correlate with, and may be deduced from, the identity of the target genes which GAM547 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8703] Nucleotide sequences of the GAM547 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM547 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM547 are further described hereinbelow with reference to Table Table1.

[8704] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM547 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8705] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 548 (GAM548) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8706] GAM548 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM548 was detected is described hereinabove with reference to Figs. 2-8.

[8707] GAM548 gene, herein designated GAM GENE, and GAM548 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8708] GAM548 gene, herein designated GAM GENE, encodes a GAM548 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM548 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM548 precursor RNA is designated SEQ ID:521, and is provided hereinbelow with refer-

ence to the sequence listing part.

[8709] GAM548 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8710] An enzyme complex designated DICER COMPLEX, dices the GAM548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM548 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM548 RNA is designated SEQ ID:2197, and is provided hereinbelow with reference to the sequence listing part.

[8711] GAM548 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM548 target RNA, herein designated GAM TARGET RNA.

GAM548 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8712] GAM548 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM548 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM548 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM548 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM548 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8713] The complementary binding of GAM548 RNA, herein designated GAM RNA, to target binding sites on GAM548 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM548 target RNA, herein designated GAM TARGET RNA, into GAM548 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8714] It is appreciated that GAM548 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM548 target genes. The mRNA of each one of this plurality of GAM548 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM548 RNA, herein designated GAM RNA, and which when bound by GAM548 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM548 target proteins.

[8715] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM548 gene, herein designated GAM GENE, on one or more GAM548 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8716] It is yet further appreciated that specific functions, and accordingly utilities, of GAM548 correlate with, and may be deduced from, the identity of the target genes which GAM548 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8717] Nucleotide sequences of the GAM548 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM548 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM548 are further described hereinbelow with reference to Table Table1.

[8718] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM548 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8719] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 549 (GAM549) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8720] GAM549 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM549 was detected is described hereinabove with reference to Figs. 2-8.

[8721] GAM549 gene, herein designated GAM GENE, and GAM549 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8722] GAM549 gene, herein designated GAM GENE, encodes a GAM549 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM549 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM549 precursor RNA is designated SEQ ID:522, and is provided hereinbelow with reference to the sequence listing part.

[8723] GAM549 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8724] An enzyme complex designated DICER COMPLEX, dices the GAM549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM549 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM549 RNA is designated SEQ ID:2198, and is provided hereinbelow with reference to the sequence listing part.

[8725] GAM549 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM549 target RNA, herein designated GAM TARGET RNA. GAM549 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8726] GAM549 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM549 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM549 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM549 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM549 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8727] The complementary binding of GAM549 RNA, herein designated GAM RNA, to target binding sites on GAM549 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM549 target RNA, herein designated GAM TARGET RNA, into GAM549 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8728] It is appreciated that GAM549 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM549 target genes. The mRNA of each one of this plu-

rality of GAM549 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM549 RNA, herein designated GAM RNA, and which when bound by GAM549 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM549 target proteins.

[8729] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM549 gene, herein designated GAM GENE, on one or more GAM549 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8730] It is yet further appreciated that specific functions, and accordingly utilities, of GAM549 correlate with, and may be deduced from, the identity of the target genes which GAM549 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8731] Nucleotide sequences of the GAM549 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM549 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM549 are further described hereinbelow with reference to Table Table1.

[8732] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM549 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8733] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 550 (GAM550) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[8734] GAM550 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM550 was detected is described hereinabove with reference to Figs. 2-8.

[8735] GAM550 gene, herein designated GAM GENE, and GAM550 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8736] GAM550 gene, herein designated GAM GENE, encodes a GAM550 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM550 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM550 precursor RNA is designated SEQ ID:523, and is provided hereinbelow with reference to the sequence listing part.

[8737] GAM550 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8738] An enzyme complex designated DICER COMPLEX, dices the GAM550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM550 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM550 RNA is designated SEQ ID:2199, and is provided hereinbelow with reference to the sequence listing part.

[8739] GAM550 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM550 target RNA, herein designated GAM TARGET RNA. GAM550 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8740] GAM550 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM550 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM550 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM550 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM550 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8741] The complementary binding of GAM550 RNA, herein designated GAM RNA, to target binding sites on GAM550 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM550 target RNA, herein designated GAM TARGET RNA, into GAM550 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8742] It is appreciated that GAM550 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM550 target genes. The mRNA of each one of this plurality of GAM550 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM550 RNA, herein designated GAM RNA, and which when bound by GAM550 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM550 target proteins.

[8743] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM550 gene, herein designated GAM GENE, on one or more GAM550 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8744] It is yet further appreciated that specific functions, and accordingly utilities, of GAM550 correlate with, and may be deduced from, the identity of the target genes which GAM550 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8745] Nucleotide sequences of the GAM550 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM550 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM550 are further described hereinbelow with reference to Table Table1.

[8746] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM550 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8747] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 551 (GAM551) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8748] GAM551 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM551 was detected is described hereinabove with reference to Figs. 2-8.

[8749] GAM551 gene, herein designated GAM GENE, and GAM551 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8750] GAM551 gene, herein designated GAM GENE, encodes a GAM551 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM551 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM551 precursor RNA is desig-

nated SEQ ID:524, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:524 is located at position 7819273 relative to contig NT_023935.13, on chromosome 9.

[8751] GAM551 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8752] An enzyme complex designated DICER COMPLEX, dices the GAM551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM551 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM551 RNA is designated SEQ ID:2200, and is provided hereinbelow with reference to the sequence listing part.

[8753] GAM551 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM551 target RNA, herein designated GAM TARGET RNA. GAM551 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8754] GAM551 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM551 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM551 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM551 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM551 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8755] The complementary binding of GAM551 RNA, herein designated GAM RNA, to target binding sites on GAM551 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM551 target RNA, herein designated GAM TARGET RNA, into GAM551 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8756] It is appreciated that GAM551 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM551 target genes. The mRNA of each one of this plurality of GAM551 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM551 RNA, herein designated GAM RNA, and which when bound by GAM551 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM551 target proteins.

[8757] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM551 gene, herein designated GAM GENE, on one or more GAM551 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8758] It is yet further appreciated that specific functions, and accordingly utilities, of GAM551 correlate with, and may be deduced from, the identity of the target genes which GAM551 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8759] Nucleotide sequences of the GAM551 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM551 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM551 are further described hereinbelow with reference to Table Table1.

[8760] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM551 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8761] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 552 (GAM552) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8762] GAM552 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM552 was detected is described hereinabove with reference to Figs. 2-8.

[8763] GAM552 gene, herein designated GAM GENE, and GAM552 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8764] GAM552 gene, herein designated GAM GENE, encodes a GAM552 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM552 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM552 precursor RNA is designated SEQ ID:525, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:525 is located at position 8681475 relative to contig NT_017568.11, on chromosome 9.

[8765] GAM552 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[8766] An enzyme complex designated DICER COMPLEX, dices the GAM552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM552 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM552 RNA is designated SEQ ID:2201, and is provided hereinbelow with reference to the sequence listing part.

[8767] GAM552 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM552 target RNA, herein designated GAM TARGET RNA. GAM552 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8768] GAM552 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM552 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM552 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM552 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM552 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8769] The complementary binding of GAM552 RNA, herein designated GAM RNA, to target binding sites on GAM552 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM552 target RNA, herein designated GAM TARGET RNA, into GAM552 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8770] It is appreciated that GAM552 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM552 target genes. The mRNA of each one of this plurality of GAM552 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM552 RNA, herein designated GAM RNA, and which when bound by GAM552 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM552 target proteins.

[8771] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM552 gene, herein designated GAM GENE, on one or more GAM552 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8772] It is yet further appreciated that specific functions, and accordingly utilities, of GAM552 correlate with, and may be deduced from, the identity of the target genes which GAM552 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8773] Nucleotide sequences of the GAM552 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM552 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM552 are further described hereinbelow with reference to Table Table1.

[8774] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM552 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8775] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 553 (GAM553) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8776] GAM553 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM553 was detected is described hereinabove with reference to Figs. 2-8.

[8777] GAM553 gene, herein designated GAM GENE, and GAM553 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8778] GAM553 gene, herein designated GAM GENE, encodes a GAM553 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM553 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM553 precursor RNA is designated SEQ ID:526, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:526 is located at position 4062832 relative to con-

tig NT_035235.2, on chromosome 12.

[8779] GAM553 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8780] An enzyme complex designated DICER COMPLEX, dices the GAM553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM553 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM553 RNA is designated SEQ ID:2202, and is provided hereinbelow with reference to the sequence listing part.

[8781] GAM553 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM553 target RNA, herein designated GAM TARGET RNA.

GAM553 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8782] GAM553 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM553 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM553 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM553 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM553 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8783] The complementary binding of GAM553 RNA, herein designated GAM RNA, to target binding sites on GAM553 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM553 target RNA, herein designated GAM TARGET RNA, into GAM553 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8784] It is appreciated that GAM553 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM553 target genes. The mRNA of each one of this plurality of GAM553 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM553 RNA, herein designated GAM RNA, and which when bound by GAM553 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM553 target proteins.

[8785] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM553 gene, herein designated GAM GENE, on one or more GAM553 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8786] It is yet further appreciated that specific functions, and accordingly utilities, of GAM553 correlate with, and may be deduced from, the identity of the target genes which GAM553 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8787] Nucleotide sequences of the GAM553 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM553 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM553 are further described hereinbelow with reference to Table Table1.

[8788] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM553 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8789] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 554 (GAM554) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8790] GAM554 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM554 was detected is described hereinabove with reference to Figs. 2-8.

[8791] GAM554 gene, herein designated GAM GENE, and GAM554 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8792] GAM554 gene, herein designated GAM GENE, encodes a GAM554 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM554 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM554 precursor RNA is designated SEQ ID:527, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:527 is located at position 1698742 relative to contig NT_028309.8, on chromosome 11.

[8793] GAM554 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8794] An enzyme complex designated DICER COMPLEX, dices the GAM554 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM554 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM554 RNA is designated SEQ ID:2203, and is provided hereinbelow with reference to the sequence listing part.

[8795] GAM554 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM554 target RNA, herein designated GAM TARGET RNA. GAM554 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8796] GAM554 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM554 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM554 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM554 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM554 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8797] The complementary binding of GAM554 RNA, herein designated GAM RNA, to target binding sites on GAM554 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM554 target RNA, herein designated GAM TARGET RNA, into GAM554 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8798] It is appreciated that GAM554 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM554 target genes. The mRNA of each one of this plurality of GAM554 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM554 RNA, herein designated GAM RNA, and which when bound by GAM554 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM554 target proteins.

[8799] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM554 gene, herein designated GAM GENE, on one or more GAM554 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8800] It is yet further appreciated that specific functions, and accordingly utilities, of GAM554 correlate with, and may be deduced from, the identity of the target genes which GAM554 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8801] Nucleotide sequences of the GAM554 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM554 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM554 are further described hereinbelow with reference to Table Table1.

[8802] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM554 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8803] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

555 (GAM555) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8804] GAM555 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM555 was detected is described hereinabove with reference to Figs. 2-8.

[8805] GAM555 gene, herein designated GAM GENE, and GAM555 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8806] GAM555 gene, herein designated GAM GENE, encodes a GAM555 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM555 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM555 precursor RNA is designated SEQ ID:528, and is provided hereinbelow with reference to the sequence listing part.

[8807] GAM555 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8808] An enzyme complex designated DICER COMPLEX, dices the GAM555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM555 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM555 RNA is designated SEQ ID:2204, and is provided hereinbelow with reference to the sequence listing part.

[8809] GAM555 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM555 target RNA, herein designated GAM TARGET RNA. GAM555 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8810] GAM555 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM555 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM555 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM555 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM555 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8811] The complementary binding of GAM555 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM555 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM555 target RNA, herein designated GAM TARGET RNA, into GAM555 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8812] It is appreciated that GAM555 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM555 target genes. The mRNA of each one of this plurality of GAM555 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM555 RNA, herein designated GAM RNA, and which when bound by GAM555 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM555 target proteins.

[8813] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM555 gene, herein designated GAM GENE, on one or more GAM555 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8814] It is yet further appreciated that specific functions, and accordingly utilities, of GAM555 correlate with, and may be deduced from, the identity of the target genes which GAM555 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8815] Nucleotide sequences of the GAM555 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM555 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM555 are further described hereinbelow with reference to Table Table1.

[8816] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM555 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8817] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 556 (GAM556) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8818] GAM556 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM556 was detected is described hereinabove with reference to Figs. 2-8.

[8819] GAM556 gene, herein designated GAM GENE, and GAM556 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8820] GAM556 gene, herein designated GAM GENE, encodes a GAM556 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM556 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM556 precursor RNA is designated SEQ ID:529, and is provided hereinbelow with reference to the sequence listing part.

[8821] GAM556 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8822] An enzyme complex designated DICER COMPLEX, dices the GAM556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM556 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM556 RNA is designated SEQ ID:2205, and is provided hereinbelow with reference to the sequence listing part.

[8823] GAM556 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM556 target RNA, herein designated GAM TARGET RNA. GAM556 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8824] GAM556 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM556 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM556 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM556 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM556 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8825] The complementary binding of GAM556 RNA, herein designated GAM RNA, to target binding sites on GAM556 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM556 target RNA, herein designated GAM TARGET RNA, into GAM556 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8826] It is appreciated that GAM556 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM556 target genes. The mRNA of each one of this plurality of GAM556 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM556 RNA, herein designated GAM RNA, and which when bound by GAM556 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM556 target proteins.

[8827] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM556 gene, herein designated GAM GENE, on one or more GAM556 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8828] It is yet further appreciated that specific functions, and accordingly utilities, of GAM556 correlate with, and may be deduced from, the identity of the target genes which GAM556 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8829] Nucleotide sequences of the GAM556 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM556 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM556 are further described hereinbelow with reference to Table Table1.

[8830] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM556 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8831] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 557 (GAM557) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8832] GAM557 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM557 was detected is described hereinabove with reference to Figs. 2-8.

[8833] GAM557 gene, herein designated GAM GENE, and GAM557 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8834] GAM557 gene, herein designated GAM GENE, encodes a GAM557 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM557 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM557 precursor RNA is designated SEQ ID:530, and is provided hereinbelow with reference to the sequence listing part.

[8835] GAM557 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8836] An enzyme complex designated DICER COMPLEX, dices

the GAM557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM557 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM557 RNA is designated SEQ ID:2206, and is provided hereinbelow with reference to the sequence listing part.

[8837] GAM557 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM557 target RNA, herein designated GAM TARGET RNA. GAM557 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8838] GAM557 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM557 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM557

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM557 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM557 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8839] The complementary binding of GAM557 RNA, herein designated GAM RNA, to target binding sites on GAM557 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM557 target RNA, herein designated GAM TARGET RNA, into GAM557 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8840] It is appreciated that GAM557 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM557 target genes. The mRNA of each one of this plurality of GAM557 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM557 RNA, herein designated GAM RNA, and which when bound by GAM557 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM557 target proteins.

[8841] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM557 gene, herein designated GAM GENE, on one or more GAM557 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8842] It is yet further appreciated that specific functions, and accordingly utilities, of GAM557 correlate with, and may be deduced from, the identity of the target genes which GAM557 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8843] Nucleotide sequences of the GAM557 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM557 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM557 are further described hereinbelow with reference to Table Table1.

[8844] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM557 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8845] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 558 (GAM558) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8846] GAM558 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM558 was detected is described hereinabove with reference to Figs. 2-8.

[8847] GAM558 gene, herein designated GAM GENE, and GAM558 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8848] GAM558 gene, herein designated GAM GENE, encodes a GAM558 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM558 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM558 precursor RNA is designated SEQ ID:531, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:531 is located at position 2349693 relative to contig NT_021907.13, on chromosome 1.

[8849] GAM558 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8850] An enzyme complex designated DICER COMPLEX, dices the GAM558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM558 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM558 RNA is designated SEQ ID:2207, and is provided hereinbelow with reference to the sequence listing part.

[8851] GAM558 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM558 target RNA, herein designated GAM TARGET RNA.

GAM558 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8852] GAM558 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM558 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM558 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM558 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM558 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8853] The complementary binding of GAM558 RNA, herein designated GAM RNA, to target binding sites on GAM558 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM558 target RNA, herein designated GAM TARGET RNA, into GAM558 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8854] It is appreciated that GAM558 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM558 target genes. The mRNA of each one of this plurality of GAM558 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM558 RNA, herein designated GAM RNA, and which when bound by GAM558 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM558 target proteins.

[8855] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM558 gene, herein designated GAM GENE, on one or more GAM558 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8856] It is yet further appreciated that specific functions, and accordingly utilities, of GAM558 correlate with, and may be deduced from, the identity of the target genes which GAM558 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8857] Nucleotide sequences of the GAM558 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM558 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM558 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM558 are further described hereinbelow with reference to Table Table1.

[8858] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM558 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8859] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 559 (GAM559) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8860] GAM559 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM559 was detected is described hereinabove with reference to Figs. 2-8.

[8861] GAM559 gene, herein designated GAM GENE, and GAM559 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8862] GAM559 gene, herein designated GAM GENE, encodes a GAM559 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM559 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM559 precursor RNA is designated SEQ ID:532, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:532 is located at position 4851368 relative to contig NT_022517.13, on chromosome 3.

[8863] GAM559 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8864] An enzyme complex designated DICER COMPLEX, dices the GAM559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM559 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM559 RNA is designated SEQ ID:2208, and is provided hereinbelow with reference to the sequence listing part.

[8865] GAM559 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM559 target RNA, herein designated GAM TARGET RNA. GAM559 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8866] GAM559 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM559 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM559 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM559 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM559 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8867] The complementary binding of GAM559 RNA, herein designated GAM RNA, to target binding sites on GAM559 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM559 target RNA, herein designated GAM TARGET RNA, into GAM559 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8868] It is appreciated that GAM559 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM559 target genes. The mRNA of each one of this plu-

rality of GAM559 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM559 RNA, herein designated GAM RNA, and which when bound by GAM559 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM559 target proteins.

[8869] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM559 gene, herein designated GAM GENE, on one or more GAM559 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8870] It is yet further appreciated that specific functions, and accordingly utilities, of GAM559 correlate with, and may be deduced from, the identity of the target genes which GAM559 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8871] Nucleotide sequences of the GAM559 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM559 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM559 are further described hereinbelow with reference to Table Table1.

[8872] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM559 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8873] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 560 (GAM560) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[8874] GAM560 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM560 was detected is described hereinabove with reference to Figs. 2-8.

[8875] GAM560 gene, herein designated GAM GENE, and GAM560 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8876] GAM560 gene, herein designated GAM GENE, encodes a GAM560 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM560 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM560 precursor RNA is designated SEQ ID:533, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:533 is located at position 11259454 relative to contig NT_007592.11, on chromosome 6.

[8877] GAM560 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8878] An enzyme complex designated DICER COMPLEX, dices the GAM560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM560 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM560 RNA is designated SEQ ID:2209, and is provided hereinbelow with reference to the sequence listing part.

[8879] GAM560 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM560 target RNA, herein designated GAM TARGET RNA. GAM560 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8880] GAM560 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM560 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM560 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM560 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM560 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8881] The complementary binding of GAM560 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM560 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM560 target RNA, herein designated GAM TARGET RNA, into GAM560 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8882] It is appreciated that GAM560 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM560 target genes. The mRNA of each one of this plurality of GAM560 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM560 RNA, herein designated GAM RNA, and which when bound by GAM560 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM560 target proteins.

[8883] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM560 gene, herein designated GAM GENE, on one or more GAM560 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8884] It is yet further appreciated that specific functions, and accordingly utilities, of GAM560 correlate with, and may be deduced from, the identity of the target genes which GAM560 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8885] Nucleotide sequences of the GAM560 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM560 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM560 are further described hereinbelow with reference to Table Table1.

[8886] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM560 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8887] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 561 (GAM561) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8888] GAM561 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM561 was detected is described hereinabove with reference to Figs. 2-8.

[8889] GAM561 gene, herein designated GAM GENE, and GAM561 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8890] GAM561 gene, herein designated GAM GENE, encodes a GAM561 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM561 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM561 precursor RNA is designated SEQ ID:534, and is provided hereinbelow with reference to the sequence listing part.

[8891] GAM561 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8892] An enzyme complex designated DICER COMPLEX, dices the GAM561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM561 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM561 RNA is designated SEQ ID:2210, and is provided hereinbelow with reference to the sequence listing part.

[8893] GAM561 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM561 target RNA, herein designated GAM TARGET RNA. GAM561 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8894] GAM561 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM561 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM561 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM561 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM561 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8895] The complementary binding of GAM561 RNA, herein designated GAM RNA, to target binding sites on GAM561 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM561 target RNA, herein designated GAM TARGET RNA, into GAM561 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8896] It is appreciated that GAM561 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM561 target genes. The mRNA of each one of this plurality of GAM561 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM561 RNA, herein designated GAM RNA, and which when bound by GAM561 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM561 target proteins.

[8897] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM561 gene, herein designated GAM GENE, on one or more GAM561 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8898] It is yet further appreciated that specific functions, and accordingly utilities, of GAM561 correlate with, and may be deduced from, the identity of the target genes which GAM561 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8899] Nucleotide sequences of the GAM561 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM561 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM561 are further described hereinbelow with reference to Table Table1.

[8900] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM561 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8901] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 562 (GAM562) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8902] GAM562 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM562 was detected is described hereinabove with reference to Figs. 2-8.

[8903] GAM562 gene, herein designated GAM GENE, and GAM562 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8904] GAM562 gene, herein designated GAM GENE, encodes a GAM562 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM562 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM562 precursor RNA is designated SEQ ID:535, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:535 is located at position 5766805 relative to contig NT_005204.11, on chromosome 2.

[8905] GAM562 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM562 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[8906] An enzyme complex designated DICER COMPLEX, dices the GAM562 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM562 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM562 RNA is designated SEQ ID:2211, and is provided hereinbelow with reference to the sequence listing part.

[8907] GAM562 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM562 target RNA, herein designated GAM TARGET RNA. GAM562 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8908] GAM562 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM562 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM562 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM562 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM562 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8909] The complementary binding of GAM562 RNA, herein designated GAM RNA, to target binding sites on GAM562 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM562 target RNA, herein designated GAM TARGET RNA, into GAM562 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8910] It is appreciated that GAM562 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM562 target genes. The mRNA of each one of this plurality of GAM562 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM562 RNA, herein designated GAM RNA, and which when bound by GAM562 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM562 target proteins.

[8911] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM562 gene, herein designated GAM GENE, on one or more GAM562 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8912] It is yet further appreciated that specific functions, and accordingly utilities, of GAM562 correlate with, and may be deduced from, the identity of the target genes which GAM562 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8913] Nucleotide sequences of the GAM562 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM562 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM562 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM562 are further described hereinbelow with reference to Table Table1.

[8914] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM562 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8915] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 563 (GAM563) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8916] GAM563 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM563 was detected is described hereinabove with reference to Figs. 2-8.

[8917] GAM563 gene, herein designated GAM GENE, and GAM563 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8918] GAM563 gene, herein designated GAM GENE, encodes a GAM563 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM563 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM563 precursor RNA is designated SEQ ID:536, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:536 is located at position 3533591 relative to con-

tig NT_022171.11, on chromosome 2.

[8919] GAM563 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8920] An enzyme complex designated DICER COMPLEX, dices the GAM563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM563 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM563 RNA is designated SEQ ID:2212, and is provided hereinbelow with reference to the sequence listing part.

[8921] GAM563 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM563 target RNA, herein designated GAM TARGET RNA.

GAM563 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8922] GAM563 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM563 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM563 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM563 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM563 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8923] The complementary binding of GAM563 RNA, herein designated GAM RNA, to target binding sites on GAM563 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM563 target RNA, herein designated GAM TARGET RNA, into GAM563 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8924] It is appreciated that GAM563 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM563 target genes. The mRNA of each one of this plurality of GAM563 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM563 RNA, herein designated GAM RNA, and which when bound by GAM563 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM563 target proteins.

[8925] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM563 gene, herein designated GAM GENE, on one or more GAM563 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8926] It is yet further appreciated that specific functions, and accordingly utilities, of GAM563 correlate with, and may be deduced from, the identity of the target genes which GAM563 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8927] Nucleotide sequences of the GAM563 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM563 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM563 are further described hereinbelow with reference to Table Table1.

[8928] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM563 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8929] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 564 (GAM564) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8930] GAM564 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM564 was detected is described hereinabove with reference to Figs. 2-8.

[8931] GAM564 gene, herein designated GAM GENE, and GAM564 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8932] GAM564 gene, herein designated GAM GENE, encodes a GAM564 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM564 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM564 precursor RNA is designated SEQ ID:537, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:537 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[8933] GAM564 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8934] An enzyme complex designated DICER COMPLEX, dices the GAM564 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM564 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM564 RNA is designated SEQ ID:2213, and is provided hereinbelow with reference to the sequence listing part.

[8935] GAM564 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM564 target RNA, herein designated GAM TARGET RNA. GAM564 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8936] GAM564 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM564 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM564 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM564 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM564 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8937] The complementary binding of GAM564 RNA, herein designated GAM RNA, to target binding sites on GAM564 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM564 target RNA, herein designated GAM TARGET RNA, into GAM564 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8938] It is appreciated that GAM564 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM564 target genes. The mRNA of each one of this plurality of GAM564 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM564 RNA, herein designated GAM RNA, and which when bound by GAM564 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM564 target proteins.

[8939] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM564 gene, herein designated GAM GENE, on one or more GAM564 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8940] It is yet further appreciated that specific functions, and accordingly utilities, of GAM564 correlate with, and may be deduced from, the identity of the target genes which GAM564 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8941] Nucleotide sequences of the GAM564 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM564 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM564 are further described hereinbelow with reference to Table Table1.

[8942] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM564 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8943] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

565 (GAM565) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8944] GAM565 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM565 was detected is described hereinabove with reference to Figs. 2-8.

[8945] GAM565 gene, herein designated GAM GENE, and GAM565 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8946] GAM565 gene, herein designated GAM GENE, encodes a GAM565 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM565 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM565 precursor RNA is designated SEQ ID:538, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:538 is located at position 1183698 relative to contig NT_029289.7, on chromosome 5.

[8947] GAM565 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM565 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8948] An enzyme complex designated DICER COMPLEX, dices the GAM565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM565 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM565 RNA is designated SEQ ID:2214, and is provided hereinbelow with reference to the sequence listing part.

[8949] GAM565 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM565 target RNA, herein designated GAM TARGET RNA. GAM565 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8950] GAM565 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM565 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM565 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM565 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM565 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[8951] The complementary binding of GAM565 RNA, herein designated GAM RNA, to target binding sites on GAM565 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM565 target RNA, herein designated GAM TARGET RNA, into GAM565 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8952] It is appreciated that GAM565 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM565 target genes. The mRNA of each one of this plurality of GAM565 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM565 RNA, herein designated GAM RNA, and which when bound by GAM565 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM565 target proteins.

[8953] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM565 gene, herein designated GAM GENE, on one or

more GAM565 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8954] It is yet further appreciated that specific functions, and accordingly utilities, of GAM565 correlate with, and may be deduced from, the identity of the target genes which GAM565 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8955] Nucleotide sequences of the GAM565 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM565 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM565 are further de-

scribed hereinbelow with reference to Table Table1.

[8956] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM565 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8957] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 566 (GAM566) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8958] GAM566 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM566 was detected is described hereinabove with reference to Figs. 2-8.

[8959] GAM566 gene, herein designated GAM GENE, and GAM566 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8960] GAM566 gene, herein designated GAM GENE, encodes a GAM566 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM566 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM566 precursor RNA is designated SEQ ID:539, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:539 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[8961] GAM566 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8962] An enzyme complex designated DICER COMPLEX, dices the GAM566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM566 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM566 RNA is designated SEQ ID:2215, and is provided hereinbelow with reference to the sequence listing part.

[8963] GAM566 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM566 target RNA, herein designated GAM TARGET RNA. GAM566 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8964] GAM566 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM566 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM566 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM566 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM566 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8965] The complementary binding of GAM566 RNA, herein designated GAM RNA, to target binding sites on GAM566 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM566 target RNA, herein designated GAM TARGET RNA, into GAM566 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8966] It is appreciated that GAM566 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM566 target genes. The mRNA of each one of this plurality of GAM566 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM566 RNA, herein designated GAM RNA, and which when bound by GAM566 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM566 target proteins.

[8967] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM566 gene, herein designated GAM GENE, on one or more GAM566 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8968] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM566 correlate with, and may be deduced from, the identity of the target genes which GAM566 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8969] Nucleotide sequences of the GAM566 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM566 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM566 are further described hereinbelow with reference to Table Table1.

[8970] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM566 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8971] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 567 (GAM567) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8972] GAM567 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM567 was detected is described hereinabove with reference to Figs. 2-8.

[8973] GAM567 gene, herein designated GAM GENE, and GAM567 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8974] GAM567 gene, herein designated GAM GENE, encodes a GAM567 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM567 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM567 precursor RNA is designated SEQ ID:540, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:540 is located at position 35745 relative to contig NT_005832.12, on chromosome 3.

[8975] GAM567 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8976] An enzyme complex designated DICER COMPLEX, dices the GAM567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM567 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM567 RNA is designated SEQ ID:2216, and is provided hereinbelow with reference to the sequence listing part.

[8977] GAM567 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM567 target RNA, herein designated GAM TARGET RNA. GAM567 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[8978] GAM567 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM567 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM567 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM567 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM567 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8979] The complementary binding of GAM567 RNA, herein designated GAM RNA, to target binding sites on GAM567 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM567 target RNA, herein designated GAM TARGET RNA, into GAM567 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8980] It is appreciated that GAM567 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM567 target genes. The mRNA of each one of this plurality of GAM567 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM567 RNA, herein designated GAM RNA, and which when bound by GAM567 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM567 target proteins.

[8981] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM567 gene, herein designated GAM GENE, on one or more GAM567 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8982] It is yet further appreciated that specific functions, and accordingly utilities, of GAM567 correlate with, and may be deduced from, the identity of the target genes which GAM567 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[8983] Nucleotide sequences of the GAM567 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM567 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM567 are further described hereinbelow with reference to Table Table1.

[8984] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM567 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8985] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 568 (GAM568) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[8986] GAM568 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM568 was detected is described hereinabove with reference to Figs. 2-8.

[8987] GAM568 gene, herein designated GAM GENE, and GAM568 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[8988] GAM568 gene, herein designated GAM GENE, encodes a GAM568 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM568 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM568 precursor RNA is designated SEQ ID:541, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:541 is located at position 1654428 relative to contig NT_005986.13, on chromosome 3.

[8989] GAM568 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[8990] An enzyme complex designated DICER COMPLEX, dices the GAM568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM568 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM568 RNA is designated SEQ ID:2217, and is provided hereinbelow with reference to the sequence listing part.

[8991] GAM568 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM568 target RNA, herein designated GAM TARGET RNA. GAM568 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[8992] GAM568 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM568 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM568 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM568 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM568 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[8993] The complementary binding of GAM568 RNA, herein designated GAM RNA, to target binding sites on GAM568 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM568 target RNA, herein designated GAM TARGET RNA, into GAM568 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[8994] It is appreciated that GAM568 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM568 target genes. The mRNA of each one of this plurality of GAM568 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM568 RNA, herein designated GAM RNA, and which when bound by

GAM568 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM568 target proteins.

[8995] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM568 gene, herein designated GAM GENE, on one or more GAM568 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[8996] It is yet further appreciated that specific functions, and accordingly utilities, of GAM568 correlate with, and may be deduced from, the identity of the target genes which GAM568 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[8997] Nucleotide sequences of the GAM568 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM568 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM568 are further described hereinbelow with reference to Table Table1.

[8998] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM568 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[8999] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 569 (GAM569) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9000] GAM569 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM569 was detected is described hereinabove

with reference to Figs. 2-8.

[9001] GAM569 gene, herein designated GAM GENE, and GAM569 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9002] GAM569 gene, herein designated GAM GENE, encodes a GAM569 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM569 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM569 precursor RNA is designated SEQ ID:542, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:542 is located at position 3004691 relative to contig NT_004852.13, on chromosome 1.

[9003] GAM569 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[9004] An enzyme complex designated DICER COMPLEX, dices the GAM569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM569 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM569 RNA is designated SEQ ID:2218, and is provided hereinbelow with reference to the sequence listing part.

[9005] GAM569 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM569 target RNA, herein designated GAM TARGET RNA.
GAM569 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9006] GAM569 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM569 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM569 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM569 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM569 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9007] The complementary binding of GAM569 RNA, herein designated GAM RNA, to target binding sites on GAM569 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM569 target RNA, herein desig-

nated GAM TARGET RNA, into GAM569 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9008] It is appreciated that GAM569 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM569 target genes. The mRNA of each one of this plurality of GAM569 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM569 RNA, herein designated GAM RNA, and which when bound by GAM569 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM569 target proteins.

[9009] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM569 gene, herein designated GAM GENE, on one or more GAM569 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9010] It is yet further appreciated that specific functions, and accordingly utilities, of GAM569 correlate with, and may be deduced from, the identity of the target genes which GAM569 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9011] Nucleotide sequences of the GAM569 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM569 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM569 are further described hereinbelow with reference to Table Table1.

[9012] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM569 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[9013] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 570 (GAM570) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9014] GAM570 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM570 was detected is described hereinabove with reference to Figs. 2-8.

[9015] GAM570 gene, herein designated GAM GENE, and GAM570 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9016] GAM570 gene, herein designated GAM GENE, encodes a GAM570 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM570 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM570 precursor RNA is designated SEQ ID:543, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:543 is located at position 2369688 relative to contig NT_030059.8, on chromosome 10.

[9017] GAM570 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9018] An enzyme complex designated DICER COMPLEX, dices the GAM570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM570 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM570 RNA is designated SEQ ID:2219, and is provided hereinbelow with reference to the sequence listing part.

[9019] GAM570 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM570 target RNA, herein designated GAM TARGET RNA. GAM570 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9020] GAM570 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM570 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM570 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM570 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM570

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9021] The complementary binding of GAM570 RNA, herein designated GAM RNA, to target binding sites on GAM570 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM570 target RNA, herein designated GAM TARGET RNA, into GAM570 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9022] It is appreciated that GAM570 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM570 target genes. The mRNA of each one of this plurality of GAM570 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM570 RNA, herein designated GAM RNA, and which when bound by GAM570 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM570 target proteins.

[9023] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM570 gene, herein designated GAM GENE, on one or more GAM570 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9024] It is yet further appreciated that specific functions, and accordingly utilities, of GAM570 correlate with, and may be deduced from, the identity of the target genes which GAM570 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9025] Nucleotide sequences of the GAM570 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM570 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM570 are further described hereinbelow with reference to Table Table1.

[9026] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM570 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9027] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 571 (GAM571) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9028] GAM571 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM571 was detected is described hereinabove with reference to Figs. 2-8.

[9029] GAM571 gene, herein designated GAM GENE, and GAM571 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[9030] GAM571 gene, herein designated GAM GENE, encodes a GAM571 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM571 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM571 precursor RNA is designated SEQ ID:544, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:544 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[9031] GAM571 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9032] An enzyme complex designated DICER COMPLEX, dices

the GAM571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM571 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM571 RNA is designated SEQ ID:2220, and is provided hereinbelow with reference to the sequence listing part.

[9033] GAM571 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM571 target RNA, herein designated GAM TARGET RNA. GAM571 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9034] GAM571 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM571 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM571

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM571 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM571 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9035] The complementary binding of GAM571 RNA, herein designated GAM RNA, to target binding sites on GAM571 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM571 target RNA, herein designated GAM TARGET RNA, into GAM571 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9036] It is appreciated that GAM571 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM571 target genes. The mRNA of each one of this plurality of GAM571 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM571 RNA, herein designated GAM RNA, and which when bound by GAM571 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM571 target proteins.

[9037] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM571 gene, herein designated GAM GENE, on one or more GAM571 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9038] It is yet further appreciated that specific functions, and accordingly utilities, of GAM571 correlate with, and may be deduced from, the identity of the target genes which GAM571 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9039] Nucleotide sequences of the GAM571 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM571 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM571 are further described hereinbelow with reference to Table Table1.

[9040] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM571 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9041] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 572 (GAM572) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9042] GAM572 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM572 was detected is described hereinabove with reference to Figs. 2-8.

[9043] GAM572 gene, herein designated GAM GENE, and GAM572 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9044] GAM572 gene, herein designated GAM GENE, encodes a GAM572 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM572 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM572 precursor RNA is designated SEQ ID:545, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:545 is located at position 13961449 relative to contig NT_009151.13, on chromosome 11.

[9045] GAM572 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9046] An enzyme complex designated DICER COMPLEX, dices the GAM572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM572 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM572 RNA is designated SEQ ID:2221, and is provided hereinbelow with reference to the sequence listing part.

[9047] GAM572 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM572 target RNA, herein designated GAM TARGET RNA.

GAM572 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9048] GAM572 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM572 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM572 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM572 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM572 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9049] The complementary binding of GAM572 RNA, herein designated GAM RNA, to target binding sites on GAM572 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM572 target RNA, herein designated GAM TARGET RNA, into GAM572 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9050] It is appreciated that GAM572 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM572 target genes. The mRNA of each one of this plurality of GAM572 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM572 RNA, herein designated GAM RNA, and which when bound by GAM572 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM572 target proteins.

[9051] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM572 gene, herein designated GAM GENE, on one or more GAM572 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9052] It is yet further appreciated that specific functions, and accordingly utilities, of GAM572 correlate with, and may be deduced from, the identity of the target genes which GAM572 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9053] Nucleotide sequences of the GAM572 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM572 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM572 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM572 are further described hereinbelow with reference to Table Table1.

[9054] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM572 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9055] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 573 (GAM573) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9056] GAM573 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM573 was detected is described hereinabove with reference to Figs. 2-8.

[9057] GAM573 gene, herein designated GAM GENE, and GAM573 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9058] GAM573 gene, herein designated GAM GENE, encodes a GAM573 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM573 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM573 precursor RNA is designated SEQ ID:546, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:546 is located at position 86501 relative to contig NT_011594.9, on chromosome X.

[9059] GAM573 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9060] An enzyme complex designated DICER COMPLEX, dices the GAM573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM573 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM573 RNA is designated SEQ ID:2222, and is provided hereinbelow with reference to the sequence listing part.

[9061] GAM573 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM573 target RNA, herein designated GAM TARGET RNA. GAM573 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9062] GAM573 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM573 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM573 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM573 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM573 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9063] The complementary binding of GAM573 RNA, herein designated GAM RNA, to target binding sites on GAM573 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM573 target RNA, herein designated GAM TARGET RNA, into GAM573 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9064] It is appreciated that GAM573 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM573 target genes. The mRNA of each one of this plu-

rality of GAM573 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM573 RNA, herein designated GAM RNA, and which when bound by GAM573 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM573 target proteins.

[9065] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM573 gene, herein designated GAM GENE, on one or more GAM573 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9066] It is yet further appreciated that specific functions, and accordingly utilities, of GAM573 correlate with, and may be deduced from, the identity of the target genes which GAM573 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9067] Nucleotide sequences of the GAM573 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM573 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM573 are further described hereinbelow with reference to Table Table1.

[9068] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM573 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9069] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 574 (GAM574) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[9070] GAM574 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM574 was detected is described hereinabove with reference to Figs. 2-8.

[9071] GAM574 gene, herein designated GAM GENE, and GAM574 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9072] GAM574 gene, herein designated GAM GENE, encodes a GAM574 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM574 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM574 precursor RNA is designated SEQ ID:547, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:547 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[9073] GAM574 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9074] An enzyme complex designated DICER COMPLEX, dices the GAM574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM574 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM574 RNA is designated SEQ ID:2223, and is provided hereinbelow with reference to the sequence listing part.

[9075] GAM574 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM574 target RNA, herein designated GAM TARGET RNA. GAM574 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9076] GAM574 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM574 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM574 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM574 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM574 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9077] The complementary binding of GAM574 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM574 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM574 target RNA, herein designated GAM TARGET RNA, into GAM574 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9078] It is appreciated that GAM574 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM574 target genes. The mRNA of each one of this plurality of GAM574 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM574 RNA, herein designated GAM RNA, and which when bound by GAM574 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM574 target proteins.

[9079] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM574 gene, herein designated GAM GENE, on one or more GAM574 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9080] It is yet further appreciated that specific functions, and accordingly utilities, of GAM574 correlate with, and may be deduced from, the identity of the target genes which GAM574 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9081] Nucleotide sequences of the GAM574 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM574 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM574 are further described hereinbelow with reference to Table Table1.

[9082] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM574 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9083] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 575 (GAM575) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9084] GAM575 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM575 was detected is described hereinabove with reference to Figs. 2-8.

[9085] GAM575 gene, herein designated GAM GENE, and GAM575 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9086] GAM575 gene, herein designated GAM GENE, encodes a GAM575 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM575 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM575 precursor RNA is designated SEQ ID:548, and is provided hereinbelow with reference to the sequence listing part.

[9087] GAM575 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9088] An enzyme complex designated DICER COMPLEX, dices the GAM575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM575 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM575 RNA is designated SEQ ID:2224, and is provided hereinbelow with reference to the sequence listing part.

[9089] GAM575 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM575 target RNA, herein designated GAM TARGET RNA. GAM575 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9090] GAM575 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM575 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM575 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM575 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM575 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9091] The complementary binding of GAM575 RNA, herein designated GAM RNA, to target binding sites on GAM575 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM575 target RNA, herein designated GAM TARGET RNA, into GAM575 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9092] It is appreciated that GAM575 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM575 target genes. The mRNA of each one of this plurality of GAM575 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM575 RNA, herein designated GAM RNA, and which when bound by GAM575 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM575 target proteins.

[9093] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM575 gene, herein designated GAM GENE, on one or more GAM575 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9094] It is yet further appreciated that specific functions, and accordingly utilities, of GAM575 correlate with, and may be deduced from, the identity of the target genes which GAM575 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9095] Nucleotide sequences of the GAM575 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM575 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM575 are further described hereinbelow with reference to Table Table1.

[9096] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM575 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9097] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 576 (GAM576) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9098] GAM576 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM576 was detected is described hereinabove with reference to Figs. 2-8.

[9099] GAM576 gene, herein designated GAM GENE, and GAM576 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9100] GAM576 gene, herein designated GAM GENE, encodes a GAM576 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM576 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM576 precursor RNA is designated SEQ ID:549, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:549 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[9101] GAM576 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[9102] An enzyme complex designated DICER COMPLEX, dices the GAM576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM576 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM576 RNA is designated SEQ ID:2225, and is provided hereinbelow with reference to the sequence listing part.

[9103] GAM576 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM576 target RNA, herein designated GAM TARGET RNA. GAM576 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9104] GAM576 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM576 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM576 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM576 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM576 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9105] The complementary binding of GAM576 RNA, herein designated GAM RNA, to target binding sites on GAM576 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM576 target RNA, herein designated GAM TARGET RNA, into GAM576 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9106] It is appreciated that GAM576 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM576 target genes. The mRNA of each one of this plurality of GAM576 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM576 RNA, herein designated GAM RNA, and which when bound by GAM576 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM576 target proteins.

[9107] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM576 gene, herein designated GAM GENE, on one or more GAM576 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9108] It is yet further appreciated that specific functions, and accordingly utilities, of GAM576 correlate with, and may be deduced from, the identity of the target genes which GAM576 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9109] Nucleotide sequences of the GAM576 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM576 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM576 are further described hereinbelow with reference to Table Table1.

[9110] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM576 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9111] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 577 (GAM577) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9112] GAM577 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM577 was detected is described hereinabove with reference to Figs. 2-8.

[9113] GAM577 gene, herein designated GAM GENE, and GAM577 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9114] GAM577 gene, herein designated GAM GENE, encodes a GAM577 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM577 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM577 precursor RNA is designated SEQ ID:550, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:550 is located at position 716274 relative to contig

NT_006111.13, on chromosome 4.

[9115] GAM577 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM577 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9116] An enzyme complex designated DICER COMPLEX, dices the GAM577 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM577 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM577 RNA is designated SEQ ID:2226, and is provided hereinbelow with reference to the sequence listing part.

[9117] GAM577 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM577 target RNA, herein designated GAM TARGET RNA.

GAM577 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9118] GAM577 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM577 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM577 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM577 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM577 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9119] The complementary binding of GAM577 RNA, herein designated GAM RNA, to target binding sites on GAM577 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM577 target RNA, herein designated GAM TARGET RNA, into GAM577 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9120] It is appreciated that GAM577 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM577 target genes. The mRNA of each one of this plurality of GAM577 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM577 RNA, herein designated GAM RNA, and which when bound by GAM577 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM577 target proteins.

[9121] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM577 gene, herein designated GAM GENE, on one or more GAM577 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9122] It is yet further appreciated that specific functions, and accordingly utilities, of GAM577 correlate with, and may be deduced from, the identity of the target genes which GAM577 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9123] Nucleotide sequences of the GAM577 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM577 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM577 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM577 are further described hereinbelow with reference to Table Table1.

[9124] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM577 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9125] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 578 (GAM578) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9126] GAM578 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM578 was detected is described hereinabove with reference to Figs. 2-8.

[9127] GAM578 gene, herein designated GAM GENE, and GAM578 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9128] GAM578 gene, herein designated GAM GENE, encodes a GAM578 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM578 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM578 precursor RNA is designated SEQ ID:551, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:551 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[9129] GAM578 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[9130] SEQ ID:99321 detected in mouse EST Accession AA144533.1.

[9131] SEQ ID:99322 detected in mouse EST Accession AA671455.1.

[9132] SEQ ID:99323 detected in mouse EST Accession BE943987.1.

[9133] SEQ ID:99324 detected in mouse EST Accession

BE691447.1.

[9134] SEQ ID:99325 detected in mouse EST Accession BG808025.1.

[9135] SEQ ID:99326 detected in mouse EST Accession BG808010.1.

[9136] SEQ ID:99327 detected in mouse EST Accession BG807850.1.

[9137] SEQ ID:99328 detected in mouse EST Accession BG805970.1.

[9138] SEQ ID:99329 detected in mouse EST Accession AW208601.1.

[9139] SEQ ID:99330 detected in mouse EST Accession BB610842.1.

[9140] SEQ ID:99331 detected in mouse EST Accession BB609859.1.

[9141] SEQ ID:99332 detected in mouse EST Accession AW824753.1.

[9142] SEQ ID:99333 detected in mouse EST Accession BE691413.1.

[9143] SEQ ID:99335 detected in mouse EST Accession BG145596.1.

[9144] SEQ ID:99336 detected in mouse EST Accession BE692802.1.

[9145] GAM578 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9146] An enzyme complex designated DICER COMPLEX, dices the GAM578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM578 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM578 RNA is designated SEQ ID:2227, and is provided hereinbelow with reference to the sequence listing part.

[9147] GAM578 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM578

target RNA, herein designated GAM TARGET RNA.

GAM578 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9148] GAM578 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM578 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM578 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM578 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM578 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9149] The complementary binding of GAM578 RNA, herein designated GAM RNA, to target binding sites on GAM578 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM578 target RNA, herein designated GAM TARGET RNA, into GAM578 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9150] It is appreciated that GAM578 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM578 target genes. The mRNA of each one of this plurality of GAM578 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM578 RNA, herein designated GAM RNA, and which when bound by GAM578 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM578 target proteins.

[9151] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM578 gene, herein designated GAM GENE, on one or more GAM578 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9152] It is yet further appreciated that specific functions, and accordingly utilities, of GAM578 correlate with, and may be deduced from, the identity of the target genes which GAM578 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9153] Nucleotide sequences of the GAM578 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM578 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM578 are further described hereinbelow with reference to Table Table1.

[9154] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM578 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9155] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 579 (GAM579) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9156] GAM579 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM579 was detected is described hereinabove with reference to Figs. 2-8.

[9157] GAM579 gene, herein designated GAM GENE, and GAM579 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9158] GAM579 gene, herein designated GAM GENE, encodes a

GAM579 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM579 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM579 precursor RNA is designated SEQ ID:552, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:552 is located at position 1392324 relative to contig NT_025319.11, on chromosome X.

[9159] GAM579 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9160] An enzyme complex designated DICER COMPLEX, dices the GAM579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM579 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM579 RNA is designated SEQ ID:2228, and is provided hereinbelow with reference to the sequence listing part.

[9161] GAM579 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM579 target RNA, herein designated GAM TARGET RNA. GAM579 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9162] GAM579 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM579 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM579 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM579 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM579 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9163] The complementary binding of GAM579 RNA, herein designated GAM RNA, to target binding sites on GAM579 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM579 target RNA, herein designated GAM TARGET RNA, into GAM579 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9164] It is appreciated that GAM579 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM579 target genes. The mRNA of each one of this plurality of GAM579 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM579 RNA, herein designated GAM RNA, and which when bound by GAM579 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM579 target proteins.

[9165] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM579 gene, herein designated GAM GENE, on one or more GAM579 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[9166] It is yet further appreciated that specific functions, and accordingly utilities, of GAM579 correlate with, and may be deduced from, the identity of the target genes which GAM579 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9167] Nucleotide sequences of the GAM579 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM579 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM579 are further described hereinbelow with reference to Table Table1.

[9168] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM579 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9169] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 580 (GAM580) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[9170] GAM580 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM580 was detected is described hereinabove with reference to Figs. 2-8.

[9171] GAM580 gene, herein designated GAM GENE, and GAM580 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9172] GAM580 gene, herein designated GAM GENE, encodes a GAM580 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM580 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM580 precursor RNA is designated SEQ ID:553, and is provided hereinbelow with reference to the sequence listing part.

[9173] GAM580 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9174] An enzyme complex designated DICER COMPLEX, dices the GAM580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM580 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM580 RNA is designated SEQ ID:2229, and is provided hereinbelow with reference to the sequence listing part.

[9175] GAM580 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM580 target RNA, herein designated GAM TARGET RNA.
GAM580 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[9176] GAM580 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM580 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM580 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM580 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM580 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9177] The complementary binding of GAM580 RNA, herein designated GAM RNA, to target binding sites on GAM580 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM580 target RNA, herein designated GAM TARGET RNA, into GAM580 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9178] It is appreciated that GAM580 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM580 target genes. The mRNA of each one of this plurality of GAM580 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM580 RNA, herein designated GAM RNA, and which when bound by GAM580 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM580 target proteins.

[9179] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM580 gene, herein designated GAM GENE, on one or more GAM580 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9180] It is yet further appreciated that specific functions, and accordingly utilities, of GAM580 correlate with, and may be deduced from, the identity of the target genes which GAM580 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9181] Nucleotide sequences of the GAM580 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM580 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM580 are further described hereinbelow with reference to Table Table1.

[9182] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM580 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9183] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 581 (GAM581) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9184] GAM581 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM581 was detected is described hereinabove with reference to Figs. 2-8.

[9185] GAM581 gene, herein designated GAM GENE, and GAM581 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9186] GAM581 gene, herein designated GAM GENE, encodes a GAM581 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM581 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM581 precursor RNA is designated SEQ ID:554, and is provided hereinbelow with reference to the sequence listing part.

[9187] GAM581 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[9188] SEQ ID:99814 detected in mouse EST Accession BB610842.1.

[9189] SEQ ID:99815 detected in mouse EST Accession BE692068.1.

[9190] SEQ ID:99816 detected in mouse EST Accession AA144533.1.

[9191] SEQ ID:99817 detected in mouse EST Accession BE691447.1.

[9192] SEQ ID:99818 detected in mouse EST Accession BE335742.1.

[9193] SEQ ID:99819 detected in mouse EST Accession AA671455.1.

[9194] SEQ ID:99820 detected in mouse EST Accession AW824753.1.

[9195] SEQ ID:99821 detected in mouse EST Accession

BE691413.1.

[9196] SEQ ID:99822 detected in mouse EST Accession BG808025.1.

[9197] SEQ ID:99823 detected in mouse EST Accession BG808010.1.

[9198] SEQ ID:99824 detected in mouse EST Accession BG807850.1.

[9199] SEQ ID:99825 detected in mouse EST Accession BG805970.1.

[9200] SEQ ID:99826 detected in mouse EST Accession BE692802.1.

[9201] SEQ ID:99827 detected in mouse EST Accession BG145596.1.

[9202] SEQ ID:99828 detected in mouse EST Accession AW208601.1.

[9203] GAM581 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9204] An enzyme complex designated DICER COMPLEX, dices the GAM581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM581 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM581 RNA is designated SEQ ID:2230, and is provided hereinbelow with reference to the sequence listing part.

[9205] GAM581 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM581 target RNA, herein designated GAM TARGET RNA. GAM581 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9206] GAM581 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM581 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM581 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM581 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM581 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9207] The complementary binding of GAM581 RNA, herein designated GAM RNA, to target binding sites on GAM581 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM581 target RNA, herein designated GAM TARGET RNA, into GAM581 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9208] It is appreciated that GAM581 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM581 target genes. The mRNA of each one of this plurality of GAM581 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM581 RNA, herein designated GAM RNA, and which when bound by GAM581 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM581 target proteins.

[9209] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM581 gene, herein designated GAM GENE, on one or more GAM581 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[9210] It is yet further appreciated that specific functions, and accordingly utilities, of GAM581 correlate with, and may be deduced from, the identity of the target genes which GAM581 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9211] Nucleotide sequences of the GAM581 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM581 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM581 are further described hereinbelow with reference to Table Table1.

[9212] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM581 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9213] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 582 (GAM582) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[9214] GAM582 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM582 was detected is described hereinabove with reference to Figs. 2-8.

[9215] GAM582 gene, herein designated GAM GENE, and GAM582 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9216] GAM582 gene, herein designated GAM GENE, encodes a GAM582 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM582 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM582 precursor RNA is designated SEQ ID:555, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:555 is located at position 2779777 relative to contig NT_015280.13, on chromosome 8.

[9217] GAM582 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9218] An enzyme complex designated DICER COMPLEX, dices the GAM582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM582 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM582 RNA is designated SEQ ID:2231, and is provided hereinbelow with reference to the sequence listing part.

[9219] GAM582 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM582 target RNA, herein designated GAM TARGET RNA. GAM582 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9220] GAM582 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM582 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM582 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM582 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM582 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9221] The complementary binding of GAM582 RNA, herein designated GAM RNA, to target binding sites on GAM582 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM582 target RNA, herein designated GAM TARGET RNA, into GAM582 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9222] It is appreciated that GAM582 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM582 target genes. The mRNA of each one of this plurality of GAM582 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM582 RNA, herein designated GAM RNA, and which when bound by GAM582 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM582 target proteins.

[9223] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM582 gene, herein designated GAM GENE, on one or more GAM582 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9224] It is yet further appreciated that specific functions, and accordingly utilities, of GAM582 correlate with, and may be deduced from, the identity of the target genes which GAM582 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9225] Nucleotide sequences of the GAM582 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM582 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM582 are further described hereinbelow with reference to Table Table1.

[9226] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM582 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9227] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 583 (GAM583) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9228] GAM583 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM583 was detected is described hereinabove with reference to Figs. 2-8.

[9229] GAM583 gene, herein designated GAM GENE, and GAM583 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9230] GAM583 gene, herein designated GAM GENE, encodes a GAM583 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM583 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM583 precursor RNA is designated SEQ ID:556, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:556 is located at position 3102351 relative to contig NT_011109.13, on chromosome 19.

[9231] GAM583 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9232] An enzyme complex designated DICER COMPLEX, dices the GAM583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM583 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM583 RNA is designated SEQ ID:2232, and is provided hereinbelow with reference to the sequence listing part.

[9233] GAM583 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM583 target RNA, herein designated GAM TARGET RNA. GAM583 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9234] GAM583 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM583 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM583 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM583 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM583 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9235] The complementary binding of GAM583 RNA, herein designated GAM RNA, to target binding sites on GAM583 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM583 target RNA, herein designated GAM TARGET RNA, into GAM583 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9236] It is appreciated that GAM583 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM583 target genes. The mRNA of each one of this plurality of GAM583 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM583 RNA, herein designated GAM RNA, and which when bound by GAM583 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM583 target proteins.

[9237] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM583 gene, herein designated GAM GENE, on one or more GAM583 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9238] It is yet further appreciated that specific functions, and accordingly utilities, of GAM583 correlate with, and may

be deduced from, the identity of the target genes which GAM583 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9239] Nucleotide sequences of the GAM583 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM583 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM583 are further described hereinbelow with reference to Table Table1.

[9240] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM583 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9241] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 584 (GAM584) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9242] GAM584 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM584 was detected is described hereinabove with reference to Figs. 2-8.

[9243] GAM584 gene, herein designated GAM GENE, and GAM584 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9244] GAM584 gene, herein designated GAM GENE, encodes a GAM584 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM584 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM584 precursor RNA is designated SEQ ID:557, and is provided hereinbelow with reference to the sequence listing part.

[9245] GAM584 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[9246] An enzyme complex designated DICER COMPLEX, dices the GAM584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM584 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM584 RNA is designated SEQ ID:2233, and is provided hereinbelow with reference to the sequence listing part.

[9247] GAM584 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM584 target RNA, herein designated GAM TARGET RNA.
GAM584 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9248] GAM584 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM584 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM584 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM584 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM584 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9249] The complementary binding of GAM584 RNA, herein designated GAM RNA, to target binding sites on GAM584 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM584 target RNA, herein desig-

nated GAM TARGET RNA, into GAM584 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9250] It is appreciated that GAM584 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM584 target genes. The mRNA of each one of this plurality of GAM584 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM584 RNA, herein designated GAM RNA, and which when bound by GAM584 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM584 target proteins.

[9251] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM584 gene, herein designated GAM GENE, on one or more GAM584 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9252] It is yet further appreciated that specific functions, and accordingly utilities, of GAM584 correlate with, and may be deduced from, the identity of the target genes which GAM584 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9253] Nucleotide sequences of the GAM584 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM584 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM584 are further described hereinbelow with reference to Table Table1.

[9254] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM584 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[9255] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 585 (GAM585) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9256] GAM585 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM585 was detected is described hereinabove with reference to Figs. 2-8.

[9257] GAM585 gene, herein designated GAM GENE, and GAM585 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9258] GAM585 gene, herein designated GAM GENE, encodes a GAM585 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM585 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM585 precursor RNA is designated SEQ ID:558, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:558 is located at position 10031168 relative to contig NT_006431.11, on chromosome 5.

[9259] GAM585 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9260] An enzyme complex designated DICER COMPLEX, dices the GAM585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM585 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM585 RNA is designated SEQ ID:2234, and is provided hereinbelow with reference to the sequence listing part.

[9261] GAM585 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM585 target RNA, herein designated GAM TARGET RNA. GAM585 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9262] GAM585 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM585 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM585 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM585 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM585

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9263] The complementary binding of GAM585 RNA, herein designated GAM RNA, to target binding sites on GAM585 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM585 target RNA, herein designated GAM TARGET RNA, into GAM585 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9264] It is appreciated that GAM585 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM585 target genes. The mRNA of each one of this plurality of GAM585 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM585 RNA, herein designated GAM RNA, and which when bound by GAM585 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM585 target proteins.

[9265] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM585 gene, herein designated GAM GENE, on one or more GAM585 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9266] It is yet further appreciated that specific functions, and accordingly utilities, of GAM585 correlate with, and may be deduced from, the identity of the target genes which GAM585 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9267] Nucleotide sequences of the GAM585 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM585 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM585 are further described hereinbelow with reference to Table Table1.

[9268] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM585 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9269] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 586 (GAM586) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9270] GAM586 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM586 was detected is described hereinabove with reference to Figs. 2-8.

[9271] GAM586 gene, herein designated GAM GENE, and GAM586 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[9272] GAM586 gene, herein designated GAM GENE, encodes a GAM586 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM586 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM586 precursor RNA is designated SEQ ID:559, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:559 is located at position 2459976 relative to contig NT_015805.11, on chromosome 2.

[9273] GAM586 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9274] An enzyme complex designated DICER COMPLEX, dices

the GAM586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM586 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM586 RNA is designated SEQ ID:2235, and is provided hereinbelow with reference to the sequence listing part.

[9275] GAM586 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM586 target RNA, herein designated GAM TARGET RNA. GAM586 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9276] GAM586 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM586 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM586

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM586 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM586 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9277] The complementary binding of GAM586 RNA, herein designated GAM RNA, to target binding sites on GAM586 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM586 target RNA, herein designated GAM TARGET RNA, into GAM586 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9278] It is appreciated that GAM586 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM586 target genes. The mRNA of each one of this plurality of GAM586 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM586 RNA, herein designated GAM RNA, and which when bound by GAM586 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM586 target proteins.

[9279] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM586 gene, herein designated GAM GENE, on one or more GAM586 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9280] It is yet further appreciated that specific functions, and accordingly utilities, of GAM586 correlate with, and may be deduced from, the identity of the target genes which GAM586 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9281] Nucleotide sequences of the GAM586 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM586 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM586 are further described hereinbelow with reference to Table Table1.

[9282] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM586 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9283] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 587 (GAM587) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9284] GAM587 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM587 was detected is described hereinabove with reference to Figs. 2-8.

[9285] GAM587 gene, herein designated GAM GENE, and GAM587 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9286] GAM587 gene, herein designated GAM GENE, encodes a GAM587 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM587 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM587 precursor RNA is designated SEQ ID:560, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:560 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[9287] GAM587 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9288] An enzyme complex designated DICER COMPLEX, dices the GAM587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM587 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM587 RNA is designated SEQ ID:2236, and is provided hereinbelow with reference to the sequence listing part.

[9289] GAM587 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM587 target RNA, herein designated GAM TARGET RNA.

GAM587 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9290] GAM587 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM587 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM587 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM587 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM587 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9291] The complementary binding of GAM587 RNA, herein designated GAM RNA, to target binding sites on GAM587 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM587 target RNA, herein designated GAM TARGET RNA, into GAM587 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9292] It is appreciated that GAM587 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM587 target genes. The mRNA of each one of this plurality of GAM587 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM587 RNA, herein designated GAM RNA, and which when bound by GAM587 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM587 target proteins.

[9293] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM587 gene, herein designated GAM GENE, on one or more GAM587 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9294] It is yet further appreciated that specific functions, and accordingly utilities, of GAM587 correlate with, and may be deduced from, the identity of the target genes which GAM587 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9295] Nucleotide sequences of the GAM587 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM587 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM587 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM587 are further described hereinbelow with reference to Table Table1.

[9296] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM587 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9297] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 588 (GAM588) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9298] GAM588 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM588 was detected is described hereinabove with reference to Figs. 2-8.

[9299] GAM588 gene, herein designated GAM GENE, and GAM588 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9300] GAM588 gene, herein designated GAM GENE, encodes a GAM588 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM588 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM588 precursor RNA is designated SEQ ID:561, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:561 is located at position 437366 relative to contig NT_031847.6, on chromosome 10.

[9301] GAM588 has 40 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[9302] SEQ ID:98573 detected in mouse EST Accession AW240290.1.

[9303] SEQ ID:98574 detected in mouse EST Accession AI466465.1.

[9304] SEQ ID:98575 detected in mouse EST Accession AI386303.1.

[9305] SEQ ID:98576 detected in mouse EST Accession BE332557.1.

[9306] SEQ ID:98577 detected in mouse EST Accession

BE138169.1.

[9307] SEQ ID:98578 detected in mouse EST Accession AA833390.1.

[9308] SEQ ID:98580 detected in mouse EST Accession AI322688.1.

[9309] SEQ ID:98581 detected in mouse EST Accession BE954450.1.

[9310] SEQ ID:98582 detected in mouse EST Accession AI892771.1.

[9311] SEQ ID:98583 detected in mouse EST Accession AI152626.1.

[9312] SEQ ID:98584 detected in mouse EST Accession AA518310.1.

[9313] SEQ ID:98585 detected in mouse EST Accession AA153863.1.

[9314] SEQ ID:98586 detected in mouse EST Accession BE628853.1.

[9315] SEQ ID:98587 detected in mouse EST Accession AI786482.1.

[9316] SEQ ID:98588 detected in mouse EST Accession AA138462.1.

[9317] SEQ ID:98589 detected in mouse EST Accession BI440887.1.

[9318] SEQ ID:98590 detected in mouse EST Accession AA597003.1.

[9319] SEQ ID:98591 detected in mouse EST Accession BG807589.1.

[9320] SEQ ID:98592 detected in mouse EST Accession BG801685.1.

[9321] SEQ ID:98593 detected in mouse EST Accession BG965057.1.

[9322] SEQ ID:98594 detected in mouse EST Accession BF788592.1.

[9323] SEQ ID:98595 detected in mouse EST Accession BF783978.1.

[9324] SEQ ID:98596 detected in mouse EST Accession BI109599.1.

[9325] SEQ ID:98597 detected in mouse EST Accession BE306388.1.

[9326] SEQ ID:98598 detected in mouse EST Accession BF122743.1.

[9327] SEQ ID:98599 detected in mouse EST Accession BI251323.1.

[9328] SEQ ID:98600 detected in mouse EST Accession BE570270.1.

[9329] SEQ ID:98601 detected in mouse EST Accession

AW488506.1.

[9330] SEQ ID:98602 detected in mouse EST Accession AI020141.1.

[9331] SEQ ID:98603 detected in mouse EST Accession AA048592.1.

[9332] SEQ ID:98604 detected in mouse EST Accession AA270221.1.

[9333] SEQ ID:98605 detected in mouse EST Accession AA154986.1.

[9334] SEQ ID:98606 detected in mouse EST Accession AA072931.1.

[9335] SEQ ID:98607 detected in mouse EST Accession AA462619.1.

[9336] SEQ ID:98608 detected in mouse EST Accession AA023591.1.

[9337] SEQ ID:98609 detected in mouse EST Accession AA268161.1.

[9338] SEQ ID:98611 detected in mouse EST Accession BG969557.1.

[9339] SEQ ID:98612 detected in mouse EST Accession BI650316.1.

[9340] SEQ ID:98613 detected in mouse EST Accession BG867629.1.

[9341] SEQ ID:98614 detected in mouse EST Accession BI685815.1.

[9342] GAM588 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9343] An enzyme complex designated DICER COMPLEX, dices the GAM588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM588 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM588 RNA is designated SEQ ID:2237, and is provided hereinbelow with reference to the sequence listing part.

[9344] GAM588 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM588 target RNA, herein designated GAM TARGET RNA. GAM588 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9345] GAM588 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM588 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM588 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM588 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM588

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9346] The complementary binding of GAM588 RNA, herein designated GAM RNA, to target binding sites on GAM588 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM588 target RNA, herein designated GAM TARGET RNA, into GAM588 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9347] It is appreciated that GAM588 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM588 target genes. The mRNA of each one of this plurality of GAM588 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM588 RNA, herein designated GAM RNA, and which when bound by GAM588 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM588 target proteins.

[9348] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM588 gene, herein designated GAM GENE, on one or more GAM588 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9349] It is yet further appreciated that specific functions, and accordingly utilities, of GAM588 correlate with, and may be deduced from, the identity of the target genes which GAM588 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9350] Nucleotide sequences of the GAM588 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM588 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM588 are further described hereinbelow with reference to Table Table1.

[9351] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM588 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9352] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 589 (GAM589) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9353] GAM589 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM589 was detected is described hereinabove with reference to Figs. 2-8.

[9354] GAM589 gene, herein designated GAM GENE, and GAM589 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[9355] GAM589 gene, herein designated GAM GENE, encodes a GAM589 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM589 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM589 precursor RNA is designated SEQ ID:562, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:562 is located at position 2865607 relative to contig NT_011512.7, on chromosome 21.

[9356] GAM589 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9357] An enzyme complex designated DICER COMPLEX, dices

the GAM589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM589 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM589 RNA is designated SEQ ID:2238, and is provided hereinbelow with reference to the sequence listing part.

[9358] GAM589 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM589 target RNA, herein designated GAM TARGET RNA. GAM589 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9359] GAM589 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM589 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM589

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM589 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM589 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9360] The complementary binding of GAM589 RNA, herein designated GAM RNA, to target binding sites on GAM589 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM589 target RNA, herein designated GAM TARGET RNA, into GAM589 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9361] It is appreciated that GAM589 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM589 target genes. The mRNA of each one of this plurality of GAM589 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM589 RNA, herein designated GAM RNA, and which when bound by GAM589 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM589 target proteins.

[9362] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM589 gene, herein designated GAM GENE, on one or more GAM589 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9363] It is yet further appreciated that specific functions, and accordingly utilities, of GAM589 correlate with, and may be deduced from, the identity of the target genes which GAM589 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9364] Nucleotide sequences of the GAM589 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM589 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM589 are further described hereinbelow with reference to Table Table1.

[9365] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM589 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9366] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 590 (GAM590) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9367] GAM590 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM590 was detected is described hereinabove with reference to Figs. 2-8.

[9368] GAM590 gene, herein designated GAM GENE, and GAM590 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9369] GAM590 gene, herein designated GAM GENE, encodes a GAM590 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM590 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM590 precursor RNA is designated SEQ ID:563, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:563 is located at position 6294508 relative to contig NT_024981.11, on chromosome 18.

[9370] GAM590 has a highly conserved, expressed mouse ho-

molog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98953, which mouse homolog is detected in mouse EST accession BE198095.1.

[9371] GAM590 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9372] An enzyme complex designated DICER COMPLEX, dices the GAM590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM590 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM590 RNA is designated SEQ ID:2239, and is provided hereinbelow with reference to the sequence listing part.

[9373] GAM590 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM590 target RNA, herein designated GAM TARGET RNA. GAM590 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9374] GAM590 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM590 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM590 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM590 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM590 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9375] The complementary binding of GAM590 RNA, herein designated GAM RNA, to target binding sites on GAM590 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM590 target RNA, herein designated GAM TARGET RNA, into GAM590 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9376] It is appreciated that GAM590 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM590 target genes. The mRNA of each one of this plurality of GAM590 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM590 RNA, herein designated GAM RNA, and which when bound by GAM590 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM590 target proteins.

[9377] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM590 gene, herein designated GAM GENE, on one or more GAM590 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9378] It is yet further appreciated that specific functions, and accordingly utilities, of GAM590 correlate with, and may be deduced from, the identity of the target genes which GAM590 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9379] Nucleotide sequences of the GAM590 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM590 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM590 are further described hereinbelow with reference to Table Table1.

[9380] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM590 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9381] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 591 (GAM591) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9382] GAM591 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM591 was detected is described hereinabove with reference to Figs. 2-8.

[9383] GAM591 gene, herein designated GAM GENE, and GAM591 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9384] GAM591 gene, herein designated GAM GENE, encodes a GAM591 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM591 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM591 precursor RNA is designated SEQ ID:564, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:564 is located at position 424570 relative to contig NT_035431.2, on chromosome 17.

[9385] GAM591 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[9386] An enzyme complex designated DICER COMPLEX, dices the GAM591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM591 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM591 RNA is designated SEQ ID:2240, and is provided hereinbelow with reference to the sequence listing part.

[9387] GAM591 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM591 target RNA, herein designated GAM TARGET RNA. GAM591 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9388] GAM591 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM591 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM591 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM591 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM591 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9389] The complementary binding of GAM591 RNA, herein designated GAM RNA, to target binding sites on GAM591 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM591 target RNA, herein designated GAM TARGET RNA, into GAM591 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9390] It is appreciated that GAM591 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM591 target genes. The mRNA of each one of this plurality of GAM591 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM591 RNA, herein designated GAM RNA, and which when bound by GAM591 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM591 target proteins.

[9391] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM591 gene, herein designated GAM GENE, on one or more GAM591 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9392] It is yet further appreciated that specific functions, and accordingly utilities, of GAM591 correlate with, and may be deduced from, the identity of the target genes which GAM591 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9393] Nucleotide sequences of the GAM591 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM591 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM591 are further described hereinbelow with reference to Table Table1.

[9394] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM591 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9395] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 592 (GAM592) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9396] GAM592 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM592 was detected is described hereinabove with reference to Figs. 2-8.

[9397] GAM592 gene, herein designated GAM GENE, and GAM592 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9398] GAM592 gene, herein designated GAM GENE, encodes a GAM592 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM592 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM592 precursor RNA is designated SEQ ID:565, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:565 is located at position 2554140 relative to con-

tig NT_004852.13, on chromosome 1.

[9399] GAM592 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9400] An enzyme complex designated DICER COMPLEX, dices the GAM592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM592 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM592 RNA is designated SEQ ID:2241, and is provided hereinbelow with reference to the sequence listing part.

[9401] GAM592 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM592 target RNA, herein designated GAM TARGET RNA.

GAM592 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9402] GAM592 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM592 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM592 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM592 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM592 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9403] The complementary binding of GAM592 RNA, herein designated GAM RNA, to target binding sites on GAM592 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM592 target RNA, herein designated GAM TARGET RNA, into GAM592 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9404] It is appreciated that GAM592 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM592 target genes. The mRNA of each one of this plurality of GAM592 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM592 RNA, herein designated GAM RNA, and which when bound by GAM592 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM592 target proteins.

[9405] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM592 gene, herein designated GAM GENE, on one or more GAM592 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9406] It is yet further appreciated that specific functions, and accordingly utilities, of GAM592 correlate with, and may be deduced from, the identity of the target genes which GAM592 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9407] Nucleotide sequences of the GAM592 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM592 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM592 are further described hereinbelow with reference to Table Table1.

[9408] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM592 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9409] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 593 (GAM593) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9410] GAM593 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM593 was detected is described hereinabove with reference to Figs. 2-8.

[9411] GAM593 gene, herein designated GAM GENE, and GAM593 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9412] GAM593 gene, herein designated GAM GENE, encodes a GAM593 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM593 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM593 precursor RNA is designated SEQ ID:566, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:566 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[9413] GAM593 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9414] An enzyme complex designated DICER COMPLEX, dices the GAM593 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM593 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM593 RNA is designated SEQ ID:2242, and is provided hereinbelow with reference to the sequence listing part.

[9415] GAM593 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM593 target RNA, herein designated GAM TARGET RNA. GAM593 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9416] GAM593 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM593 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM593 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM593 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM593 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9417] The complementary binding of GAM593 RNA, herein designated GAM RNA, to target binding sites on GAM593 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM593 target RNA, herein designated GAM TARGET RNA, into GAM593 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9418] It is appreciated that GAM593 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM593 target genes. The mRNA of each one of this plurality of GAM593 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM593 RNA, herein designated GAM RNA, and which when bound by GAM593 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM593 target proteins.

[9419] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM593 gene, herein designated GAM GENE, on one or more GAM593 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9420] It is yet further appreciated that specific functions, and accordingly utilities, of GAM593 correlate with, and may be deduced from, the identity of the target genes which GAM593 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9421] Nucleotide sequences of the GAM593 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM593 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM593 are further described hereinbelow with reference to Table Table1.

[9422] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM593 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9423] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

594 (GAM594) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9424] GAM594 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM594 was detected is described hereinabove with reference to Figs. 2-8.

[9425] GAM594 gene, herein designated GAM GENE, and GAM594 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9426] GAM594 gene, herein designated GAM GENE, encodes a GAM594 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM594 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM594 precursor RNA is designated SEQ ID:567, and is provided hereinbelow with reference to the sequence listing part.

[9427] GAM594 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9428] An enzyme complex designated DICER COMPLEX, dices the GAM594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM594 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM594 RNA is designated SEQ ID:2243, and is provided hereinbelow with reference to the sequence listing part.

[9429] GAM594 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM594 target RNA, herein designated GAM TARGET RNA. GAM594 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9430] GAM594 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM594 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM594 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM594 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM594 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9431] The complementary binding of GAM594 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM594 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM594 target RNA, herein designated GAM TARGET RNA, into GAM594 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9432] It is appreciated that GAM594 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM594 target genes. The mRNA of each one of this plurality of GAM594 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM594 RNA, herein designated GAM RNA, and which when bound by GAM594 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM594 target proteins.

[9433] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM594 gene, herein designated GAM GENE, on one or more GAM594 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9434] It is yet further appreciated that specific functions, and accordingly utilities, of GAM594 correlate with, and may be deduced from, the identity of the target genes which GAM594 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9435] Nucleotide sequences of the GAM594 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM594 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM594 are further described hereinbelow with reference to Table Table1.

[9436] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM594 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9437] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 595 (GAM595) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9438] GAM595 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM595 was detected is described hereinabove with reference to Figs. 2-8.

[9439] GAM595 gene, herein designated GAM GENE, and GAM595 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9440] GAM595 gene, herein designated GAM GENE, encodes a GAM595 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM595 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM595 precursor RNA is designated SEQ ID:568, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:568 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[9441] GAM595 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9442] An enzyme complex designated DICER COMPLEX, dices the GAM595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM595 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM595 RNA is designated SEQ ID:2244, and is provided hereinbelow with reference to the sequence listing part.

[9443] GAM595 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM595 target RNA, herein designated GAM TARGET RNA. GAM595 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9444] GAM595 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM595 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM595 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM595 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM595 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9445] The complementary binding of GAM595 RNA, herein designated GAM RNA, to target binding sites on GAM595 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM595 target RNA, herein designated GAM TARGET RNA, into GAM595 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9446] It is appreciated that GAM595 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM595 target genes. The mRNA of each one of this plurality of GAM595 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM595 RNA,

herein designated GAM RNA, and which when bound by GAM595 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM595 target proteins.

[9447] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM595 gene, herein designated GAM GENE, on one or more GAM595 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9448] It is yet further appreciated that specific functions, and accordingly utilities, of GAM595 correlate with, and may be deduced from, the identity of the target genes which

GAM595 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9449] Nucleotide sequences of the GAM595 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM595 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM595 are further described hereinbelow with reference to Table Table1.

[9450] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM595 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9451] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 596 (GAM596) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9452] GAM596 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM596 was detected is described hereinabove with reference to Figs. 2-8.

[9453] GAM596 gene, herein designated GAM GENE, and GAM596 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9454] GAM596 gene, herein designated GAM GENE, encodes a GAM596 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM596 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM596 precursor RNA is designated SEQ ID:569, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:569 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[9455] GAM596 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9456] An enzyme complex designated DICER COMPLEX, dices the GAM596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM596 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM596 RNA is designated SEQ ID:2245, and is provided hereinbelow with reference to the sequence listing part.

[9457] GAM596 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM596 target RNA, herein designated GAM TARGET RNA. GAM596 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9458] GAM596 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM596 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM596 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM596 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM596 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9459] The complementary binding of GAM596 RNA, herein designated GAM RNA, to target binding sites on GAM596 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM596 target RNA, herein designated GAM TARGET RNA, into GAM596 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9460] It is appreciated that GAM596 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM596 target genes. The mRNA of each one of this plurality of GAM596 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM596 RNA, herein designated GAM RNA, and which when bound by GAM596 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM596 target proteins.

[9461] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM596 gene, herein designated GAM GENE, on one or more GAM596 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9462] It is yet further appreciated that specific functions, and accordingly utilities, of GAM596 correlate with, and may be deduced from, the identity of the target genes which GAM596 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9463] Nucleotide sequences of the GAM596 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM596 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM596 are further described hereinbelow with reference to Table Table1.

[9464] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM596 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9465] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 597 (GAM597) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9466] GAM597 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM597 was detected is described hereinabove with reference to Figs. 2-8.

[9467] GAM597 gene, herein designated GAM GENE, and GAM597 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9468] GAM597 gene, herein designated GAM GENE, encodes a GAM597 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM597 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM597 precursor RNA is designated SEQ ID:570, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:570 is located at position 4256971 relative to contig NT_008046.11, on chromosome 8.

[9469] GAM597 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99359, which mouse homolog is detected in mouse EST accession AW476224.1.

[9470] GAM597 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9471] An enzyme complex designated DICER COMPLEX, dices the GAM597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM597 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM597 RNA is designated SEQ ID:2246, and is provided hereinbelow with reference to the sequence listing part.

[9472] GAM597 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM597 target RNA, herein designated GAM TARGET RNA. GAM597 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9473] GAM597 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM597 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM597 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM597 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM597 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9474] The complementary binding of GAM597 RNA, herein designated GAM RNA, to target binding sites on GAM597 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM597 target RNA, herein designated GAM TARGET RNA, into GAM597 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9475] It is appreciated that GAM597 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM597 target genes. The mRNA of each one of this plurality of GAM597 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM597 RNA, herein designated GAM RNA, and which when bound by GAM597 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM597 target proteins.

[9476] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM597 gene, herein designated GAM GENE, on one or more GAM597 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9477] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM597 correlate with, and may be deduced from, the identity of the target genes which GAM597 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9478] Nucleotide sequences of the GAM597 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM597 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM597 are further described hereinbelow with reference to Table Table1.

[9479] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM597 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9480] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 598 (GAM598) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9481] GAM598 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM598 was detected is described hereinabove with reference to Figs. 2-8.

[9482] GAM598 gene, herein designated GAM GENE, and GAM598 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9483] GAM598 gene, herein designated GAM GENE, encodes a GAM598 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM598 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM598 precursor RNA is designated SEQ ID:571, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:571 is located at position 65722 relative to contig NT_010755.11, on chromosome 17.

[9484] GAM598 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9485] An enzyme complex designated DICER COMPLEX, dices the GAM598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM598 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM598 RNA is designated SEQ ID:2247, and is provided hereinbelow with reference to the sequence listing part.

[9486] GAM598 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM598 target RNA, herein designated GAM TARGET RNA.
GAM598 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[9487] GAM598 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM598 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM598 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM598 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM598 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9488] The complementary binding of GAM598 RNA, herein designated GAM RNA, to target binding sites on GAM598 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM598 target RNA, herein designated GAM TARGET RNA, into GAM598 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9489] It is appreciated that GAM598 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM598 target genes. The mRNA of each one of this plurality of GAM598 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM598 RNA, herein designated GAM RNA, and which when bound by GAM598 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM598 target proteins.

[9490] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM598 gene, herein designated GAM GENE, on one or more GAM598 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9491] It is yet further appreciated that specific functions, and accordingly utilities, of GAM598 correlate with, and may be deduced from, the identity of the target genes which GAM598 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9492] Nucleotide sequences of the GAM598 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM598 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM598 are further described hereinbelow with reference to Table Table1.

[9493] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM598 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9494] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 599 (GAM599) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9495] GAM599 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM599 was detected is described hereinabove with reference to Figs. 2-8.

[9496] GAM599 gene, herein designated GAM GENE, and GAM599 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9497] GAM599 gene, herein designated GAM GENE, encodes a GAM599 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM599 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM599 precursor RNA is designated SEQ ID:572, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:572 is located at position 7678827 relative to contig NT_004852.13, on chromosome 1.

[9498] GAM599 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9499] An enzyme complex designated DICER COMPLEX, dices the GAM599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM599 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM599 RNA is designated SEQ ID:2248, and is provided hereinbelow with reference to the sequence listing part.

[9500] GAM599 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM599 target RNA, herein designated GAM TARGET RNA. GAM599 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9501] GAM599 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM599 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM599 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM599 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM599 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9502] The complementary binding of GAM599 RNA, herein designated GAM RNA, to target binding sites on GAM599 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM599 target RNA, herein designated GAM TARGET RNA, into GAM599 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9503] It is appreciated that GAM599 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM599 target genes. The mRNA of each one of this plurality of GAM599 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM599 RNA, herein designated GAM RNA, and which when bound by

GAM599 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM599 target proteins.

[9504] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM599 gene, herein designated GAM GENE, on one or more GAM599 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9505] It is yet further appreciated that specific functions, and accordingly utilities, of GAM599 correlate with, and may be deduced from, the identity of the target genes which GAM599 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[9506] Nucleotide sequences of the GAM599 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM599 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM599 are further described hereinbelow with reference to Table Table1.

[9507] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM599 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9508] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 600 (GAM600) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9509] GAM600 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM600 was detected is described hereinabove

with reference to Figs. 2-8.

[9510] GAM600 gene, herein designated GAM GENE, and GAM600 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9511] GAM600 gene, herein designated GAM GENE, encodes a GAM600 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM600 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM600 precursor RNA is designated SEQ ID:573, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:573 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[9512] GAM600 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[9513] SEQ ID:99474 detected in mouse EST Accession AA671455.1.

[9514] SEQ ID:99475 detected in mouse EST Accession

BE943987.1.

[9515] SEQ ID:99476 detected in mouse EST Accession BE691447.1.

[9516] SEQ ID:99477 detected in mouse EST Accession BG808025.1.

[9517] SEQ ID:99478 detected in mouse EST Accession BG808010.1.

[9518] SEQ ID:99479 detected in mouse EST Accession BG807850.1.

[9519] SEQ ID:99480 detected in mouse EST Accession BG805970.1.

[9520] SEQ ID:99481 detected in mouse EST Accession BG145596.1.

[9521] SEQ ID:99482 detected in mouse EST Accession BE692802.1.

[9522] SEQ ID:99483 detected in mouse EST Accession AW208601.1.

[9523] SEQ ID:99484 detected in mouse EST Accession BB610842.1.

[9524] SEQ ID:99485 detected in mouse EST Accession AA144533.1.

[9525] SEQ ID:99486 detected in mouse EST Accession AW824753.1.

[9526] SEQ ID:99487 detected in mouse EST Accession BE691413.1.

[9527] SEQ ID:99497 detected in mouse EST Accession BB609859.1.

[9528] GAM600 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9529] An enzyme complex designated DICER COMPLEX, dices the GAM600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM600 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM600 RNA is designated SEQ ID:2249, and is provided hereinbelow with reference to the sequence listing part.

[9530] GAM600 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM600 target RNA, herein designated GAM TARGET RNA. GAM600 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9531] GAM600 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM600 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM600 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM600 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM600 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9532] The complementary binding of GAM600 RNA, herein designated GAM RNA, to target binding sites on GAM600 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM600 target RNA, herein designated GAM TARGET RNA, into GAM600 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9533] It is appreciated that GAM600 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM600 target genes. The mRNA of each one of this plurality of GAM600 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM600 RNA, herein designated GAM RNA, and which when bound by GAM600 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM600 target proteins.

[9534] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM600 gene, herein designated GAM GENE, on one or more GAM600 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9535] It is yet further appreciated that specific functions, and accordingly utilities, of GAM600 correlate with, and may be deduced from, the identity of the target genes which GAM600 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9536] Nucleotide sequences of the GAM600 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM600 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM600 are further described hereinbelow with reference to Table Table1.

[9537] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM600 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9538] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 601 (GAM601) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9539] GAM601 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM601 was detected is described hereinabove with reference to Figs. 2-8.

[9540] GAM601 gene, herein designated GAM GENE, and GAM601 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9541] GAM601 gene, herein designated GAM GENE, encodes a GAM601 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM601 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM601 precursor RNA is designated SEQ ID:574, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:574 is located at position 989877 relative to contig NT_023666.13, on chromosome 8.

[9542] GAM601 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[9543] An enzyme complex designated DICER COMPLEX, dices the GAM601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM601 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM601 RNA is designated SEQ ID:2250, and is provided hereinbelow with reference to the sequence listing part.

[9544] GAM601 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM601 target RNA, herein designated GAM TARGET RNA. GAM601 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9545] GAM601 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM601 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM601 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM601 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM601 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9546] The complementary binding of GAM601 RNA, herein designated GAM RNA, to target binding sites on GAM601 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM601 target RNA, herein designated GAM TARGET RNA, into GAM601 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9547] It is appreciated that GAM601 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM601 target genes. The mRNA of each one of this plurality of GAM601 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM601 RNA, herein designated GAM RNA, and which when bound by GAM601 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM601 target proteins.

[9548] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM601 gene, herein designated GAM GENE, on one or more GAM601 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9549] It is yet further appreciated that specific functions, and accordingly utilities, of GAM601 correlate with, and may be deduced from, the identity of the target genes which GAM601 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9550] Nucleotide sequences of the GAM601 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM601 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM601 are further described hereinbelow with reference to Table Table1.

[9551] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM601 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9552] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 602 (GAM602) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9553] GAM602 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM602 was detected is described hereinabove with reference to Figs. 2-8.

[9554] GAM602 gene, herein designated GAM GENE, and GAM602 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9555] GAM602 gene, herein designated GAM GENE, encodes a GAM602 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM602 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM602 precursor RNA is designated SEQ ID:575, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:575 is located at position 3434864 relative to con-

tig NT_009714.13, on chromosome 12.

[9556] GAM602 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99502, which mouse homolog is detected in mouse EST accession BG288438.1.

[9557] GAM602 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9558] An enzyme complex designated DICER COMPLEX, dices the GAM602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM602 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM602 RNA is designated SEQ ID:2251, and is provided hereinbelow with reference to the sequence listing part.

[9559] GAM602 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM602 target RNA, herein designated GAM TARGET RNA. GAM602 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9560] GAM602 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM602 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM602 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM602 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM602 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9561] The complementary binding of GAM602 RNA, herein designated GAM RNA, to target binding sites on GAM602 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM602 target RNA, herein designated GAM TARGET RNA, into GAM602 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9562] It is appreciated that GAM602 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM602 target genes. The mRNA of each one of this plurality of GAM602 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM602 RNA,

herein designated GAM RNA, and which when bound by GAM602 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM602 target proteins.

[9563] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM602 gene, herein designated GAM GENE, on one or more GAM602 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9564] It is yet further appreciated that specific functions, and accordingly utilities, of GAM602 correlate with, and may be deduced from, the identity of the target genes which

GAM602 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9565] Nucleotide sequences of the GAM602 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM602 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM602 are further described hereinbelow with reference to Table Table1.

[9566] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM602 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9567] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 603 (GAM603) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9568] GAM603 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM603 was detected is described hereinabove with reference to Figs. 2-8.

[9569] GAM603 gene, herein designated GAM GENE, and GAM603 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9570] GAM603 gene, herein designated GAM GENE, encodes a GAM603 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM603 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM603 precursor RNA is designated SEQ ID:576, and is provided hereinbelow with reference to the sequence listing part.

[9571] GAM603 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[9572] SEQ ID:99507 detected in mouse EST Accession BI659161.1.

[9573] SEQ ID:99512 detected in mouse EST Accession BI690616.1.

[9574] SEQ ID:99513 detected in mouse EST Accession BI688304.1.

[9575] GAM603 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM603 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9576] An enzyme complex designated DICER COMPLEX, dices the GAM603 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM603 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM603 RNA is designated SEQ ID:2252, and is provided hereinbelow with reference to the sequence listing part.

[9577] GAM603 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM603 target RNA, herein designated GAM TARGET RNA. GAM603 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9578] GAM603 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM603 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM603 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM603 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM603

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9579] The complementary binding of GAM603 RNA, herein designated GAM RNA, to target binding sites on GAM603 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM603 target RNA, herein designated GAM TARGET RNA, into GAM603 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9580] It is appreciated that GAM603 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM603 target genes. The mRNA of each one of this plurality of GAM603 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM603 RNA, herein designated GAM RNA, and which when bound by GAM603 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM603 target proteins.

[9581] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM603 gene, herein designated GAM GENE, on one or more GAM603 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9582] It is yet further appreciated that specific functions, and accordingly utilities, of GAM603 correlate with, and may be deduced from, the identity of the target genes which GAM603 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9583] Nucleotide sequences of the GAM603 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM603 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM603 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM603 are further described hereinbelow with reference to Table Table1.

[9584] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM603 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9585] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 604 (GAM604) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9586] GAM604 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM604 was detected is described hereinabove with reference to Figs. 2-8.

[9587] GAM604 gene, herein designated GAM GENE, and GAM604 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[9588] GAM604 gene, herein designated GAM GENE, encodes a GAM604 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM604 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM604 precursor RNA is designated SEQ ID:577, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:577 is located at position 1235058 relative to contig NT_009526.11, on chromosome 12.

[9589] GAM604 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[9590] SEQ ID:100038 detected in mouse EST Accession AI326210.1.

[9591] SEQ ID:100039 detected in mouse EST Accession BI965652.1.

[9592] SEQ ID:100064 detected in mouse EST Accession BI965972.1.

[9593] GAM604 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9594] An enzyme complex designated DICER COMPLEX, dices the GAM604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM604 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM604 RNA is designated SEQ ID:2253, and is provided hereinbelow with reference to the sequence listing part.

[9595] GAM604 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM604

target RNA, herein designated GAM TARGET RNA.

GAM604 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9596] GAM604 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM604 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM604 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM604 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM604 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9597] The complementary binding of GAM604 RNA, herein designated GAM RNA, to target binding sites on GAM604 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM604 target RNA, herein designated GAM TARGET RNA, into GAM604 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9598] It is appreciated that GAM604 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM604 target genes. The mRNA of each one of this plurality of GAM604 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM604 RNA, herein designated GAM RNA, and which when bound by GAM604 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM604 target proteins.

[9599] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM604 gene, herein designated GAM GENE, on one or more GAM604 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9600] It is yet further appreciated that specific functions, and accordingly utilities, of GAM604 correlate with, and may be deduced from, the identity of the target genes which GAM604 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9601] Nucleotide sequences of the GAM604 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM604 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM604 are further described hereinbelow with reference to Table Table1.

[9602] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM604 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9603] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 605 (GAM605) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9604] GAM605 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM605 was detected is described hereinabove with reference to Figs. 2-8.

[9605] GAM605 gene, herein designated GAM GENE, and GAM605 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9606] GAM605 gene, herein designated GAM GENE, encodes a

GAM605 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM605 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM605 precursor RNA is designated SEQ ID:578, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:578 is located at position 1485137 relative to contig NT_022171.11, on chromosome 2.

[9607] GAM605 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9608] An enzyme complex designated DICER COMPLEX, dices the GAM605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM605 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM605 RNA is designated SEQ ID:2254, and is provided hereinbelow with reference to the sequence listing part.

[9609] GAM605 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM605 target RNA, herein designated GAM TARGET RNA.
GAM605 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9610] GAM605 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM605 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM605 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM605 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM605 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9611] The complementary binding of GAM605 RNA, herein designated GAM RNA, to target binding sites on GAM605 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM605 target RNA, herein designated GAM TARGET RNA, into GAM605 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9612] It is appreciated that GAM605 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM605 target genes. The mRNA of each one of this plurality of GAM605 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM605 RNA, herein designated GAM RNA, and which when bound by GAM605 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM605 target proteins.

[9613] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM605 gene, herein designated GAM GENE, on one or more GAM605 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[9614] It is yet further appreciated that specific functions, and accordingly utilities, of GAM605 correlate with, and may be deduced from, the identity of the target genes which GAM605 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9615] Nucleotide sequences of the GAM605 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM605 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM605 are further described hereinbelow with reference to Table Table1.

[9616] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM605 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9617] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 606 (GAM606) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[9618] GAM606 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM606 was detected is described hereinabove with reference to Figs. 2-8.

[9619] GAM606 gene, herein designated GAM GENE, and GAM606 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9620] GAM606 gene, herein designated GAM GENE, encodes a GAM606 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM606 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM606 precursor RNA is designated SEQ ID:579, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:579 is located at position 2593972 relative to contig NT_008176.13, on chromosome 8.

[9621] GAM606 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9622] An enzyme complex designated DICER COMPLEX, dices the GAM606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM606 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM606 RNA is designated SEQ ID:2255, and is provided hereinbelow with reference to the sequence listing part.

[9623] GAM606 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM606 target RNA, herein designated GAM TARGET RNA. GAM606 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9624] GAM606 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM606 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM606 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM606 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM606 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9625] The complementary binding of GAM606 RNA, herein designated GAM RNA, to target binding sites on GAM606 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM606 target RNA, herein designated GAM TARGET RNA, into GAM606 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9626] It is appreciated that GAM606 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM606 target genes. The mRNA of each one of this plurality of GAM606 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM606 RNA, herein designated GAM RNA, and which when bound by GAM606 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM606 target proteins.

[9627] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM606 gene, herein designated GAM GENE, on one or more GAM606 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9628] It is yet further appreciated that specific functions, and accordingly utilities, of GAM606 correlate with, and may be deduced from, the identity of the target genes which GAM606 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9629] Nucleotide sequences of the GAM606 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM606 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM606 are further described hereinbelow with reference to Table Table1.

[9630] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM606 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9631] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 607 (GAM607) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9632] GAM607 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM607 was detected is described hereinabove with reference to Figs. 2-8.

[9633] GAM607 gene, herein designated GAM GENE, and GAM607 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9634] GAM607 gene, herein designated GAM GENE, encodes a GAM607 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM607 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM607 precursor RNA is designated SEQ ID:580, and is provided hereinbelow with reference to the sequence listing part.

[9635] GAM607 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9636] An enzyme complex designated DICER COMPLEX, dices the GAM607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM607 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM607 RNA is designated SEQ ID:2256, and is provided hereinbelow with reference to the sequence listing part.

[9637] GAM607 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM607 target RNA, herein designated GAM TARGET RNA. GAM607 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9638] GAM607 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM607 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM607 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM607 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM607 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9639] The complementary binding of GAM607 RNA, herein designated GAM RNA, to target binding sites on GAM607 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM607 target RNA, herein designated GAM TARGET RNA, into GAM607 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9640] It is appreciated that GAM607 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM607 target genes. The mRNA of each one of this plurality of GAM607 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM607 RNA, herein designated GAM RNA, and which when bound by

GAM607 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM607 target proteins.

[9641] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM607 gene, herein designated GAM GENE, on one or more GAM607 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9642] It is yet further appreciated that specific functions, and accordingly utilities, of GAM607 correlate with, and may be deduced from, the identity of the target genes which GAM607 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[9643] Nucleotide sequences of the GAM607 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM607 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM607 are further described hereinbelow with reference to Table Table1.

[9644] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM607 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9645] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 608 (GAM608) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9646] GAM608 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM608 was detected is described hereinabove

with reference to Figs. 2-8.

[9647] GAM608 gene, herein designated GAM GENE, and GAM608 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9648] GAM608 gene, herein designated GAM GENE, encodes a GAM608 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM608 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM608 precursor RNA is designated SEQ ID:581, and is provided hereinbelow with reference to the sequence listing part.

[9649] GAM608 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9650] An enzyme complex designated DICER COMPLEX, dices the GAM608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM608 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM608 RNA is designated SEQ ID:2257, and is provided hereinbelow with reference to the sequence listing part.

[9651] GAM608 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM608 target RNA, herein designated GAM TARGET RNA. GAM608 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9652] GAM608 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM608 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM608 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM608 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM608 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9653] The complementary binding of GAM608 RNA, herein designated GAM RNA, to target binding sites on GAM608 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM608 target RNA, herein designated GAM TARGET RNA, into GAM608 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[9654] It is appreciated that GAM608 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM608 target genes. The mRNA of each one of this plurality of GAM608 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM608 RNA, herein designated GAM RNA, and which when bound by GAM608 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM608 target proteins.

[9655] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM608 gene, herein designated GAM GENE, on one or more GAM608 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9656] It is yet further appreciated that specific functions, and accordingly utilities, of GAM608 correlate with, and may be deduced from, the identity of the target genes which GAM608 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9657] Nucleotide sequences of the GAM608 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM608 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM608 are further described hereinbelow with reference to Table Table1.

[9658] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM608 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9659] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 609 (GAM609) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9660] GAM609 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM609 was detected is described hereinabove with reference to Figs. 2-8.

[9661] GAM609 gene, herein designated GAM GENE, and GAM609 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9662] GAM609 gene, herein designated GAM GENE, encodes a GAM609 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM609 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM609 precursor RNA is designated SEQ ID:582, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:582 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[9663] GAM609 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[9664] SEQ ID:98560 detected in mouse EST Accession AA144533.1.

[9665] SEQ ID:98561 detected in mouse EST Accession AA671455.1.

[9666] SEQ ID:98562 detected in mouse EST Accession AW824753.1.

[9667] SEQ ID:98563 detected in mouse EST Accession BE943987.1.

[9668] SEQ ID:98564 detected in mouse EST Accession BE691413.1.

[9669] SEQ ID:98565 detected in mouse EST Accession BE691447.1.

[9670] SEQ ID:98566 detected in mouse EST Accession BG808025.1.

[9671] SEQ ID:98567 detected in mouse EST Accession BG808010.1.

[9672] SEQ ID:98568 detected in mouse EST Accession BG807850.1.

[9673] SEQ ID:98569 detected in mouse EST Accession BG805970.1.

[9674] SEQ ID:98570 detected in mouse EST Accession BG145596.1.

[9675] SEQ ID:98571 detected in mouse EST Accession BE692802.1.

[9676] SEQ ID:98572 detected in mouse EST Accession BB609859.1.

[9677] SEQ ID:98579 detected in mouse EST Accession AW208601.1.

[9678] SEQ ID:98610 detected in mouse EST Accession BB610842.1.

[9679] GAM609 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9680] An enzyme complex designated DICER COMPLEX, dices

the GAM609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM609 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM609 RNA is designated SEQ ID:2258, and is provided hereinbelow with reference to the sequence listing part.

[9681] GAM609 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM609 target RNA, herein designated GAM TARGET RNA.
GAM609 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9682] GAM609 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM609 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM609

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM609 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM609 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9683] The complementary binding of GAM609 RNA, herein designated GAM RNA, to target binding sites on GAM609 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM609 target RNA, herein designated GAM TARGET RNA, into GAM609 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9684] It is appreciated that GAM609 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM609 target genes. The mRNA of each one of this plurality of GAM609 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM609 RNA, herein designated GAM RNA, and which when bound by GAM609 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM609 target proteins.

[9685] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM609 gene, herein designated GAM GENE, on one or more GAM609 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9686] It is yet further appreciated that specific functions, and accordingly utilities, of GAM609 correlate with, and may be deduced from, the identity of the target genes which GAM609 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9687] Nucleotide sequences of the GAM609 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM609 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM609 are further described hereinbelow with reference to Table Table1.

[9688] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM609 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9689] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 610 (GAM610) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9690] GAM610 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM610 was detected is described hereinabove with reference to Figs. 2-8.

[9691] GAM610 gene, herein designated GAM GENE, and GAM610 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9692] GAM610 gene, herein designated GAM GENE, encodes a GAM610 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM610 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM610 precursor RNA is designated SEQ ID:583, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:583 is located at position 1364370 relative to contig NT_035014.2, on chromosome 9.

[9693] GAM610 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9694] An enzyme complex designated DICER COMPLEX, dices the GAM610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM610 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM610 RNA is designated SEQ ID:2259, and is provided hereinbelow with reference to the sequence listing part.

[9695] GAM610 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM610 target RNA, herein designated GAM TARGET RNA.

GAM610 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9696] GAM610 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM610 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM610 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM610 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM610 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9697] The complementary binding of GAM610 RNA, herein designated GAM RNA, to target binding sites on GAM610 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM610 target RNA, herein designated GAM TARGET RNA, into GAM610 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9698] It is appreciated that GAM610 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM610 target genes. The mRNA of each one of this plurality of GAM610 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM610 RNA, herein designated GAM RNA, and which when bound by GAM610 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM610 target proteins.

[9699] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM610 gene, herein designated GAM GENE, on one or more GAM610 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9700] It is yet further appreciated that specific functions, and accordingly utilities, of GAM610 correlate with, and may be deduced from, the identity of the target genes which GAM610 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9701] Nucleotide sequences of the GAM610 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM610 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM610 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM610 are further described hereinbelow with reference to Table Table1.

[9702] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM610 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9703] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 611 (GAM611) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9704] GAM611 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM611 was detected is described hereinabove with reference to Figs. 2-8.

[9705] GAM611 gene, herein designated GAM GENE, and GAM611 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9706] GAM611 gene, herein designated GAM GENE, encodes a GAM611 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM611 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM611 precursor RNA is designated SEQ ID:584, and is provided hereinbelow with reference to the sequence listing part.

[9707] GAM611 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9708] An enzyme complex designated DICER COMPLEX, dices the GAM611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM611 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM611 RNA is designated SEQ ID:2260, and is provided hereinbelow with reference to the sequence listing part.

[9709] GAM611 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM611 target RNA, herein designated GAM TARGET RNA. GAM611 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9710] GAM611 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM611 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM611 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM611 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM611 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9711] The complementary binding of GAM611 RNA, herein designated GAM RNA, to target binding sites on GAM611 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM611 target RNA, herein designated GAM TARGET RNA, into GAM611 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9712] It is appreciated that GAM611 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM611 target genes. The mRNA of each one of this plurality of GAM611 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM611 RNA, herein designated GAM RNA, and which when bound by GAM611 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM611 target proteins.

[9713] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM611 gene, herein designated GAM GENE, on one or more GAM611 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9714] It is yet further appreciated that specific functions, and accordingly utilities, of GAM611 correlate with, and may

be deduced from, the identity of the target genes which GAM611 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9715] Nucleotide sequences of the GAM611 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM611 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM611 are further described hereinbelow with reference to Table Table1.

[9716] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM611 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9717] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 612 (GAM612) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9718] GAM612 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM612 was detected is described hereinabove with reference to Figs. 2-8.

[9719] GAM612 gene, herein designated GAM GENE, and GAM612 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9720] GAM612 gene, herein designated GAM GENE, encodes a GAM612 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM612 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM612 precursor RNA is designated SEQ ID:585, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:585 is located at position 17488567 relative to contig NT_011520.8, on chromosome 22.

[9721] GAM612 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM612 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9722] An enzyme complex designated DICER COMPLEX, dices the GAM612 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM612 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM612 RNA is designated SEQ ID:2261, and is provided hereinbelow with reference to the sequence listing part.

[9723] GAM612 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM612 target RNA, herein designated GAM TARGET RNA. GAM612 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9724] GAM612 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM612 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM612 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM612 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM612 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9725] The complementary binding of GAM612 RNA, herein designated GAM RNA, to target binding sites on GAM612 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM612 target RNA, herein designated GAM TARGET RNA, into GAM612 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9726] It is appreciated that GAM612 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM612 target genes. The mRNA of each one of this plurality of GAM612 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM612 RNA, herein designated GAM RNA, and which when bound by GAM612 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM612 target proteins.

[9727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM612 gene, herein designated GAM GENE, on one or more GAM612 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9728] It is yet further appreciated that specific functions, and accordingly utilities, of GAM612 correlate with, and may be deduced from, the identity of the target genes which GAM612 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9729] Nucleotide sequences of the GAM612 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM612 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM612 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM612 are further described hereinbelow with reference to Table Table1.

[9730] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM612 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9731] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 613 (GAM613) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9732] GAM613 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM613 was detected is described hereinabove with reference to Figs. 2-8.

[9733] GAM613 gene, herein designated GAM GENE, and GAM613 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9734] GAM613 gene, herein designated GAM GENE, encodes a GAM613 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM613 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM613 precursor RNA is desig-

nated SEQ ID:586, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:586 is located at position 2349675 relative to contig NT_021907.13, on chromosome 1.

[9735] GAM613 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9736] An enzyme complex designated DICER COMPLEX, dices the GAM613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM613 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM613 RNA is designated SEQ ID:2262, and is provided hereinbelow with reference to the sequence listing part.

[9737] GAM613 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM613 target RNA, herein designated GAM TARGET RNA. GAM613 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9738] GAM613 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM613 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM613 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM613 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM613 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9739] The complementary binding of GAM613 RNA, herein designated GAM RNA, to target binding sites on GAM613 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM613 target RNA, herein designated GAM TARGET RNA, into GAM613 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9740] It is appreciated that GAM613 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM613 target genes. The mRNA of each one of this plurality of GAM613 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM613 RNA, herein designated GAM RNA, and which when bound by GAM613 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM613 target proteins.

[9741] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM613 gene, herein designated GAM GENE, on one or more GAM613 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9742] It is yet further appreciated that specific functions, and accordingly utilities, of GAM613 correlate with, and may be deduced from, the identity of the target genes which GAM613 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9743] Nucleotide sequences of the GAM613 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM613 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM613 are further described hereinbelow with reference to Table Table1.

[9744] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM613 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9745] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 614 (GAM614) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9746] GAM614 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM614 was detected is described hereinabove with reference to Figs. 2-8.

[9747] GAM614 gene, herein designated GAM GENE, and GAM614 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9748] GAM614 gene, herein designated GAM GENE, encodes a GAM614 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM614 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM614 precursor RNA is designated SEQ ID:587, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:587 is located at position 4531567 relative to contig NT_011657.11, on chromosome X.

[9749] GAM614 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[9750] An enzyme complex designated DICER COMPLEX, dices the GAM614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM614 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM614 RNA is designated SEQ ID:2263, and is provided hereinbelow with reference to the sequence listing part.

[9751] GAM614 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM614 target RNA, herein designated GAM TARGET RNA. GAM614 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9752] GAM614 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM614 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM614 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM614 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM614 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9753] The complementary binding of GAM614 RNA, herein designated GAM RNA, to target binding sites on GAM614 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM614 target RNA, herein designated GAM TARGET RNA, into GAM614 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9754] It is appreciated that GAM614 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM614 target genes. The mRNA of each one of this plurality of GAM614 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM614 RNA, herein designated GAM RNA, and which when bound by GAM614 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM614 target proteins.

[9755] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM614 gene, herein designated GAM GENE, on one or more GAM614 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9756] It is yet further appreciated that specific functions, and accordingly utilities, of GAM614 correlate with, and may be deduced from, the identity of the target genes which GAM614 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9757] Nucleotide sequences of the GAM614 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM614 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM614 are further described hereinbelow with reference to Table Table1.

[9758] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM614 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9759] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 615 (GAM615) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9760] GAM615 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM615 was detected is described hereinabove with reference to Figs. 2-8.

[9761] GAM615 gene, herein designated GAM GENE, and GAM615 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9762] GAM615 gene, herein designated GAM GENE, encodes a GAM615 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM615 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM615 precursor RNA is designated SEQ ID:588, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:588 is located at position 4532539 relative to con-

tig NT_035212.2, on chromosome 12.

[9763] GAM615 has 10 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[9764] SEQ ID:99275 detected in mouse EST Accession AA981127.1.

[9765] SEQ ID:99276 detected in mouse EST Accession BF318901.1.

[9766] SEQ ID:99277 detected in mouse EST Accession AA410034.1.

[9767] SEQ ID:99278 detected in mouse EST Accession BG073066.1.

[9768] SEQ ID:99279 detected in mouse EST Accession BI686879.1.

[9769] SEQ ID:99280 detected in mouse EST Accession BI150489.1.

[9770] SEQ ID:99281 detected in mouse EST Accession BF318900.1.

[9771] SEQ ID:99282 detected in mouse EST Accession BF462203.1.

[9772] SEQ ID:99295 detected in mouse EST Accession

AW548168.1.

[9773] SEQ ID:99296 detected in mouse EST Accession BE570198.1.

[9774] GAM615 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9775] An enzyme complex designated DICER COMPLEX, dices the GAM615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM615 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM615 RNA is designated SEQ ID:2264, and is provided

hereinbelow with reference to the sequence listing part.

[9776] GAM615 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM615 target RNA, herein designated GAM TARGET RNA.
GAM615 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9777] GAM615 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM615 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM615 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM615 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM615 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9778] The complementary binding of GAM615 RNA, herein designated GAM RNA, to target binding sites on GAM615 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM615 target RNA, herein designated GAM TARGET RNA, into GAM615 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9779] It is appreciated that GAM615 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM615 target genes. The mRNA of each one of this plurality of GAM615 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM615 RNA, herein designated GAM RNA, and which when bound by GAM615 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM615 tar-

get proteins.

[9780] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM615 gene, herein designated GAM GENE, on one or more GAM615 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9781] It is yet further appreciated that specific functions, and accordingly utilities, of GAM615 correlate with, and may be deduced from, the identity of the target genes which GAM615 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9782] Nucleotide sequences of the GAM615 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM615 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM615 are further described hereinbelow with reference to Table Table1.

[9783] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM615 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9784] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 616 (GAM616) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9785] GAM616 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM616 was detected is described hereinabove with reference to Figs. 2-8.

[9786] GAM616 gene, herein designated GAM GENE, and

GAM616 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9787] GAM616 gene, herein designated GAM GENE, encodes a GAM616 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM616 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM616 precursor RNA is designated SEQ ID:589, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:589 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[9788] GAM616 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9789] An enzyme complex designated DICER COMPLEX, dices the GAM616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM616 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM616 RNA is designated SEQ ID:2265, and is provided hereinbelow with reference to the sequence listing part.

[9790] GAM616 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM616 target RNA, herein designated GAM TARGET RNA. GAM616 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9791] GAM616 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM616 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM616 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM616 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM616 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9792] The complementary binding of GAM616 RNA, herein designated GAM RNA, to target binding sites on GAM616 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM616 target RNA, herein designated GAM TARGET RNA, into GAM616 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[9793] It is appreciated that GAM616 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM616 target genes. The mRNA of each one of this plurality of GAM616 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM616 RNA, herein designated GAM RNA, and which when bound by GAM616 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM616 target proteins.

[9794] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM616 gene, herein designated GAM GENE, on one or more GAM616 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9795] It is yet further appreciated that specific functions, and accordingly utilities, of GAM616 correlate with, and may be deduced from, the identity of the target genes which GAM616 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9796] Nucleotide sequences of the GAM616 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM616 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM616 are further described hereinbelow with reference to Table Table1.

[9797] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM616 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9798] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 617 (GAM617) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9799] GAM617 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM617 was detected is described hereinabove with reference to Figs. 2-8.

[9800] GAM617 gene, herein designated GAM GENE, and GAM617 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9801] GAM617 gene, herein designated GAM GENE, encodes a GAM617 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM617 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM617 precursor RNA is designated SEQ ID:590, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:590 is located at position 24546770 relative to contig NT_011512.7, on chromosome 21.

[9802] GAM617 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[9803] SEQ ID:99244 detected in mouse EST Accession BG277409.1.

[9804] SEQ ID:99246 detected in mouse EST Accession BE197325.1.

[9805] GAM617 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9806] An enzyme complex designated DICER COMPLEX, dices the GAM617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM617 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM617 RNA is designated SEQ ID:2266, and is provided hereinbelow with reference to the sequence listing part.

[9807] GAM617 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM617 target RNA, herein designated GAM TARGET RNA. GAM617 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9808] GAM617 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM617 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM617 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM617 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM617 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9809] The complementary binding of GAM617 RNA, herein designated GAM RNA, to target binding sites on GAM617 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM617 target RNA, herein designated GAM TARGET RNA, into GAM617 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9810] It is appreciated that GAM617 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM617 target genes. The mRNA of each one of this plu-

rality of GAM617 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM617 RNA, herein designated GAM RNA, and which when bound by GAM617 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM617 target proteins.

[9811] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM617 gene, herein designated GAM GENE, on one or more GAM617 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9812] It is yet further appreciated that specific functions, and accordingly utilities, of GAM617 correlate with, and may be deduced from, the identity of the target genes which GAM617 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9813] Nucleotide sequences of the GAM617 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM617 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM617 are further described hereinbelow with reference to Table Table1.

[9814] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM617 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9815] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 618 (GAM618) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[9816] GAM618 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM618 was detected is described hereinabove with reference to Figs. 2-8.

[9817] GAM618 gene, herein designated GAM GENE, and GAM618 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9818] GAM618 gene, herein designated GAM GENE, encodes a GAM618 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM618 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM618 precursor RNA is designated SEQ ID:591, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:591 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[9819] GAM618 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9820] An enzyme complex designated DICER COMPLEX, dices the GAM618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM618 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM618 RNA is designated SEQ ID:2267, and is provided hereinbelow with reference to the sequence listing part.

[9821] GAM618 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM618 target RNA, herein designated GAM TARGET RNA. GAM618 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9822] GAM618 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM618 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM618 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM618 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM618 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9823] The complementary binding of GAM618 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM618 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM618 target RNA, herein designated GAM TARGET RNA, into GAM618 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9824] It is appreciated that GAM618 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM618 target genes. The mRNA of each one of this plurality of GAM618 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM618 RNA, herein designated GAM RNA, and which when bound by GAM618 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM618 target proteins.

[9825] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM618 gene, herein designated GAM GENE, on one or more GAM618 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9826] It is yet further appreciated that specific functions, and accordingly utilities, of GAM618 correlate with, and may be deduced from, the identity of the target genes which GAM618 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9827] Nucleotide sequences of the GAM618 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM618 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM618 are further described hereinbelow with reference to Table Table1.

[9828] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM618 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9829] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 619 (GAM619) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9830] GAM619 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM619 was detected is described hereinabove with reference to Figs. 2-8.

[9831] GAM619 gene, herein designated GAM GENE, and GAM619 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9832] GAM619 gene, herein designated GAM GENE, encodes a GAM619 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM619 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM619 precursor RNA is designated SEQ ID:592, and is provided hereinbelow with reference to the sequence listing part.

[9833] GAM619 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9834] An enzyme complex designated DICER COMPLEX, dices the GAM619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM619 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM619 RNA is designated SEQ ID:2268, and is provided hereinbelow with reference to the sequence listing part.

[9835] GAM619 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM619 target RNA, herein designated GAM TARGET RNA. GAM619 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9836] GAM619 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM619 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM619 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM619 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM619 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9837] The complementary binding of GAM619 RNA, herein designated GAM RNA, to target binding sites on GAM619 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM619 target RNA, herein designated GAM TARGET RNA, into GAM619 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9838] It is appreciated that GAM619 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM619 target genes. The mRNA of each one of this plurality of GAM619 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM619 RNA, herein designated GAM RNA, and which when bound by GAM619 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM619 target proteins.

[9839] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM619 gene, herein designated GAM GENE, on one or more GAM619 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9840] It is yet further appreciated that specific functions, and accordingly utilities, of GAM619 correlate with, and may be deduced from, the identity of the target genes which GAM619 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9841] Nucleotide sequences of the GAM619 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM619 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM619 are further described hereinbelow with reference to Table Table1.

[9842] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM619 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9843] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 620 (GAM620) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9844] GAM620 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM620 was detected is described hereinabove with reference to Figs. 2-8.

[9845] GAM620 gene, herein designated GAM GENE, and GAM620 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9846] GAM620 gene, herein designated GAM GENE, encodes a GAM620 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM620 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM620 precursor RNA is designated SEQ ID:593, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:593 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[9847] GAM620 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[9848] An enzyme complex designated DICER COMPLEX, dices the GAM620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM620 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM620 RNA is designated SEQ ID:2269, and is provided hereinbelow with reference to the sequence listing part.

[9849] GAM620 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM620 target RNA, herein designated GAM TARGET RNA. GAM620 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9850] GAM620 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM620 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM620 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM620 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM620 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9851] The complementary binding of GAM620 RNA, herein designated GAM RNA, to target binding sites on GAM620 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM620 target RNA, herein designated GAM TARGET RNA, into GAM620 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9852] It is appreciated that GAM620 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM620 target genes. The mRNA of each one of this plurality of GAM620 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM620 RNA, herein designated GAM RNA, and which when bound by GAM620 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM620 target proteins.

[9853] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM620 gene, herein designated GAM GENE, on one or more GAM620 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9854] It is yet further appreciated that specific functions, and accordingly utilities, of GAM620 correlate with, and may be deduced from, the identity of the target genes which GAM620 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9855] Nucleotide sequences of the GAM620 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM620 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM620 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM620 are further described hereinbelow with reference to Table Table1.

[9856] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM620 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9857] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 621 (GAM621) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9858] GAM621 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM621 was detected is described hereinabove with reference to Figs. 2-8.

[9859] GAM621 gene, herein designated GAM GENE, and GAM621 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9860] GAM621 gene, herein designated GAM GENE, encodes a GAM621 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM621 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM621 precursor RNA is designated SEQ ID:594, and is provided hereinbelow with reference to the sequence listing part.

[9861] GAM621 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9862] An enzyme complex designated DICER COMPLEX, dices the GAM621 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM621 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM621 RNA is designated SEQ ID:2270, and is provided hereinbelow with reference to the sequence listing part.

[9863] GAM621 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM621 target RNA, herein designated GAM TARGET RNA.

GAM621 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9864] GAM621 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM621 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM621 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM621 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM621 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9865] The complementary binding of GAM621 RNA, herein designated GAM RNA, to target binding sites on GAM621 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM621 target RNA, herein designated GAM TARGET RNA, into GAM621 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9866] It is appreciated that GAM621 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM621 target genes. The mRNA of each one of this plurality of GAM621 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM621 RNA, herein designated GAM RNA, and which when bound by GAM621 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM621 target proteins.

[9867] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM621 gene, herein designated GAM GENE, on one or more GAM621 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9868] It is yet further appreciated that specific functions, and accordingly utilities, of GAM621 correlate with, and may be deduced from, the identity of the target genes which GAM621 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9869] Nucleotide sequences of the GAM621 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM621 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM621 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM621 are further described hereinbelow with reference to Table Table1.

[9870] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM621 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9871] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 622 (GAM622) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9872] GAM622 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM622 was detected is described hereinabove with reference to Figs. 2-8.

[9873] GAM622 gene, herein designated GAM GENE, and GAM622 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9874] GAM622 gene, herein designated GAM GENE, encodes a GAM622 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM622 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM622 precursor RNA is designated SEQ ID:595, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:595 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[9875] GAM622 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[9876] SEQ ID:99247 detected in mouse EST Accession AA144533.1.

[9877] SEQ ID:99248 detected in mouse EST Accession BE691447.1.

[9878] SEQ ID:99249 detected in mouse EST Accession AW208601.1.

[9879] SEQ ID:99250 detected in mouse EST Accession BB610842.1.

[9880] SEQ ID:99251 detected in mouse EST Accession

BB609859.1.

[9881] SEQ ID:99252 detected in mouse EST Accession AA671455.1.

[9882] SEQ ID:99253 detected in mouse EST Accession AW824753.1.

[9883] SEQ ID:99254 detected in mouse EST Accession BE691413.1.

[9884] SEQ ID:99255 detected in mouse EST Accession BG145596.1.

[9885] SEQ ID:99256 detected in mouse EST Accession BE692802.1.

[9886] SEQ ID:99257 detected in mouse EST Accession BE943987.1.

[9887] SEQ ID:99258 detected in mouse EST Accession BG808025.1.

[9888] SEQ ID:99259 detected in mouse EST Accession BG808010.1.

[9889] SEQ ID:99260 detected in mouse EST Accession BG807850.1.

[9890] SEQ ID:99261 detected in mouse EST Accession BG805970.1.

[9891] GAM622 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM622 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9892] An enzyme complex designated DICER COMPLEX, dices the GAM622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM622 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM622 RNA is designated SEQ ID:2271, and is provided hereinbelow with reference to the sequence listing part.

[9893] GAM622 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM622 target RNA, herein designated GAM TARGET RNA. GAM622 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9894] GAM622 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM622 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM622 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM622 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM622 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[9895] The complementary binding of GAM622 RNA, herein designated GAM RNA, to target binding sites on GAM622 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM622 target RNA, herein designated GAM TARGET RNA, into GAM622 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9896] It is appreciated that GAM622 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM622 target genes. The mRNA of each one of this plurality of GAM622 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM622 RNA, herein designated GAM RNA, and which when bound by GAM622 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM622 target proteins.

[9897] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM622 gene, herein designated GAM GENE, on one or

more GAM622 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9898] It is yet further appreciated that specific functions, and accordingly utilities, of GAM622 correlate with, and may be deduced from, the identity of the target genes which GAM622 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9899] Nucleotide sequences of the GAM622 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM622 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM622 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM622 are further de-

scribed hereinbelow with reference to Table Table1.

[9900] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM622 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9901] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 623 (GAM623) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9902] GAM623 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM623 was detected is described hereinabove with reference to Figs. 2-8.

[9903] GAM623 gene, herein designated GAM GENE, and GAM623 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9904] GAM623 gene, herein designated GAM GENE, encodes a GAM623 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM623 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM623 precursor RNA is designated SEQ ID:596, and is provided hereinbelow with reference to the sequence listing part.

[9905] GAM623 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99283, which mouse homolog is detected in mouse EST accession BG963903.1.

[9906] GAM623 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9907] An enzyme complex designated DICER COMPLEX, dices the GAM623 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM623 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM623 RNA is designated SEQ ID:2272, and is provided hereinbelow with reference to the sequence listing part.

[9908] GAM623 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM623 target RNA, herein designated GAM TARGET RNA. GAM623 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9909] GAM623 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM623 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM623 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM623 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM623 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9910] The complementary binding of GAM623 RNA, herein designated GAM RNA, to target binding sites on GAM623 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM623 target RNA, herein designated GAM TARGET RNA, into GAM623 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9911] It is appreciated that GAM623 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM623 target genes. The mRNA of each one of this plurality of GAM623 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM623 RNA, herein designated GAM RNA, and which when bound by GAM623 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM623 target proteins.

[9912] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM623 gene, herein designated GAM GENE, on one or more GAM623 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9913] It is yet further appreciated that specific functions, and accordingly utilities, of GAM623 correlate with, and may be deduced from, the identity of the target genes which GAM623 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9914] Nucleotide sequences of the GAM623 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM623 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM623 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM623 are further described hereinbelow with reference to Table Table1.

[9915] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM623 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9916] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

624 (GAM624) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9917] GAM624 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM624 was detected is described hereinabove with reference to Figs. 2-8.

[9918] GAM624 gene, herein designated GAM GENE, and GAM624 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9919] GAM624 gene, herein designated GAM GENE, encodes a GAM624 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM624 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM624 precursor RNA is designated SEQ ID:597, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:597 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[9920] GAM624 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM624 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9921] An enzyme complex designated DICER COMPLEX, dices the GAM624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM624 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM624 RNA is designated SEQ ID:2273, and is provided hereinbelow with reference to the sequence listing part.

[9922] GAM624 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM624 target RNA, herein designated GAM TARGET RNA. GAM624 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9923] GAM624 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM624 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM624 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM624 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM624 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[9924] The complementary binding of GAM624 RNA, herein designated GAM RNA, to target binding sites on GAM624 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM624 target RNA, herein designated GAM TARGET RNA, into GAM624 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9925] It is appreciated that GAM624 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM624 target genes. The mRNA of each one of this plurality of GAM624 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM624 RNA, herein designated GAM RNA, and which when bound by GAM624 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM624 target proteins.

[9926] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM624 gene, herein designated GAM GENE, on one or

more GAM624 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9927] It is yet further appreciated that specific functions, and accordingly utilities, of GAM624 correlate with, and may be deduced from, the identity of the target genes which GAM624 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9928] Nucleotide sequences of the GAM624 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM624 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM624 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM624 are further de-

scribed hereinbelow with reference to Table Table1.

[9929] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM624 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9930] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 625 (GAM625) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9931] GAM625 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM625 was detected is described hereinabove with reference to Figs. 2-8.

[9932] GAM625 gene, herein designated GAM GENE, and GAM625 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9933] GAM625 gene, herein designated GAM GENE, encodes a GAM625 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM625 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM625 precursor RNA is designated SEQ ID:598, and is provided hereinbelow with reference to the sequence listing part.

[9934] GAM625 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9935] An enzyme complex designated DICER COMPLEX, dices the GAM625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM625 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM625 RNA is designated SEQ ID:2274, and is provided hereinbelow with reference to the sequence listing part.

[9936] GAM625 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM625 target RNA, herein designated GAM TARGET RNA. GAM625 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9937] GAM625 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM625 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM625 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM625 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM625 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9938] The complementary binding of GAM625 RNA, herein designated GAM RNA, to target binding sites on GAM625 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM625 target RNA, herein designated GAM TARGET RNA, into GAM625 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9939] It is appreciated that GAM625 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM625 target genes. The mRNA of each one of this plurality of GAM625 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM625 RNA,

herein designated GAM RNA, and which when bound by GAM625 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM625 target proteins.

[9940] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM625 gene, herein designated GAM GENE, on one or more GAM625 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9941] It is yet further appreciated that specific functions, and accordingly utilities, of GAM625 correlate with, and may be deduced from, the identity of the target genes which

GAM625 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9942] Nucleotide sequences of the GAM625 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM625 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM625 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM625 are further described hereinbelow with reference to Table Table1.

[9943] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM625 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9944] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 626 (GAM626) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9945] GAM626 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM626 was detected is described hereinabove with reference to Figs. 2-8.

[9946] GAM626 gene, herein designated GAM GENE, and GAM626 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9947] GAM626 gene, herein designated GAM GENE, encodes a GAM626 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM626 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM626 precursor RNA is designated SEQ ID:599, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:599 is located at position 6065304 relative to contig NT_023974.13, on chromosome 9.

[9948] GAM626 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9949] An enzyme complex designated DICER COMPLEX, dices the GAM626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM626 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM626 RNA is designated SEQ ID:2275, and is provided hereinbelow with reference to the sequence listing part.

[9950] GAM626 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM626 target RNA, herein designated GAM TARGET RNA. GAM626 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9951] GAM626 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM626 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM626 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM626 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM626 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9952] The complementary binding of GAM626 RNA, herein designated GAM RNA, to target binding sites on GAM626 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM626 target RNA, herein designated GAM TARGET RNA, into GAM626 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9953] It is appreciated that GAM626 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM626 target genes. The mRNA of each one of this plurality of GAM626 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM626 RNA, herein designated GAM RNA, and which when bound by GAM626 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM626 target proteins.

[9954] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM626 gene, herein designated GAM GENE, on one or more GAM626 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9955] It is yet further appreciated that specific functions, and accordingly utilities, of GAM626 correlate with, and may be deduced from, the identity of the target genes which GAM626 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9956] Nucleotide sequences of the GAM626 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM626 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM626 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM626 are further described hereinbelow with reference to Table Table1.

[9957] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM626 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9958] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 627 (GAM627) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9959] GAM627 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM627 was detected is described hereinabove with reference to Figs. 2-8.

[9960] GAM627 gene, herein designated GAM GENE, and GAM627 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9961] GAM627 gene, herein designated GAM GENE, encodes a GAM627 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM627 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM627 precursor RNA is designated SEQ ID:600, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:600 is located at position 280476 relative to contig NT_007758.8, on chromosome 7.

[9962] GAM627 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9963] An enzyme complex designated DICER COMPLEX, dices the GAM627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM627 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM627 RNA is designated SEQ ID:2276, and is provided

hereinbelow with reference to the sequence listing part.

[9964] GAM627 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM627 target RNA, herein designated GAM TARGET RNA.
GAM627 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9965] GAM627 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM627 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM627 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM627 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM627 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9966] The complementary binding of GAM627 RNA, herein designated GAM RNA, to target binding sites on GAM627 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM627 target RNA, herein designated GAM TARGET RNA, into GAM627 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9967] It is appreciated that GAM627 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM627 target genes. The mRNA of each one of this plurality of GAM627 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM627 RNA, herein designated GAM RNA, and which when bound by GAM627 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM627 tar-

get proteins.

[9968] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM627 gene, herein designated GAM GENE, on one or more GAM627 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9969] It is yet further appreciated that specific functions, and accordingly utilities, of GAM627 correlate with, and may be deduced from, the identity of the target genes which GAM627 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9970] Nucleotide sequences of the GAM627 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM627 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM627 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM627 are further described hereinbelow with reference to Table Table1.

[9971] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM627 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9972]

[9973] Fig. 8 further provides a conceptual description of a novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 628 (GAM628) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9974] GAM628 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM628 was detected is described hereinabove with reference to Figs. 2-8.

[9975] GAM628 gene, herein designated GAM GENE, and GAM628 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9976] GAM628 gene, herein designated GAM GENE, encodes a GAM628 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM628 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM628 precursor RNA is designated SEQ ID:601, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:601 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[9977] GAM628 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[9978] An enzyme complex designated DICER COMPLEX, dices the GAM628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM628 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM628 RNA is designated SEQ ID:2277, and is provided hereinbelow with reference to the sequence listing part.

[9979] GAM628 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM628 target RNA, herein designated GAM TARGET RNA. GAM628 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9980] GAM628 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM628 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM628 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM628 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM628 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9981] The complementary binding of GAM628 RNA, herein designated GAM RNA, to target binding sites on GAM628 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM628 target RNA, herein designated GAM TARGET RNA, into GAM628 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9982] It is appreciated that GAM628 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM628 target genes. The mRNA of each one of this plurality of GAM628 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM628 RNA, herein designated GAM RNA, and which when bound by GAM628 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM628 target proteins.

[9983] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM628 gene, herein designated GAM GENE, on one or more GAM628 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9984] It is yet further appreciated that specific functions, and accordingly utilities, of GAM628 correlate with, and may be deduced from, the identity of the target genes which GAM628 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9985] Nucleotide sequences of the GAM628 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM628 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM628 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM628 are further described hereinbelow with reference to Table Table1.

[9986] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM628 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[9987] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 629 (GAM629) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[9988] GAM629 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM629 was detected is described hereinabove with reference to Figs. 2-8.

[9989] GAM629 gene, herein designated GAM GENE, and GAM629 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[9990] GAM629 gene, herein designated GAM GENE, encodes a GAM629 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM629 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM629 precursor RNA is designated SEQ ID:602, and is provided hereinbelow with reference to the sequence listing part.

[9991] GAM629 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[9992] An enzyme complex designated DICER COMPLEX, dices the GAM629 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM629 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM629 RNA is designated SEQ ID:2278, and is provided hereinbelow with reference to the sequence listing part.

[9993] GAM629 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM629 target RNA, herein designated GAM TARGET RNA.

GAM629 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[9994] GAM629 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM629 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM629 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM629 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM629 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[9995] The complementary binding of GAM629 RNA, herein designated GAM RNA, to target binding sites on GAM629 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM629 target RNA, herein designated GAM TARGET RNA, into GAM629 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[9996] It is appreciated that GAM629 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM629 target genes. The mRNA of each one of this plurality of GAM629 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM629 RNA, herein designated GAM RNA, and which when bound by GAM629 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM629 target proteins.

[9997] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM629 gene, herein designated GAM GENE, on one or more GAM629 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[9998] It is yet further appreciated that specific functions, and accordingly utilities, of GAM629 correlate with, and may be deduced from, the identity of the target genes which GAM629 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[9999] Nucleotide sequences of the GAM629 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM629 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM629 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM629 are further described hereinbelow with reference to Table Table1.

[10000] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM629 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10001] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 630 (GAM630) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10002] GAM630 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM630 was detected is described hereinabove with reference to Figs. 2-8.

[10003] GAM630 gene, herein designated GAM GENE, and GAM630 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10004] GAM630 gene, herein designated GAM GENE, encodes a GAM630 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM630 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM630 precursor RNA is designated SEQ ID:603, and is provided hereinbelow with reference to the sequence listing part.

[10005] GAM630 has 14 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[10006] SEQ ID:97976 detected in mouse EST Accession AI060752.1.

[10007] SEQ ID:97985 detected in mouse EST Accession AA546767.1.

[10008] SEQ ID:97986 detected in mouse EST Accession AA184326.1.

[10009] SEQ ID:98617 detected in mouse EST Accession AL022643.1.

[10010] SEQ ID:98618 detected in mouse EST Accession AI060752.1.

[10011] SEQ ID:98619 detected in mouse EST Accession

BF452099.1.

[10012] SEQ ID:98620 detected in mouse EST Accession AA546767.1.

[10013] SEQ ID:98623 detected in mouse EST Accession BI453661.1.

[10014] SEQ ID:98627 detected in mouse EST Accession BE531895.1.

[10015] SEQ ID:98628 detected in mouse EST Accession AA184326.1.

[10016] SEQ ID:98629 detected in mouse EST Accession AL022643.1.

[10017] SEQ ID:98630 detected in mouse EST Accession BF452099.1.

[10018] SEQ ID:98631 detected in mouse EST Accession BI453661.1.

[10019] SEQ ID:98632 detected in mouse EST Accession BE531895.1.

[10020] GAM630 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10021] An enzyme complex designated DICER COMPLEX, dices the GAM630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM630 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM630 RNA is designated SEQ ID:2279, and is provided hereinbelow with reference to the sequence listing part.

[10022] GAM630 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM630 target RNA, herein designated GAM TARGET RNA.
GAM630 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10023] GAM630 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM630 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM630 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM630 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM630 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10024] The complementary binding of GAM630 RNA, herein designated GAM RNA, to target binding sites on GAM630 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM630 target RNA, herein designated GAM TARGET RNA, into GAM630 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10025] It is appreciated that GAM630 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM630 target genes. The mRNA of each one of this plurality of GAM630 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM630 RNA, herein designated GAM RNA, and which when bound by GAM630 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM630 target proteins.

[10026] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM630 gene, herein designated GAM GENE, on one or more GAM630 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10027] It is yet further appreciated that specific functions, and accordingly utilities, of GAM630 correlate with, and may be deduced from, the identity of the target genes which GAM630 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10028] Nucleotide sequences of the GAM630 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM630 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM630 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM630 are further described hereinbelow with reference to Table Table1.

[10029] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM630 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10030] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 631 (GAM631) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10031] GAM631 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM631 was detected is described hereinabove with reference to Figs. 2-8.

[10032] GAM631 gene, herein designated GAM GENE, and GAM631 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10033] GAM631 gene, herein designated GAM GENE, encodes a GAM631 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM631 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM631 precursor RNA is desig-

nated SEQ ID:604, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:604 is located at position 1422451 relative to contig NT_031915.4, on chromosome 19.

[10034] GAM631 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10035] An enzyme complex designated DICER COMPLEX, dices the GAM631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM631 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM631 RNA is designated SEQ ID:2280, and is provided hereinbelow with reference to the sequence listing part.

[10036] GAM631 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM631 target RNA, herein designated GAM TARGET RNA. GAM631 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10037] GAM631 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM631 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM631 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM631 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM631 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10038] The complementary binding of GAM631 RNA, herein designated GAM RNA, to target binding sites on GAM631 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM631 target RNA, herein designated GAM TARGET RNA, into GAM631 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10039] It is appreciated that GAM631 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM631 target genes. The mRNA of each one of this plurality of GAM631 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM631 RNA, herein designated GAM RNA, and which when bound by GAM631 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM631 target proteins.

[10040] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM631 gene, herein designated GAM GENE, on one or more GAM631 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10041] It is yet further appreciated that specific functions, and accordingly utilities, of GAM631 correlate with, and may be deduced from, the identity of the target genes which GAM631 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10042] Nucleotide sequences of the GAM631 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM631 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM631 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM631 are further described hereinbelow with reference to Table Table1.

[10043] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM631 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10044] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 632 (GAM632) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10045] GAM632 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM632 was detected is described hereinabove with reference to Figs. 2-8.

[10046] GAM632 gene, herein designated GAM GENE, and GAM632 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10047] GAM632 gene, herein designated GAM GENE, encodes a GAM632 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM632 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM632 precursor RNA is designated SEQ ID:605, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:605 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[10048] GAM632 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[10049] An enzyme complex designated DICER COMPLEX, dices the GAM632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM632 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM632 RNA is designated SEQ ID:2281, and is provided hereinbelow with reference to the sequence listing part.

[10050] GAM632 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM632 target RNA, herein designated GAM TARGET RNA. GAM632 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10051] GAM632 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM632 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM632 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM632 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM632 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10052] The complementary binding of GAM632 RNA, herein designated GAM RNA, to target binding sites on GAM632 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM632 target RNA, herein designated GAM TARGET RNA, into GAM632 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10053] It is appreciated that GAM632 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM632 target genes. The mRNA of each one of this plurality of GAM632 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM632 RNA, herein designated GAM RNA, and which when bound by GAM632 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM632 target proteins.

[10054] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM632 gene, herein designated GAM GENE, on one or more GAM632 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10055] It is yet further appreciated that specific functions, and accordingly utilities, of GAM632 correlate with, and may be deduced from, the identity of the target genes which GAM632 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10056] Nucleotide sequences of the GAM632 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM632 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM632 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM632 are further described hereinbelow with reference to Table Table1.

[10057] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM632 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10058] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 633 (GAM633) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10059] GAM633 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM633 was detected is described hereinabove with reference to Figs. 2-8.

[10060] GAM633 gene, herein designated GAM GENE, and GAM633 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10061] GAM633 gene, herein designated GAM GENE, encodes a GAM633 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM633 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM633 precursor RNA is designated SEQ ID:606, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:606 is located at position 33703762 relative to

contig NT_007592.11, on chromosome 6.

[10062] GAM633 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10063] An enzyme complex designated DICER COMPLEX, dices the GAM633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM633 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM633 RNA is designated SEQ ID:2282, and is provided hereinbelow with reference to the sequence listing part.

[10064] GAM633 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM633 target RNA, herein designated GAM TARGET RNA.

GAM633 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10065] GAM633 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM633 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM633 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM633 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM633 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10066] The complementary binding of GAM633 RNA, herein designated GAM RNA, to target binding sites on GAM633 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM633 target RNA, herein designated GAM TARGET RNA, into GAM633 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10067] It is appreciated that GAM633 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM633 target genes. The mRNA of each one of this plurality of GAM633 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM633 RNA, herein designated GAM RNA, and which when bound by GAM633 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM633 target proteins.

[10068] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM633 gene, herein designated GAM GENE, on one or more GAM633 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10069] It is yet further appreciated that specific functions, and accordingly utilities, of GAM633 correlate with, and may be deduced from, the identity of the target genes which GAM633 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10070] Nucleotide sequences of the GAM633 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM633 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM633 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM633 are further described hereinbelow with reference to Table Table1.

[10071] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM633 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10072] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 634 (GAM634) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10073] GAM634 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM634 was detected is described hereinabove with reference to Figs. 2-8.

[10074] GAM634 gene, herein designated GAM GENE, and GAM634 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10075] GAM634 gene, herein designated GAM GENE, encodes a GAM634 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM634 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM634 precursor RNA is designated SEQ ID:607, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:607 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[10076] GAM634 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10077] An enzyme complex designated DICER COMPLEX, dices the GAM634 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM634 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM634 RNA is designated SEQ ID:2283, and is provided hereinbelow with reference to the sequence listing part.

[10078] GAM634 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM634 target RNA, herein designated GAM TARGET RNA. GAM634 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10079] GAM634 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM634 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM634 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM634 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM634 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10080] The complementary binding of GAM634 RNA, herein designated GAM RNA, to target binding sites on GAM634 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM634 target RNA, herein designated GAM TARGET RNA, into GAM634 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10081] It is appreciated that GAM634 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM634 target genes. The mRNA of each one of this plurality of GAM634 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM634 RNA, herein designated GAM RNA, and which when bound by GAM634 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM634 target proteins.

[10082] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM634 gene, herein designated GAM GENE, on one or more GAM634 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10083] It is yet further appreciated that specific functions, and accordingly utilities, of GAM634 correlate with, and may be deduced from, the identity of the target genes which GAM634 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10084] Nucleotide sequences of the GAM634 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM634 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM634 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM634 are further described hereinbelow with reference to Table Table1.

[10085] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM634 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10086] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

635 (GAM635) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10087] GAM635 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM635 was detected is described hereinabove with reference to Figs. 2-8.

[10088] GAM635 gene, herein designated GAM GENE, and GAM635 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10089] GAM635 gene, herein designated GAM GENE, encodes a GAM635 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM635 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM635 precursor RNA is designated SEQ ID:608, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:608 is located at position 2183835 relative to contig NT_034383.2, on chromosome 1.

[10090] GAM635 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM635 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10091] An enzyme complex designated DICER COMPLEX, dices the GAM635 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM635 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM635 RNA is designated SEQ ID:2284, and is provided hereinbelow with reference to the sequence listing part.

[10092] GAM635 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM635 target RNA, herein designated GAM TARGET RNA. GAM635 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10093] GAM635 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM635 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM635 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM635 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM635 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[10094] The complementary binding of GAM635 RNA, herein designated GAM RNA, to target binding sites on GAM635 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM635 target RNA, herein designated GAM TARGET RNA, into GAM635 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10095] It is appreciated that GAM635 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM635 target genes. The mRNA of each one of this plurality of GAM635 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM635 RNA, herein designated GAM RNA, and which when bound by GAM635 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM635 target proteins.

[10096] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM635 gene, herein designated GAM GENE, on one or

more GAM635 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10097] It is yet further appreciated that specific functions, and accordingly utilities, of GAM635 correlate with, and may be deduced from, the identity of the target genes which GAM635 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10098] Nucleotide sequences of the GAM635 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM635 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM635 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM635 are further de-

scribed hereinbelow with reference to Table Table1.

[10099] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM635 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10100] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 636 (GAM636) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10101] GAM636 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM636 was detected is described hereinabove with reference to Figs. 2-8.

[10102] GAM636 gene, herein designated GAM GENE, and GAM636 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10103] GAM636 gene, herein designated GAM GENE, encodes a GAM636 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM636 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM636 precursor RNA is designated SEQ ID:609, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:609 is located at position 11259458 relative to contig NT_007592.11, on chromosome 6.

[10104] GAM636 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10105] An enzyme complex designated DICER COMPLEX, dices the GAM636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM636 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM636 RNA is designated SEQ ID:2285, and is provided hereinbelow with reference to the sequence listing part.

[10106] GAM636 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM636 target RNA, herein designated GAM TARGET RNA. GAM636 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10107] GAM636 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM636 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM636 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM636 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM636 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10108] The complementary binding of GAM636 RNA, herein designated GAM RNA, to target binding sites on GAM636 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM636 target RNA, herein designated GAM TARGET RNA, into GAM636 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10109] It is appreciated that GAM636 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM636 target genes. The mRNA of each one of this plurality of GAM636 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM636 RNA, herein designated GAM RNA, and which when bound by GAM636 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM636 target proteins.

[10110] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM636 gene, herein designated GAM GENE, on one or more GAM636 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10111] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM636 correlate with, and may be deduced from, the identity of the target genes which GAM636 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10112] Nucleotide sequences of the GAM636 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM636 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM636 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM636 are further described hereinbelow with reference to Table Table1.

[10113] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM636 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10114] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 637 (GAM637) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10115] GAM637 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM637 was detected is described hereinabove with reference to Figs. 2-8.

[10116] GAM637 gene, herein designated GAM GENE, and GAM637 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10117] GAM637 gene, herein designated GAM GENE, encodes a GAM637 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM637 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM637 precursor RNA is designated SEQ ID:610, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:610 is located at position 5992707 relative to contig NT_005612.11, on chromosome 3.

[10118] GAM637 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10119] An enzyme complex designated DICER COMPLEX, dices the GAM637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM637 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM637 RNA is designated SEQ ID:2286, and is provided hereinbelow with reference to the sequence listing part.

[10120] GAM637 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM637 target RNA, herein designated GAM TARGET RNA. GAM637 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[10121] GAM637 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM637 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM637 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM637 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM637 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10122] The complementary binding of GAM637 RNA, herein designated GAM RNA, to target binding sites on GAM637 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM637 target RNA, herein designated GAM TARGET RNA, into GAM637 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10123] It is appreciated that GAM637 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM637 target genes. The mRNA of each one of this plurality of GAM637 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM637 RNA, herein designated GAM RNA, and which when bound by GAM637 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM637 target proteins.

[10124] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM637 gene, herein designated GAM GENE, on one or more GAM637 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10125] It is yet further appreciated that specific functions, and accordingly utilities, of GAM637 correlate with, and may be deduced from, the identity of the target genes which GAM637 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10126] Nucleotide sequences of the GAM637 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM637 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM637 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM637 are further described hereinbelow with reference to Table Table1.

[10127] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM637 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10128] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 638 (GAM638) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10129] GAM638 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM638 was detected is described hereinabove with reference to Figs. 2-8.

[10130] GAM638 gene, herein designated GAM GENE, and GAM638 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10131] GAM638 gene, herein designated GAM GENE, encodes a GAM638 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM638 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM638 precursor RNA is designated SEQ ID:611, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:611 is located at position 4851353 relative to contig NT_022517.13, on chromosome 3.

[10132] GAM638 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10133] An enzyme complex designated DICER COMPLEX, dices the GAM638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM638 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM638 RNA is designated SEQ ID:2287, and is provided hereinbelow with reference to the sequence listing part.

[10134] GAM638 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM638 target RNA, herein designated GAM TARGET RNA. GAM638 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10135] GAM638 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM638 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM638 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM638 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM638 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10136] The complementary binding of GAM638 RNA, herein designated GAM RNA, to target binding sites on GAM638 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM638 target RNA, herein designated GAM TARGET RNA, into GAM638 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10137] It is appreciated that GAM638 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM638 target genes. The mRNA of each one of this plurality of GAM638 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM638 RNA, herein designated GAM RNA, and which when bound by

GAM638 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM638 target proteins.

[10138] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM638 gene, herein designated GAM GENE, on one or more GAM638 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10139] It is yet further appreciated that specific functions, and accordingly utilities, of GAM638 correlate with, and may be deduced from, the identity of the target genes which GAM638 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[10140] Nucleotide sequences of the GAM638 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM638 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM638 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM638 are further described hereinbelow with reference to Table Table1.

[10141] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM638 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10142] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 639 (GAM639) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10143] GAM639 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM639 was detected is described hereinabove

with reference to Figs. 2-8.

[10144] GAM639 gene, herein designated GAM GENE, and GAM639 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10145] GAM639 gene, herein designated GAM GENE, encodes a GAM639 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM639 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM639 precursor RNA is designated SEQ ID:612, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:612 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[10146] GAM639 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM639 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[10147] An enzyme complex designated DICER COMPLEX, dices the GAM639 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM639 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM639 RNA is designated SEQ ID:2288, and is provided hereinbelow with reference to the sequence listing part.

[10148] GAM639 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM639 target RNA, herein designated GAM TARGET RNA.
GAM639 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10149] GAM639 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM639 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM639 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM639 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM639 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10150] The complementary binding of GAM639 RNA, herein designated GAM RNA, to target binding sites on GAM639 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM639 target RNA, herein desig-

nated GAM TARGET RNA, into GAM639 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10151] It is appreciated that GAM639 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM639 target genes. The mRNA of each one of this plurality of GAM639 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM639 RNA, herein designated GAM RNA, and which when bound by GAM639 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM639 target proteins.

[10152] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM639 gene, herein designated GAM GENE, on one or more GAM639 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10153] It is yet further appreciated that specific functions, and accordingly utilities, of GAM639 correlate with, and may be deduced from, the identity of the target genes which GAM639 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10154] Nucleotide sequences of the GAM639 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM639 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM639 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM639 are further described hereinbelow with reference to Table Table1.

[10155] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM639 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[10156] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 640 (GAM640) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10157] GAM640 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM640 was detected is described hereinabove with reference to Figs. 2-8.

[10158] GAM640 gene, herein designated GAM GENE, and GAM640 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10159] GAM640 gene, herein designated GAM GENE, encodes a GAM640 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM640 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM640 precursor RNA is designated SEQ ID:613, and is provided hereinbelow with reference to the sequence listing part.

[10160] GAM640 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10161] An enzyme complex designated DICER COMPLEX, dices the GAM640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM640 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM640 RNA is designated SEQ ID:2289, and is provided hereinbelow with reference to the sequence listing part.

[10162] GAM640 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM640

target RNA, herein designated GAM TARGET RNA.

GAM640 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10163] GAM640 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM640 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM640 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM640 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM640 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10164] The complementary binding of GAM640 RNA, herein designated GAM RNA, to target binding sites on GAM640 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM640 target RNA, herein designated GAM TARGET RNA, into GAM640 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10165] It is appreciated that GAM640 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM640 target genes. The mRNA of each one of this plurality of GAM640 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM640 RNA, herein designated GAM RNA, and which when bound by GAM640 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM640 target proteins.

[10166] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM640 gene, herein designated GAM GENE, on one or more GAM640 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10167] It is yet further appreciated that specific functions, and accordingly utilities, of GAM640 correlate with, and may be deduced from, the identity of the target genes which GAM640 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10168] Nucleotide sequences of the GAM640 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM640 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM640 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM640 are further described hereinbelow with reference to Table Table1.

[10169] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM640 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10170] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 641 (GAM641) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10171] GAM641 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM641 was detected is described hereinabove with reference to Figs. 2-8.

[10172] GAM641 gene, herein designated GAM GENE, and GAM641 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10173] GAM641 gene, herein designated GAM GENE, encodes a

GAM641 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM641 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM641 precursor RNA is designated SEQ ID:614, and is provided hereinbelow with reference to the sequence listing part.

[10174] GAM641 has 9 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[10175] SEQ ID:100054 detected in mouse EST Accession BE631995.1.

[10176] SEQ ID:100055 detected in mouse EST Accession BG974113.1.

[10177] SEQ ID:100056 detected in mouse EST Accession BF134406.1.

[10178] SEQ ID:100057 detected in mouse EST Accession AA011740.1.

[10179] SEQ ID:100058 detected in mouse EST Accession AA032944.1.

[10180] SEQ ID:100059 detected in mouse EST Accession BG923775.1.

[10181] SEQ ID:100060 detected in mouse EST Accession BI105201.1.

[10182] SEQ ID:100061 detected in mouse EST Accession BI659868.1.

[10183] SEQ ID:100062 detected in mouse EST Accession AA413633.1.

[10184] GAM641 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM641 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10185] An enzyme complex designated DICER COMPLEX, dices the GAM641 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM641 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM641 RNA is designated SEQ ID:2290, and is provided hereinbelow with reference to the sequence listing part.

[10186] GAM641 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM641 target RNA, herein designated GAM TARGET RNA. GAM641 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10187] GAM641 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM641 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM641 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM641 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM641 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10188] The complementary binding of GAM641 RNA, herein designated GAM RNA, to target binding sites on GAM641 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM641 target RNA, herein designated GAM TARGET RNA, into GAM641 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10189] It is appreciated that GAM641 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM641 target genes. The mRNA of each one of this plurality of GAM641 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM641 RNA, herein designated GAM RNA, and which when bound by GAM641 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM641 target proteins.

[10190] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM641 gene, herein designated GAM GENE, on one or more GAM641 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10191] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM641 correlate with, and may be deduced from, the identity of the target genes which GAM641 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10192] Nucleotide sequences of the GAM641 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM641 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM641 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM641 are further described hereinbelow with reference to Table Table1.

[10193] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM641 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10194] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 642 (GAM642) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10195] GAM642 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM642 was detected is described hereinabove with reference to Figs. 2-8.

[10196] GAM642 gene, herein designated GAM GENE, and GAM642 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10197] GAM642 gene, herein designated GAM GENE, encodes a GAM642 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM642 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM642 precursor RNA is designated SEQ ID:615, and is provided hereinbelow with reference to the sequence listing part.

[10198] GAM642 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM642 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10199] An enzyme complex designated DICER COMPLEX, dices the GAM642 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM642 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM642 RNA is designated SEQ ID:2291, and is provided hereinbelow with reference to the sequence listing part.

[10200] GAM642 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM642 target RNA, herein designated GAM TARGET RNA. GAM642 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10201] GAM642 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM642 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM642 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM642 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM642 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10202] The complementary binding of GAM642 RNA, herein designated GAM RNA, to target binding sites on GAM642 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM642 target RNA, herein designated GAM TARGET RNA, into GAM642 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10203] It is appreciated that GAM642 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM642 target genes. The mRNA of each one of this plurality of GAM642 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM642 RNA, herein designated GAM RNA, and which when bound by GAM642 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM642 target proteins.

[10204] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM642 gene, herein designated GAM GENE, on one or more GAM642 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10205] It is yet further appreciated that specific functions, and accordingly utilities, of GAM642 correlate with, and may be deduced from, the identity of the target genes which GAM642 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10206] Nucleotide sequences of the GAM642 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM642 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM642 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM642 are further described hereinbelow with reference to Table Table1.

[10207] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM642 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10208] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 643 (GAM643) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10209] GAM643 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM643 was detected is described hereinabove with reference to Figs. 2-8.

[10210] GAM643 gene, herein designated GAM GENE, and GAM643 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10211] GAM643 gene, herein designated GAM GENE, encodes a GAM643 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM643 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM643 precursor RNA is designated SEQ ID:616, and is provided hereinbelow with refer-

ence to the sequence listing part.

[10212] GAM643 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM643 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10213] An enzyme complex designated DICER COMPLEX, dices the GAM643 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM643 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM643 RNA is designated SEQ ID:2292, and is provided hereinbelow with reference to the sequence listing part.

[10214] GAM643 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM643 target RNA, herein designated GAM TARGET RNA.

GAM643 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10215] GAM643 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM643 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM643 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM643 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM643 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10216] The complementary binding of GAM643 RNA, herein designated GAM RNA, to target binding sites on GAM643 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM643 target RNA, herein designated GAM TARGET RNA, into GAM643 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10217] It is appreciated that GAM643 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM643 target genes. The mRNA of each one of this plurality of GAM643 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM643 RNA, herein designated GAM RNA, and which when bound by GAM643 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM643 target proteins.

[10218] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM643 gene, herein designated GAM GENE, on one or more GAM643 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10219] It is yet further appreciated that specific functions, and accordingly utilities, of GAM643 correlate with, and may be deduced from, the identity of the target genes which GAM643 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10220] Nucleotide sequences of the GAM643 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM643 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM643 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM643 are further described hereinbelow with reference to Table Table1.

[10221] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM643 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10222] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 644 (GAM644) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10223] GAM644 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM644 was detected is described hereinabove with reference to Figs. 2-8.

[10224] GAM644 gene, herein designated GAM GENE, and GAM644 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10225] GAM644 gene, herein designated GAM GENE, encodes a GAM644 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM644 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM644 precursor RNA is designated SEQ ID:617, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:617 is located at position 53818956 relative to contig NT_026437.9, on chromosome 14.

[10226] GAM644 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM644 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10227] An enzyme complex designated DICER COMPLEX, dices the GAM644 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM644 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM644 RNA is designated SEQ ID:2293, and is provided hereinbelow with reference to the sequence listing part.

[10228] GAM644 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM644 target RNA, herein designated GAM TARGET RNA.

GAM644 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10229] GAM644 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM644 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM644 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM644 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM644 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10230] The complementary binding of GAM644 RNA, herein designated GAM RNA, to target binding sites on GAM644 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM644 target RNA, herein designated GAM TARGET RNA, into GAM644 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10231] It is appreciated that GAM644 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM644 target genes. The mRNA of each one of this plurality of GAM644 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM644 RNA, herein designated GAM RNA, and which when bound by GAM644 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM644 target proteins.

[10232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM644 gene, herein designated GAM GENE, on one or more GAM644 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10233] It is yet further appreciated that specific functions, and accordingly utilities, of GAM644 correlate with, and may be deduced from, the identity of the target genes which GAM644 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10234] Nucleotide sequences of the GAM644 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM644 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM644 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM644 are further described hereinbelow with reference to Table Table1.

[10235] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM644 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10236] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 645 (GAM645) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10237] GAM645 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM645 was detected is described hereinabove with reference to Figs. 2-8.

[10238] GAM645 gene, herein designated GAM GENE, and GAM645 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10239] GAM645 gene, herein designated GAM GENE, encodes a GAM645 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM645 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM645 precursor RNA is designated SEQ ID:618, and is provided hereinbelow with reference to the sequence listing part.

[10240] GAM645 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM645 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10241] An enzyme complex designated DICER COMPLEX, dices the GAM645 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM645 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM645 RNA is designated SEQ ID:2294, and is provided hereinbelow with reference to the sequence listing part.

[10242] GAM645 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM645 target RNA, herein designated GAM TARGET RNA. GAM645 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10243] GAM645 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM645 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM645 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM645 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM645 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10244] The complementary binding of GAM645 RNA, herein designated GAM RNA, to target binding sites on GAM645 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM645 target RNA, herein designated GAM TARGET RNA, into GAM645 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10245] It is appreciated that GAM645 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM645 target genes. The mRNA of each one of this plurality of GAM645 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM645 RNA, herein designated GAM RNA, and which when bound by GAM645 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM645 target proteins.

[10246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM645 gene, herein designated GAM GENE, on one or more GAM645 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10247] It is yet further appreciated that specific functions, and accordingly utilities, of GAM645 correlate with, and may

be deduced from, the identity of the target genes which GAM645 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10248] Nucleotide sequences of the GAM645 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM645 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM645 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM645 are further described hereinbelow with reference to Table Table1.

[10249] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM645 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10250] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 646 (GAM646) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10251] GAM646 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM646 was detected is described hereinabove with reference to Figs. 2-8.

[10252] GAM646 gene, herein designated GAM GENE, and GAM646 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10253] GAM646 gene, herein designated GAM GENE, encodes a GAM646 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM646 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM646 precursor RNA is designated SEQ ID:619, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:619 is located at position 1036024 relative to contig NT_024115.13, on chromosome 10.

[10254] GAM646 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM646 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10255] An enzyme complex designated DICER COMPLEX, dices the GAM646 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM646 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM646 RNA is designated SEQ ID:2295, and is provided hereinbelow with reference to the sequence listing part.

[10256] GAM646 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM646 target RNA, herein designated GAM TARGET RNA.
GAM646 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10257] GAM646 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM646 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM646 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM646 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM646 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10258] The complementary binding of GAM646 RNA, herein designated GAM RNA, to target binding sites on GAM646 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM646 target RNA, herein designated GAM TARGET RNA, into GAM646 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10259] It is appreciated that GAM646 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM646 target genes. The mRNA of each one of this plurality of GAM646 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM646 RNA, herein designated GAM RNA, and which when bound by GAM646 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM646 target proteins.

[10260] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM646 gene, herein designated GAM GENE, on one or more GAM646 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10261] It is yet further appreciated that specific functions, and accordingly utilities, of GAM646 correlate with, and may be deduced from, the identity of the target genes which GAM646 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10262] Nucleotide sequences of the GAM646 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM646 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM646 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM646 are further described hereinbelow with reference to Table Table1.

[10263] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM646 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10264] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 647 (GAM647) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10265] GAM647 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM647 was detected is described hereinabove with reference to Figs. 2-8.

[10266] GAM647 gene, herein designated GAM GENE, and GAM647 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10267] GAM647 gene, herein designated GAM GENE, encodes a GAM647 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM647 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM647 precursor RNA is desig-

nated SEQ ID:620, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:620 is located at position 365850 relative to contig NT_010799.11, on chromosome 17.

[10268] GAM647 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM647 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10269] An enzyme complex designated DICER COMPLEX, dices the GAM647 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM647 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM647 RNA is designated SEQ ID:2296, and is provided hereinbelow with reference to the sequence listing part.

[10270] GAM647 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM647 target RNA, herein designated GAM TARGET RNA. GAM647 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10271] GAM647 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM647 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM647 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM647 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM647 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10272] The complementary binding of GAM647 RNA, herein designated GAM RNA, to target binding sites on GAM647 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM647 target RNA, herein designated GAM TARGET RNA, into GAM647 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10273] It is appreciated that GAM647 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM647 target genes. The mRNA of each one of this plurality of GAM647 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM647 RNA, herein designated GAM RNA, and which when bound by GAM647 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM647 target proteins.

[10274] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM647 gene, herein designated GAM GENE, on one or more GAM647 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10275] It is yet further appreciated that specific functions, and accordingly utilities, of GAM647 correlate with, and may be deduced from, the identity of the target genes which GAM647 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10276] Nucleotide sequences of the GAM647 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM647 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM647 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM647 are further described hereinbelow with reference to Table Table1.

[10277] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM647 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10278] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 648 (GAM648) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10279] GAM648 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM648 was detected is described hereinabove with reference to Figs. 2-8.

[10280] GAM648 gene, herein designated GAM GENE, and GAM648 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10281] GAM648 gene, herein designated GAM GENE, encodes a GAM648 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM648 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM648 precursor RNA is designated SEQ ID:621, and is provided hereinbelow with reference to the sequence listing part.

[10282] GAM648 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM648 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10283] An enzyme complex designated DICER COMPLEX, dices

the GAM648 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM648 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM648 RNA is designated SEQ ID:2297, and is provided hereinbelow with reference to the sequence listing part.

[10284] GAM648 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM648 target RNA, herein designated GAM TARGET RNA. GAM648 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10285] GAM648 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM648 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM648

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM648 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM648 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10286] The complementary binding of GAM648 RNA, herein designated GAM RNA, to target binding sites on GAM648 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM648 target RNA, herein designated GAM TARGET RNA, into GAM648 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10287] It is appreciated that GAM648 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM648 target genes. The mRNA of each one of this plurality of GAM648 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM648 RNA, herein designated GAM RNA, and which when bound by GAM648 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM648 target proteins.

[10288] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM648 gene, herein designated GAM GENE, on one or more GAM648 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10289] It is yet further appreciated that specific functions, and accordingly utilities, of GAM648 correlate with, and may be deduced from, the identity of the target genes which GAM648 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10290] Nucleotide sequences of the GAM648 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM648 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM648 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM648 are further described hereinbelow with reference to Table Table1.

[10291] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM648 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10292] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 649 (GAM649) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10293] GAM649 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM649 was detected is described hereinabove with reference to Figs. 2-8.

[10294] GAM649 gene, herein designated GAM GENE, and GAM649 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10295] GAM649 gene, herein designated GAM GENE, encodes a GAM649 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM649 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM649 precursor RNA is designated SEQ ID:622, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:622 is located at position 985121 relative to contig NT_025273.11, on chromosome X.

[10296] GAM649 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM649 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10297] An enzyme complex designated DICER COMPLEX, dices the GAM649 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM649 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM649 RNA is designated SEQ ID:2298, and is provided hereinbelow with reference to the sequence listing part.

[10298] GAM649 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM649 target RNA, herein designated GAM TARGET RNA.

GAM649 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10299] GAM649 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM649 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM649 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM649 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM649 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10300] The complementary binding of GAM649 RNA, herein designated GAM RNA, to target binding sites on GAM649 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM649 target RNA, herein designated GAM TARGET RNA, into GAM649 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10301] It is appreciated that GAM649 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM649 target genes. The mRNA of each one of this plurality of GAM649 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM649 RNA, herein designated GAM RNA, and which when bound by GAM649 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM649 target proteins.

[10302] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM649 gene, herein designated GAM GENE, on one or more GAM649 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10303] It is yet further appreciated that specific functions, and accordingly utilities, of GAM649 correlate with, and may be deduced from, the identity of the target genes which GAM649 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10304] Nucleotide sequences of the GAM649 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM649 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM649 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM649 are further described hereinbelow with reference to Table Table1.

[10305] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM649 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10306] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 650 (GAM650) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10307] GAM650 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM650 was detected is described hereinabove with reference to Figs. 2-8.

[10308] GAM650 gene, herein designated GAM GENE, and GAM650 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10309] GAM650 gene, herein designated GAM GENE, encodes a GAM650 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM650 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM650 precursor RNA is designated SEQ ID:623, and is provided hereinbelow with reference to the sequence listing part.

[10310] GAM650 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10311] An enzyme complex designated DICER COMPLEX, dices the GAM650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM650 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM650 RNA is designated SEQ ID:2299, and is provided hereinbelow with reference to the sequence listing part.

[10312] GAM650 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM650 target RNA, herein designated GAM TARGET RNA. GAM650 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10313] GAM650 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM650 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM650 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM650 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM650 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10314] The complementary binding of GAM650 RNA, herein designated GAM RNA, to target binding sites on GAM650 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM650 target RNA, herein designated GAM TARGET RNA, into GAM650 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10315] It is appreciated that GAM650 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM650 target genes. The mRNA of each one of this plurality of GAM650 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM650 RNA, herein designated GAM RNA, and which when bound by GAM650 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM650 target proteins.

[10316] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM650 gene, herein designated GAM GENE, on one or more GAM650 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10317] It is yet further appreciated that specific functions, and accordingly utilities, of GAM650 correlate with, and may

be deduced from, the identity of the target genes which GAM650 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10318] Nucleotide sequences of the GAM650 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM650 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM650 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM650 are further described hereinbelow with reference to Table Table1.

[10319] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM650 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10320] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 651 (GAM651) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10321] GAM651 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM651 was detected is described hereinabove with reference to Figs. 2-8.

[10322] GAM651 gene, herein designated GAM GENE, and GAM651 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10323] GAM651 gene, herein designated GAM GENE, encodes a GAM651 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM651 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM651 precursor RNA is designated SEQ ID:624, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:624 is located at position 34982683 relative to contig NT_007592.11, on chromosome 6.

[10324] GAM651 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM651 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10325] An enzyme complex designated DICER COMPLEX, dices the GAM651 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM651 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM651 RNA is designated SEQ ID:2300, and is provided hereinbelow with reference to the sequence listing part.

[10326] GAM651 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM651 target RNA, herein designated GAM TARGET RNA. GAM651 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10327] GAM651 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM651 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM651 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM651 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM651 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10328] The complementary binding of GAM651 RNA, herein designated GAM RNA, to target binding sites on GAM651 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM651 target RNA, herein designated GAM TARGET RNA, into GAM651 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10329] It is appreciated that GAM651 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM651 target genes. The mRNA of each one of this plurality of GAM651 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM651 RNA, herein designated GAM RNA, and which when bound by GAM651 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM651 target proteins.

[10330] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM651 gene, herein designated GAM GENE, on one or more GAM651 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10331] It is yet further appreciated that specific functions, and accordingly utilities, of GAM651 correlate with, and may be deduced from, the identity of the target genes which GAM651 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10332] Nucleotide sequences of the GAM651 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM651 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM651 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM651 are further described hereinbelow with reference to Table Table1.

[10333] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM651 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10334] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 652 (GAM652) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10335] GAM652 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM652 was detected is described hereinabove with reference to Figs. 2-8.

[10336] GAM652 gene, herein designated GAM GENE, and GAM652 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10337] GAM652 gene, herein designated GAM GENE, encodes a GAM652 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM652 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM652 precursor RNA is desig-

nated SEQ ID:625, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:625 is located at position 28259 relative to contig NT_009526.11, on chromosome 12.

[10338] GAM652 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[10339] SEQ ID:99109 detected in mouse EST Accession BI965972.1.

[10340] SEQ ID:99110 detected in mouse EST Accession AI326210.1.

[10341] SEQ ID:99111 detected in mouse EST Accession BI965652.1.

[10342] GAM652 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM652 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[10343] An enzyme complex designated DICER COMPLEX, dices the GAM652 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM652 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM652 RNA is designated SEQ ID:2301, and is provided hereinbelow with reference to the sequence listing part.

[10344] GAM652 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM652 target RNA, herein designated GAM TARGET RNA.
GAM652 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10345] GAM652 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM652 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM652 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM652 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM652 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10346] The complementary binding of GAM652 RNA, herein designated GAM RNA, to target binding sites on GAM652 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM652 target RNA, herein desig-

nated GAM TARGET RNA, into GAM652 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10347] It is appreciated that GAM652 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM652 target genes. The mRNA of each one of this plurality of GAM652 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM652 RNA, herein designated GAM RNA, and which when bound by GAM652 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM652 target proteins.

[10348] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM652 gene, herein designated GAM GENE, on one or more GAM652 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10349] It is yet further appreciated that specific functions, and accordingly utilities, of GAM652 correlate with, and may be deduced from, the identity of the target genes which GAM652 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10350] Nucleotide sequences of the GAM652 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM652 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM652 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM652 are further described hereinbelow with reference to Table Table1.

[10351] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM652 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[10352] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 653 (GAM653) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10353] GAM653 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM653 was detected is described hereinabove with reference to Figs. 2-8.

[10354] GAM653 gene, herein designated GAM GENE, and GAM653 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10355] GAM653 gene, herein designated GAM GENE, encodes a GAM653 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM653 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM653 precursor RNA is designated SEQ ID:626, and is provided hereinbelow with reference to the sequence listing part.

[10356] GAM653 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10357] An enzyme complex designated DICER COMPLEX, dices the GAM653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM653 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM653 RNA is designated SEQ ID:2302, and is provided hereinbelow with reference to the sequence listing part.

[10358] GAM653 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM653

target RNA, herein designated GAM TARGET RNA.

GAM653 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10359] GAM653 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM653 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM653 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM653 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM653 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10360] The complementary binding of GAM653 RNA, herein designated GAM RNA, to target binding sites on GAM653 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM653 target RNA, herein designated GAM TARGET RNA, into GAM653 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10361] It is appreciated that GAM653 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM653 target genes. The mRNA of each one of this plurality of GAM653 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM653 RNA, herein designated GAM RNA, and which when bound by GAM653 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM653 target proteins.

[10362] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM653 gene, herein designated GAM GENE, on one or more GAM653 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10363] It is yet further appreciated that specific functions, and accordingly utilities, of GAM653 correlate with, and may be deduced from, the identity of the target genes which GAM653 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10364] Nucleotide sequences of the GAM653 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM653 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM653 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM653 are further described hereinbelow with reference to Table Table1.

[10365] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM653 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10366] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 654 (GAM654) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10367] GAM654 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM654 was detected is described hereinabove with reference to Figs. 2-8.

[10368] GAM654 gene, herein designated GAM GENE, and GAM654 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10369] GAM654 gene, herein designated GAM GENE, encodes a

GAM654 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM654 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM654 precursor RNA is designated SEQ ID:627, and is provided hereinbelow with reference to the sequence listing part.

[10370] GAM654 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10371] An enzyme complex designated DICER COMPLEX, dices the GAM654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM654 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM654 RNA is designated SEQ ID:2303, and is provided hereinbelow with reference to the sequence listing part.

[10372] GAM654 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM654 target RNA, herein designated GAM TARGET RNA. GAM654 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10373] GAM654 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM654 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM654 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM654 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM654 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10374] The complementary binding of GAM654 RNA, herein designated GAM RNA, to target binding sites on GAM654 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM654 target RNA, herein designated GAM TARGET RNA, into GAM654 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10375] It is appreciated that GAM654 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM654 target genes. The mRNA of each one of this plurality of GAM654 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM654 RNA, herein designated GAM RNA, and which when bound by GAM654 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM654 target proteins.

[10376] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM654 gene, herein designated GAM GENE, on one or more GAM654 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10377] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM654 correlate with, and may be deduced from, the identity of the target genes which GAM654 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10378] Nucleotide sequences of the GAM654 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM654 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM654 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM654 are further described hereinbelow with reference to Table Table1.

[10379] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM654 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10380] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 655 (GAM655) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10381] GAM655 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM655 was detected is described hereinabove with reference to Figs. 2-8.

[10382] GAM655 gene, herein designated GAM GENE, and GAM655 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10383] GAM655 gene, herein designated GAM GENE, encodes a GAM655 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM655 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM655 precursor RNA is designated SEQ ID:628, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:628 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[10384] GAM655 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM655 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10385] An enzyme complex designated DICER COMPLEX, dices the GAM655 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM655 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM655 RNA is designated SEQ ID:2304, and is provided hereinbelow with reference to the sequence listing part.

[10386] GAM655 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM655 target RNA, herein designated GAM TARGET RNA.
GAM655 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[10387] GAM655 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM655 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM655 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM655 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM655 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10388] The complementary binding of GAM655 RNA, herein designated GAM RNA, to target binding sites on GAM655 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM655 target RNA, herein designated GAM TARGET RNA, into GAM655 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10389] It is appreciated that GAM655 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM655 target genes. The mRNA of each one of this plurality of GAM655 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM655 RNA, herein designated GAM RNA, and which when bound by GAM655 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM655 target proteins.

[10390] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM655 gene, herein designated GAM GENE, on one or more GAM655 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10391] It is yet further appreciated that specific functions, and accordingly utilities, of GAM655 correlate with, and may be deduced from, the identity of the target genes which GAM655 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10392] Nucleotide sequences of the GAM655 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM655 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM655 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM655 are further described hereinbelow with reference to Table Table1.

[10393] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM655 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10394] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 656 (GAM656) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10395] GAM656 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM656 was detected is described hereinabove with reference to Figs. 2-8.

[10396] GAM656 gene, herein designated GAM GENE, and GAM656 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10397] GAM656 gene, herein designated GAM GENE, encodes a GAM656 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM656 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM656 precursor RNA is designated SEQ ID:629, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:629 is located at position 5573082 relative to contig NT_033927.3, on chromosome 11.

[10398] GAM656 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10399] An enzyme complex designated DICER COMPLEX, dices the GAM656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM656 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM656 RNA is designated SEQ ID:2305, and is provided hereinbelow with reference to the sequence listing part.

[10400] GAM656 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM656 target RNA, herein designated GAM TARGET RNA. GAM656 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10401] GAM656 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM656 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM656 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM656 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM656 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10402] The complementary binding of GAM656 RNA, herein designated GAM RNA, to target binding sites on GAM656 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM656 target RNA, herein designated GAM TARGET RNA, into GAM656 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10403] It is appreciated that GAM656 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM656 target genes. The mRNA of each one of this plurality of GAM656 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM656 RNA, herein designated GAM RNA, and which when bound by

GAM656 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM656 target proteins.

[10404] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM656 gene, herein designated GAM GENE, on one or more GAM656 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10405] It is yet further appreciated that specific functions, and accordingly utilities, of GAM656 correlate with, and may be deduced from, the identity of the target genes which GAM656 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[10406] Nucleotide sequences of the GAM656 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM656 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM656 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM656 are further described hereinbelow with reference to Table Table1.

[10407] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM656 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10408] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 657 (GAM657) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10409] GAM657 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM657 was detected is described hereinabove

with reference to Figs. 2-8.

[10410] GAM657 gene, herein designated GAM GENE, and GAM657 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10411] GAM657 gene, herein designated GAM GENE, encodes a GAM657 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM657 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM657 precursor RNA is designated SEQ ID:630, and is provided hereinbelow with reference to the sequence listing part.

[10412] GAM657 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10413] An enzyme complex designated DICER COMPLEX, dices the GAM657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM657 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM657 RNA is designated SEQ ID:2306, and is provided hereinbelow with reference to the sequence listing part.

[10414] GAM657 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM657 target RNA, herein designated GAM TARGET RNA. GAM657 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10415] GAM657 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM657 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM657 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM657 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM657 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10416] The complementary binding of GAM657 RNA, herein designated GAM RNA, to target binding sites on GAM657 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM657 target RNA, herein designated GAM TARGET RNA, into GAM657 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[10417] It is appreciated that GAM657 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM657 target genes. The mRNA of each one of this plurality of GAM657 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM657 RNA, herein designated GAM RNA, and which when bound by GAM657 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM657 target proteins.

[10418] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM657 gene, herein designated GAM GENE, on one or more GAM657 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10419] It is yet further appreciated that specific functions, and accordingly utilities, of GAM657 correlate with, and may be deduced from, the identity of the target genes which GAM657 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10420] Nucleotide sequences of the GAM657 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM657 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM657 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM657 are further described hereinbelow with reference to Table Table1.

[10421] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM657 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10422] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 658 (GAM658) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10423] GAM658 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM658 was detected is described hereinabove with reference to Figs. 2-8.

[10424] GAM658 gene, herein designated GAM GENE, and GAM658 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10425] GAM658 gene, herein designated GAM GENE, encodes a GAM658 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM658 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM658 precursor RNA is designated SEQ ID:631, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:631 is located at position 1020167 relative to contig NT_006713.11, on chromosome 5.

[10426] GAM658 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM658 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10427] An enzyme complex designated DICER COMPLEX, dices the GAM658 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM658 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM658 RNA is designated SEQ ID:2307, and is provided hereinbelow with reference to the sequence listing part.

[10428] GAM658 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM658

target RNA, herein designated GAM TARGET RNA.

GAM658 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10429] GAM658 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM658 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM658 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM658 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM658 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10430] The complementary binding of GAM658 RNA, herein designated GAM RNA, to target binding sites on GAM658 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM658 target RNA, herein designated GAM TARGET RNA, into GAM658 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10431] It is appreciated that GAM658 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM658 target genes. The mRNA of each one of this plurality of GAM658 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM658 RNA, herein designated GAM RNA, and which when bound by GAM658 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM658 target proteins.

[10432] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM658 gene, herein designated GAM GENE, on one or more GAM658 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10433] It is yet further appreciated that specific functions, and accordingly utilities, of GAM658 correlate with, and may be deduced from, the identity of the target genes which GAM658 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10434] Nucleotide sequences of the GAM658 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM658 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM658 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM658 are further described hereinbelow with reference to Table Table1.

[10435] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM658 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10436] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 659 (GAM659) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10437] GAM659 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM659 was detected is described hereinabove with reference to Figs. 2-8.

[10438] GAM659 gene, herein designated GAM GENE, and GAM659 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10439] GAM659 gene, herein designated GAM GENE, encodes a

GAM659 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM659 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM659 precursor RNA is designated SEQ ID:632, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:632 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[10440] GAM659 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM659 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10441] An enzyme complex designated DICER COMPLEX, dices the GAM659 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM659 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM659 RNA is designated SEQ ID:2308, and is provided hereinbelow with reference to the sequence listing part.

[10442] GAM659 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM659 target RNA, herein designated GAM TARGET RNA. GAM659 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10443] GAM659 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM659 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM659 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM659 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM659 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10444] The complementary binding of GAM659 RNA, herein designated GAM RNA, to target binding sites on GAM659 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM659 target RNA, herein designated GAM TARGET RNA, into GAM659 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10445] It is appreciated that GAM659 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM659 target genes. The mRNA of each one of this plurality of GAM659 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM659 RNA, herein designated GAM RNA, and which when bound by GAM659 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM659 target proteins.

[10446] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM659 gene, herein designated GAM GENE, on one or more GAM659 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[10447] It is yet further appreciated that specific functions, and accordingly utilities, of GAM659 correlate with, and may be deduced from, the identity of the target genes which GAM659 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10448] Nucleotide sequences of the GAM659 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM659 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM659 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM659 are further described hereinbelow with reference to Table Table1.

[10449] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM659 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10450] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 660 (GAM660) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[10451] GAM660 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM660 was detected is described hereinabove with reference to Figs. 2-8.

[10452] GAM660 gene, herein designated GAM GENE, and GAM660 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10453] GAM660 gene, herein designated GAM GENE, encodes a GAM660 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM660 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM660 precursor RNA is designated SEQ ID:633, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:633 is located at position 7933233 relative to contig NT_033899.3, on chromosome 11.

[10454] GAM660 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences

of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[10455] SEQ ID:99245 detected in mouse EST Accession BI411194.1.

[10456] SEQ ID:98384 detected in mouse EST Accession BI411194.1.

[10457] GAM660 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM660 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10458] An enzyme complex designated DICER COMPLEX, dices the GAM660 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM660 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM660 RNA is designated SEQ ID:2309, and is provided hereinbelow with reference to the sequence listing part.

[10459] GAM660 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM660 target RNA, herein designated GAM TARGET RNA. GAM660 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10460] GAM660 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM660 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM660 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM660 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM660 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10461] The complementary binding of GAM660 RNA, herein designated GAM RNA, to target binding sites on GAM660 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM660 target RNA, herein designated GAM TARGET RNA, into GAM660 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10462] It is appreciated that GAM660 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM660 target genes. The mRNA of each one of this plurality of GAM660 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM660 RNA,

herein designated GAM RNA, and which when bound by GAM660 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM660 target proteins.

[10463] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM660 gene, herein designated GAM GENE, on one or more GAM660 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10464] It is yet further appreciated that specific functions, and accordingly utilities, of GAM660 correlate with, and may be deduced from, the identity of the target genes which

GAM660 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10465] Nucleotide sequences of the GAM660 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM660 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM660 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM660 are further described hereinbelow with reference to Table Table1.

[10466] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM660 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10467] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 661 (GAM661) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10468] GAM661 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM661 was detected is described hereinabove with reference to Figs. 2-8.

[10469] GAM661 gene, herein designated GAM GENE, and GAM661 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10470] GAM661 gene, herein designated GAM GENE, encodes a GAM661 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM661 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM661 precursor RNA is designated SEQ ID:634, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:634 is located at position 10031168 relative to contig NT_006431.11, on chromosome 5.

[10471] GAM661 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM661 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10472] An enzyme complex designated DICER COMPLEX, dices the GAM661 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM661 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM661 RNA is designated SEQ ID:2310, and is provided hereinbelow with reference to the sequence listing part.

[10473] GAM661 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM661 target RNA, herein designated GAM TARGET RNA. GAM661 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10474] GAM661 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM661 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM661 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM661 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM661 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10475] The complementary binding of GAM661 RNA, herein designated GAM RNA, to target binding sites on GAM661 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM661 target RNA, herein designated GAM TARGET RNA, into GAM661 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10476] It is appreciated that GAM661 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM661 target genes. The mRNA of each one of this plurality of GAM661 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM661 RNA, herein designated GAM RNA, and which when bound by GAM661 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM661 target proteins.

[10477] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM661 gene, herein designated GAM GENE, on one or more GAM661 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10478] It is yet further appreciated that specific functions, and accordingly utilities, of GAM661 correlate with, and may be deduced from, the identity of the target genes which GAM661 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10479] Nucleotide sequences of the GAM661 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM661 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM661 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM661 are further described hereinbelow with reference to Table Table1.

[10480] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM661 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10481] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 662 (GAM662) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10482] GAM662 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM662 was detected is described hereinabove with reference to Figs. 2-8.

[10483] GAM662 gene, herein designated GAM GENE, and GAM662 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10484] GAM662 gene, herein designated GAM GENE, encodes a GAM662 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM662 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM662 precursor RNA is designated SEQ ID:635, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:635 is located at position 5750768 relative to contig NT_010966.11, on chromosome 18.

[10485] GAM662 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM662 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10486] An enzyme complex designated DICER COMPLEX, dices the GAM662 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM662 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM662 RNA is designated SEQ ID:2311, and is provided

hereinbelow with reference to the sequence listing part.

[10487] GAM662 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM662 target RNA, herein designated GAM TARGET RNA.

GAM662 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10488] GAM662 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM662 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM662 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM662 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM662 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10489] The complementary binding of GAM662 RNA, herein designated GAM RNA, to target binding sites on GAM662 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM662 target RNA, herein designated GAM TARGET RNA, into GAM662 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10490] It is appreciated that GAM662 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM662 target genes. The mRNA of each one of this plurality of GAM662 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM662 RNA, herein designated GAM RNA, and which when bound by GAM662 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM662 tar-

get proteins.

[10491] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM662 gene, herein designated GAM GENE, on one or more GAM662 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10492] It is yet further appreciated that specific functions, and accordingly utilities, of GAM662 correlate with, and may be deduced from, the identity of the target genes which GAM662 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10493] Nucleotide sequences of the GAM662 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM662 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM662 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM662 are further described hereinbelow with reference to Table Table1.

[10494] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM662 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10495] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 663 (GAM663) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10496] GAM663 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM663 was detected is described hereinabove with reference to Figs. 2-8.

[10497] GAM663 gene, herein designated GAM GENE, and

GAM663 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10498] GAM663 gene, herein designated GAM GENE, encodes a GAM663 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM663 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM663 precursor RNA is designated SEQ ID:636, and is provided hereinbelow with reference to the sequence listing part.

[10499] GAM663 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10500] An enzyme complex designated DICER COMPLEX, dices the GAM663 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM663 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM663 RNA is designated SEQ ID:2312, and is provided hereinbelow with reference to the sequence listing part.

[10501] GAM663 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM663 target RNA, herein designated GAM TARGET RNA. GAM663 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10502] GAM663 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM663 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM663 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM663 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM663 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10503] The complementary binding of GAM663 RNA, herein designated GAM RNA, to target binding sites on GAM663 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM663 target RNA, herein designated GAM TARGET RNA, into GAM663 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10504] It is appreciated that GAM663 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM663 target genes. The mRNA of each one of this plurality of GAM663 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM663 RNA, herein designated GAM RNA, and which when bound by GAM663 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM663 target proteins.

[10505] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM663 gene, herein designated GAM GENE, on one or more GAM663 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10506] It is yet further appreciated that specific functions, and accordingly utilities, of GAM663 correlate with, and may be deduced from, the identity of the target genes which GAM663 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10507] Nucleotide sequences of the GAM663 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM663 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM663 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM663 are further described hereinbelow with reference to Table Table1.

[10508] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM663 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10509] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

664 (GAM664) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10510] GAM664 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM664 was detected is described hereinabove with reference to Figs. 2-8.

[10511] GAM664 gene, herein designated GAM GENE, and GAM664 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10512] GAM664 gene, herein designated GAM GENE, encodes a GAM664 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM664 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM664 precursor RNA is designated SEQ ID:637, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:637 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[10513] GAM664 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM664 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10514] An enzyme complex designated DICER COMPLEX, dices the GAM664 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM664 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM664 RNA is designated SEQ ID:2313, and is provided hereinbelow with reference to the sequence listing part.

[10515] GAM664 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM664 target RNA, herein designated GAM TARGET RNA. GAM664 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10516] GAM664 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM664 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM664 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM664 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM664 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[10517] The complementary binding of GAM664 RNA, herein designated GAM RNA, to target binding sites on GAM664 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM664 target RNA, herein designated GAM TARGET RNA, into GAM664 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10518] It is appreciated that GAM664 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM664 target genes. The mRNA of each one of this plurality of GAM664 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM664 RNA, herein designated GAM RNA, and which when bound by GAM664 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM664 target proteins.

[10519] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM664 gene, herein designated GAM GENE, on one or

more GAM664 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10520] It is yet further appreciated that specific functions, and accordingly utilities, of GAM664 correlate with, and may be deduced from, the identity of the target genes which GAM664 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10521] Nucleotide sequences of the GAM664 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM664 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM664 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM664 are further de-

scribed hereinbelow with reference to Table Table1.

[10522] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM664 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10523] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 665 (GAM665) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10524] GAM665 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM665 was detected is described hereinabove with reference to Figs. 2-8.

[10525] GAM665 gene, herein designated GAM GENE, and GAM665 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10526] GAM665 gene, herein designated GAM GENE, encodes a GAM665 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM665 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM665 precursor RNA is designated SEQ ID:638, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:638 is located at position 1471884 relative to contig NT_027140.5, on chromosome 13.

[10527] GAM665 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10528] An enzyme complex designated DICER COMPLEX, dices the GAM665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM665 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM665 RNA is designated SEQ ID:2314, and is provided hereinbelow with reference to the sequence listing part.

[10529] GAM665 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM665 target RNA, herein designated GAM TARGET RNA. GAM665 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10530] GAM665 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM665 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM665 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM665 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM665 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10531] The complementary binding of GAM665 RNA, herein designated GAM RNA, to target binding sites on GAM665 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM665 target RNA, herein designated GAM TARGET RNA, into GAM665 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10532] It is appreciated that GAM665 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM665 target genes. The mRNA of each one of this plurality of GAM665 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM665 RNA, herein designated GAM RNA, and which when bound by GAM665 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM665 target proteins.

[10533] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM665 gene, herein designated GAM GENE, on one or more GAM665 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10534] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM665 correlate with, and may be deduced from, the identity of the target genes which GAM665 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10535] Nucleotide sequences of the GAM665 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM665 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM665 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM665 are further described hereinbelow with reference to Table Table1.

[10536] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM665 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10537] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 666 (GAM666) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10538] GAM666 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM666 was detected is described hereinabove with reference to Figs. 2-8.

[10539] GAM666 gene, herein designated GAM GENE, and GAM666 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10540] GAM666 gene, herein designated GAM GENE, encodes a GAM666 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM666 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM666 precursor RNA is designated SEQ ID:639, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:639 is located at position 280476 relative to contig NT_007758.8, on chromosome 7.

[10541] GAM666 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM666 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10542] An enzyme complex designated DICER COMPLEX, dices the GAM666 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM666 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM666 RNA is designated SEQ ID:2315, and is provided hereinbelow with reference to the sequence listing part.

[10543] GAM666 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM666 target RNA, herein designated GAM TARGET RNA.

GAM666 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[10544] GAM666 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM666 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM666 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM666 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM666 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10545] The complementary binding of GAM666 RNA, herein designated GAM RNA, to target binding sites on GAM666 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM666 target RNA, herein designated GAM TARGET RNA, into GAM666 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10546] It is appreciated that GAM666 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM666 target genes. The mRNA of each one of this plurality of GAM666 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM666 RNA, herein designated GAM RNA, and which when bound by GAM666 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM666 target proteins.

[10547] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM666 gene, herein designated GAM GENE, on one or more GAM666 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10548] It is yet further appreciated that specific functions, and accordingly utilities, of GAM666 correlate with, and may be deduced from, the identity of the target genes which GAM666 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10549] Nucleotide sequences of the GAM666 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM666 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM666 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM666 are further described hereinbelow with reference to Table Table1.

[10550] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM666 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10551] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 667 (GAM667) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10552] GAM667 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM667 was detected is described hereinabove with reference to Figs. 2-8.

[10553] GAM667 gene, herein designated GAM GENE, and GAM667 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10554] GAM667 gene, herein designated GAM GENE, encodes a GAM667 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM667 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM667 precursor RNA is designated SEQ ID:640, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:640 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[10555] GAM667 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM667 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10556] An enzyme complex designated DICER COMPLEX, dices the GAM667 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM667 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM667 RNA is designated SEQ ID:2316, and is provided hereinbelow with reference to the sequence listing part.

[10557] GAM667 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM667 target RNA, herein designated GAM TARGET RNA. GAM667 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10558] GAM667 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM667 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM667 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM667 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM667 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10559] The complementary binding of GAM667 RNA, herein designated GAM RNA, to target binding sites on GAM667 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM667 target RNA, herein designated GAM TARGET RNA, into GAM667 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10560] It is appreciated that GAM667 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM667 target genes. The mRNA of each one of this plurality of GAM667 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM667 RNA, herein designated GAM RNA, and which when bound by

GAM667 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM667 target proteins.

[10561] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM667 gene, herein designated GAM GENE, on one or more GAM667 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10562] It is yet further appreciated that specific functions, and accordingly utilities, of GAM667 correlate with, and may be deduced from, the identity of the target genes which GAM667 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[10563] Nucleotide sequences of the GAM667 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM667 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM667 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM667 are further described hereinbelow with reference to Table Table1.

[10564] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM667 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10565] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 668 (GAM668) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10566] GAM668 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM668 was detected is described hereinabove

with reference to Figs. 2-8.

[10567] GAM668 gene, herein designated GAM GENE, and GAM668 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10568] GAM668 gene, herein designated GAM GENE, encodes a GAM668 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM668 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM668 precursor RNA is designated SEQ ID:641, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:641 is located at position 280476 relative to contig NT_007758.8, on chromosome 7.

[10569] GAM668 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM668 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[10570] An enzyme complex designated DICER COMPLEX, dices the GAM668 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM668 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM668 RNA is designated SEQ ID:2317, and is provided hereinbelow with reference to the sequence listing part.

[10571] GAM668 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM668 target RNA, herein designated GAM TARGET RNA.
GAM668 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10572] GAM668 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM668 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM668 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM668 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM668 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10573] The complementary binding of GAM668 RNA, herein designated GAM RNA, to target binding sites on GAM668 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM668 target RNA, herein desig-

nated GAM TARGET RNA, into GAM668 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10574] It is appreciated that GAM668 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM668 target genes. The mRNA of each one of this plurality of GAM668 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM668 RNA, herein designated GAM RNA, and which when bound by GAM668 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM668 target proteins.

[10575] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM668 gene, herein designated GAM GENE, on one or more GAM668 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10576] It is yet further appreciated that specific functions, and accordingly utilities, of GAM668 correlate with, and may be deduced from, the identity of the target genes which GAM668 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10577] Nucleotide sequences of the GAM668 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM668 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM668 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM668 are further described hereinbelow with reference to Table Table1.

[10578] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM668 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[10579] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 669 (GAM669) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10580] GAM669 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM669 was detected is described hereinabove with reference to Figs. 2-8.

[10581] GAM669 gene, herein designated GAM GENE, and GAM669 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10582] GAM669 gene, herein designated GAM GENE, encodes a GAM669 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM669 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM669 precursor RNA is designated SEQ ID:642, and is provided hereinbelow with reference to the sequence listing part.

[10583] GAM669 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM669 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10584] An enzyme complex designated DICER COMPLEX, dices the GAM669 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM669 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM669 RNA is designated SEQ ID:2318, and is provided hereinbelow with reference to the sequence listing part.

[10585] GAM669 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM669

target RNA, herein designated GAM TARGET RNA.

GAM669 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10586] GAM669 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM669 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM669 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM669 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM669 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10587] The complementary binding of GAM669 RNA, herein designated GAM RNA, to target binding sites on GAM669 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM669 target RNA, herein designated GAM TARGET RNA, into GAM669 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10588] It is appreciated that GAM669 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM669 target genes. The mRNA of each one of this plurality of GAM669 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM669 RNA, herein designated GAM RNA, and which when bound by GAM669 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM669 target proteins.

[10589] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM669 gene, herein designated GAM GENE, on one or more GAM669 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10590] It is yet further appreciated that specific functions, and accordingly utilities, of GAM669 correlate with, and may be deduced from, the identity of the target genes which GAM669 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10591] Nucleotide sequences of the GAM669 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM669 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM669 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM669 are further described hereinbelow with reference to Table Table1.

[10592] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM669 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10593] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 670 (GAM670) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10594] GAM670 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM670 was detected is described hereinabove with reference to Figs. 2-8.

[10595] GAM670 gene, herein designated GAM GENE, and GAM670 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10596] GAM670 gene, herein designated GAM GENE, encodes a

GAM670 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM670 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM670 precursor RNA is designated SEQ ID:643, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:643 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[10597] GAM670 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM670 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10598] An enzyme complex designated DICER COMPLEX, dices the GAM670 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM670 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM670 RNA is designated SEQ ID:2319, and is provided hereinbelow with reference to the sequence listing part.

[10599] GAM670 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM670 target RNA, herein designated GAM TARGET RNA.
GAM670 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10600] GAM670 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM670 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM670 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM670 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM670 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10601] The complementary binding of GAM670 RNA, herein designated GAM RNA, to target binding sites on GAM670 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM670 target RNA, herein designated GAM TARGET RNA, into GAM670 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10602] It is appreciated that GAM670 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM670 target genes. The mRNA of each one of this plurality of GAM670 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM670 RNA, herein designated GAM RNA, and which when bound by GAM670 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM670 target proteins.

[10603] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM670 gene, herein designated GAM GENE, on one or more GAM670 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[10604] It is yet further appreciated that specific functions, and accordingly utilities, of GAM670 correlate with, and may be deduced from, the identity of the target genes which GAM670 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10605] Nucleotide sequences of the GAM670 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM670 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM670 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM670 are further described hereinbelow with reference to Table Table1.

[10606] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM670 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10607] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 671 (GAM671) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[10608] GAM671 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM671 was detected is described hereinabove with reference to Figs. 2-8.

[10609] GAM671 gene, herein designated GAM GENE, and GAM671 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10610] GAM671 gene, herein designated GAM GENE, encodes a GAM671 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM671 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM671 precursor RNA is designated SEQ ID:644, and is provided hereinbelow with reference to the sequence listing part.

[10611] GAM671 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[10612] SEQ ID:100043 detected in mouse EST Accession BF465648.1.

[10613] SEQ ID:100044 detected in mouse EST Accession AI591965.1.

[10614] SEQ ID:100045 detected in mouse EST Accession AA184398.1.

[10615] GAM671 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10616] An enzyme complex designated DICER COMPLEX, dices the GAM671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM671 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 97%) nucleotide sequence of GAM671 RNA is designated SEQ ID:2320, and is provided hereinbelow with reference to the sequence listing part.

[10617] GAM671 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM671 target RNA, herein designated GAM TARGET RNA. GAM671 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10618] GAM671 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM671 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM671 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM671 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM671 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10619] The complementary binding of GAM671 RNA, herein designated GAM RNA, to target binding sites on GAM671 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM671 target RNA, herein designated GAM TARGET RNA, into GAM671 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10620] It is appreciated that GAM671 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM671 target genes. The mRNA of each one of this plurality of GAM671 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM671 RNA,

herein designated GAM RNA, and which when bound by GAM671 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM671 target proteins.

[10621] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM671 gene, herein designated GAM GENE, on one or more GAM671 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10622] It is yet further appreciated that specific functions, and accordingly utilities, of GAM671 correlate with, and may be deduced from, the identity of the target genes which

GAM671 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10623] Nucleotide sequences of the GAM671 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM671 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM671 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM671 are further described hereinbelow with reference to Table Table1.

[10624] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM671 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10625] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 672 (GAM672) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10626] GAM672 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM672 was detected is described hereinabove with reference to Figs. 2-8.

[10627] GAM672 gene, herein designated GAM GENE, and GAM672 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10628] GAM672 gene, herein designated GAM GENE, encodes a GAM672 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM672 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM672 precursor RNA is designated SEQ ID:645, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:645 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[10629] GAM672 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10630] An enzyme complex designated DICER COMPLEX, dices the GAM672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM672 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM672 RNA is designated SEQ ID:2321, and is provided hereinbelow with reference to the sequence listing part.

[10631] GAM672 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM672 target RNA, herein designated GAM TARGET RNA. GAM672 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10632] GAM672 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM672 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM672 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM672 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM672 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10633] The complementary binding of GAM672 RNA, herein designated GAM RNA, to target binding sites on GAM672 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM672 target RNA, herein designated GAM TARGET RNA, into GAM672 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10634] It is appreciated that GAM672 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM672 target genes. The mRNA of each one of this plurality of GAM672 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM672 RNA, herein designated GAM RNA, and which when bound by GAM672 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM672 target proteins.

[10635] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM672 gene, herein designated GAM GENE, on one or more GAM672 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10636] It is yet further appreciated that specific functions, and accordingly utilities, of GAM672 correlate with, and may be deduced from, the identity of the target genes which GAM672 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10637] Nucleotide sequences of the GAM672 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM672 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM672 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM672 are further described hereinbelow with reference to Table Table1.

[10638] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM672 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10639] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 673 (GAM673) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10640] GAM673 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM673 was detected is described hereinabove with reference to Figs. 2-8.

[10641] GAM673 gene, herein designated GAM GENE, and GAM673 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10642] GAM673 gene, herein designated GAM GENE, encodes a GAM673 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM673 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM673 precursor RNA is designated SEQ ID:646, and is provided hereinbelow with refer-

ence to the sequence listing part.

[10643] GAM673 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10644] An enzyme complex designated DICER COMPLEX, dices the GAM673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM673 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM673 RNA is designated SEQ ID:2322, and is provided hereinbelow with reference to the sequence listing part.

[10645] GAM673 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM673 target RNA, herein designated GAM TARGET RNA.

GAM673 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10646] GAM673 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM673 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM673 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM673 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM673 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10647] The complementary binding of GAM673 RNA, herein designated GAM RNA, to target binding sites on GAM673 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM673 target RNA, herein designated GAM TARGET RNA, into GAM673 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10648] It is appreciated that GAM673 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM673 target genes. The mRNA of each one of this plurality of GAM673 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM673 RNA, herein designated GAM RNA, and which when bound by GAM673 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM673 target proteins.

[10649] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM673 gene, herein designated GAM GENE, on one or more GAM673 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10650] It is yet further appreciated that specific functions, and accordingly utilities, of GAM673 correlate with, and may be deduced from, the identity of the target genes which GAM673 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10651] Nucleotide sequences of the GAM673 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM673 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM673 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM673 are further described hereinbelow with reference to Table Table1.

[10652] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM673 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10653] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 674 (GAM674) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10654] GAM674 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM674 was detected is described hereinabove with reference to Figs. 2-8.

[10655] GAM674 gene, herein designated GAM GENE, and GAM674 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10656] GAM674 gene, herein designated GAM GENE, encodes a GAM674 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM674 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM674 precursor RNA is designated SEQ ID:647, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:647 is located at position 1654434 relative to contig NT_005986.13, on chromosome 3.

[10657] GAM674 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10658] An enzyme complex designated DICER COMPLEX, dices the GAM674 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM674 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM674 RNA is designated SEQ ID:2323, and is provided hereinbelow with reference to the sequence listing part.

[10659] GAM674 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM674 target RNA, herein designated GAM TARGET RNA. GAM674 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10660] GAM674 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM674 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM674 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM674 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM674 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10661] The complementary binding of GAM674 RNA, herein designated GAM RNA, to target binding sites on GAM674 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM674 target RNA, herein designated GAM TARGET RNA, into GAM674 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10662] It is appreciated that GAM674 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM674 target genes. The mRNA of each one of this plurality of GAM674 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM674 RNA, herein designated GAM RNA, and which when bound by GAM674 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM674 target proteins.

[10663] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM674 gene, herein designated GAM GENE, on one or more GAM674 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10664] It is yet further appreciated that specific functions, and accordingly utilities, of GAM674 correlate with, and may be deduced from, the identity of the target genes which GAM674 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10665] Nucleotide sequences of the GAM674 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM674 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM674 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM674 are further described hereinbelow with reference to Table Table1.

[10666] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM674 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10667] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

675 (GAM675) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10668] GAM675 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM675 was detected is described hereinabove with reference to Figs. 2-8.

[10669] GAM675 gene, herein designated GAM GENE, and GAM675 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10670] GAM675 gene, herein designated GAM GENE, encodes a GAM675 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM675 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM675 precursor RNA is designated SEQ ID:648, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:648 is located at position 21828628 relative to contig NT_007299.11, on chromosome 6.

[10671] GAM675 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM675 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10672] An enzyme complex designated DICER COMPLEX, dices the GAM675 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM675 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM675 RNA is designated SEQ ID:2324, and is provided hereinbelow with reference to the sequence listing part.

[10673] GAM675 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM675 target RNA, herein designated GAM TARGET RNA. GAM675 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10674] GAM675 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM675 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM675 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM675 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM675 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[10675] The complementary binding of GAM675 RNA, herein designated GAM RNA, to target binding sites on GAM675 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM675 target RNA, herein designated GAM TARGET RNA, into GAM675 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10676] It is appreciated that GAM675 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM675 target genes. The mRNA of each one of this plurality of GAM675 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM675 RNA, herein designated GAM RNA, and which when bound by GAM675 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM675 target proteins.

[10677] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM675 gene, herein designated GAM GENE, on one or

more GAM675 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10678] It is yet further appreciated that specific functions, and accordingly utilities, of GAM675 correlate with, and may be deduced from, the identity of the target genes which GAM675 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10679] Nucleotide sequences of the GAM675 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM675 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM675 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM675 are further de-

scribed hereinbelow with reference to Table Table1.

[10680] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM675 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10681] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 676 (GAM676) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10682] GAM676 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM676 was detected is described hereinabove with reference to Figs. 2-8.

[10683] GAM676 gene, herein designated GAM GENE, and GAM676 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10684] GAM676 gene, herein designated GAM GENE, encodes a GAM676 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM676 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM676 precursor RNA is designated SEQ ID:649, and is provided hereinbelow with reference to the sequence listing part.

[10685] GAM676 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM676 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10686] An enzyme complex designated DICER COMPLEX, dices the GAM676 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM676 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM676 RNA is designated SEQ ID:2325, and is provided hereinbelow with reference to the sequence listing part.

[10687] GAM676 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM676 target RNA, herein designated GAM TARGET RNA. GAM676 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10688] GAM676 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM676 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM676 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM676 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM676 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10689] The complementary binding of GAM676 RNA, herein designated GAM RNA, to target binding sites on GAM676 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM676 target RNA, herein designated GAM TARGET RNA, into GAM676 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10690] It is appreciated that GAM676 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM676 target genes. The mRNA of each one of this plurality of GAM676 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM676 RNA,

herein designated GAM RNA, and which when bound by GAM676 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM676 target proteins.

[10691] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM676 gene, herein designated GAM GENE, on one or more GAM676 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10692] It is yet further appreciated that specific functions, and accordingly utilities, of GAM676 correlate with, and may be deduced from, the identity of the target genes which

GAM676 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10693] Nucleotide sequences of the GAM676 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM676 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM676 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM676 are further described hereinbelow with reference to Table Table1.

[10694] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM676 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10695] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 677 (GAM677) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10696] GAM677 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM677 was detected is described hereinabove with reference to Figs. 2-8.

[10697] GAM677 gene, herein designated GAM GENE, and GAM677 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10698] GAM677 gene, herein designated GAM GENE, encodes a GAM677 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM677 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM677 precursor RNA is designated SEQ ID:650, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:650 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[10699] GAM677 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM677 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10700] An enzyme complex designated DICER COMPLEX, dices the GAM677 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM677 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM677 RNA is designated SEQ ID:2326, and is provided hereinbelow with reference to the sequence listing part.

[10701] GAM677 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM677 target RNA, herein designated GAM TARGET RNA. GAM677 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10702] GAM677 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM677 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM677 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM677 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM677 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10703] The complementary binding of GAM677 RNA, herein designated GAM RNA, to target binding sites on GAM677 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM677 target RNA, herein designated GAM TARGET RNA, into GAM677 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10704] It is appreciated that GAM677 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM677 target genes. The mRNA of each one of this plurality of GAM677 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM677 RNA, herein designated GAM RNA, and which when bound by GAM677 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM677 target proteins.

[10705] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM677 gene, herein designated GAM GENE, on one or more GAM677 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10706] It is yet further appreciated that specific functions, and accordingly utilities, of GAM677 correlate with, and may be deduced from, the identity of the target genes which GAM677 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10707] Nucleotide sequences of the GAM677 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM677 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM677 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM677 are further described hereinbelow with reference to Table Table1.

[10708] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM677 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10709] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 678 (GAM678) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10710] GAM678 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM678 was detected is described hereinabove with reference to Figs. 2-8.

[10711] GAM678 gene, herein designated GAM GENE, and GAM678 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10712] GAM678 gene, herein designated GAM GENE, encodes a GAM678 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM678 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM678 precursor RNA is designated SEQ ID:651, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:651 is located at position 182403 relative to contig NT_030685.4, on chromosome 5.

[10713] GAM678 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10714] An enzyme complex designated DICER COMPLEX, dices the GAM678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM678 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM678 RNA is designated SEQ ID:2327, and is provided

hereinbelow with reference to the sequence listing part.

[10715] GAM678 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM678 target RNA, herein designated GAM TARGET RNA. GAM678 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10716] GAM678 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM678 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM678 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM678 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM678 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10717] The complementary binding of GAM678 RNA, herein designated GAM RNA, to target binding sites on GAM678 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM678 target RNA, herein designated GAM TARGET RNA, into GAM678 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10718] It is appreciated that GAM678 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM678 target genes. The mRNA of each one of this plurality of GAM678 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM678 RNA, herein designated GAM RNA, and which when bound by GAM678 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM678 tar-

get proteins.

[10719] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM678 gene, herein designated GAM GENE, on one or more GAM678 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10720] It is yet further appreciated that specific functions, and accordingly utilities, of GAM678 correlate with, and may be deduced from, the identity of the target genes which GAM678 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10721] Nucleotide sequences of the GAM678 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM678 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM678 are further described hereinbelow with reference to Table Table1.

[10722] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM678 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10723] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 679 (GAM679) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10724] GAM679 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM679 was detected is described hereinabove with reference to Figs. 2-8.

[10725] GAM679 gene, herein designated GAM GENE, and

GAM679 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10726] GAM679 gene, herein designated GAM GENE, encodes a GAM679 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM679 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM679 precursor RNA is designated SEQ ID:652, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:652 is located at position 7218844 relative to contig NT_011812.10, on chromosome X.

[10727] GAM679 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM679 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10728] An enzyme complex designated DICER COMPLEX, dices the GAM679 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM679 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM679 RNA is designated SEQ ID:2328, and is provided hereinbelow with reference to the sequence listing part.

[10729] GAM679 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM679 target RNA, herein designated GAM TARGET RNA. GAM679 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10730] GAM679 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM679 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM679 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM679 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM679 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10731] The complementary binding of GAM679 RNA, herein designated GAM RNA, to target binding sites on GAM679 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM679 target RNA, herein designated GAM TARGET RNA, into GAM679 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[10732] It is appreciated that GAM679 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM679 target genes. The mRNA of each one of this plurality of GAM679 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM679 RNA, herein designated GAM RNA, and which when bound by GAM679 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM679 target proteins.

[10733] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM679 gene, herein designated GAM GENE, on one or more GAM679 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10734] It is yet further appreciated that specific functions, and accordingly utilities, of GAM679 correlate with, and may be deduced from, the identity of the target genes which GAM679 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10735] Nucleotide sequences of the GAM679 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM679 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM679 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM679 are further described hereinbelow with reference to Table Table1.

[10736] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM679 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10737] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 680 (GAM680) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10738] GAM680 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM680 was detected is described hereinabove with reference to Figs. 2-8.

[10739] GAM680 gene, herein designated GAM GENE, and GAM680 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10740] GAM680 gene, herein designated GAM GENE, encodes a GAM680 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM680 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM680 precursor RNA is designated SEQ ID:653, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:653 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[10741] GAM680 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[10742] SEQ ID:99829 detected in mouse EST Accession BB610842.1.

[10743] SEQ ID:99830 detected in mouse EST Accession BB609859.1.

[10744] SEQ ID:99831 detected in mouse EST Accession AW824753.1.

[10745] SEQ ID:99832 detected in mouse EST Accession BE943987.1.

[10746] SEQ ID:99833 detected in mouse EST Accession BG145596.1.

[10747] SEQ ID:99834 detected in mouse EST Accession BE692802.1.

[10748] SEQ ID:99835 detected in mouse EST Accession AW208601.1.

[10749] SEQ ID:99836 detected in mouse EST Accession AA144533.1.

[10750] SEQ ID:99837 detected in mouse EST Accession AA671455.1.

[10751] SEQ ID:99838 detected in mouse EST Accession BE691447.1.

[10752] SEQ ID:99840 detected in mouse EST Accession BE691413.1.

[10753] SEQ ID:99841 detected in mouse EST Accession BG808025.1.

[10754] SEQ ID:99842 detected in mouse EST Accession BG808010.1.

[10755] SEQ ID:99843 detected in mouse EST Accession BG807850.1.

[10756] SEQ ID:99844 detected in mouse EST Accession BG805970.1.

[10757] GAM680 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM680 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10758] An enzyme complex designated DICER COMPLEX, dices

the GAM680 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM680 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM680 RNA is designated SEQ ID:2329, and is provided hereinbelow with reference to the sequence listing part.

[10759] GAM680 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM680 target RNA, herein designated GAM TARGET RNA. GAM680 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10760] GAM680 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM680 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM680

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM680 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM680 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10761] The complementary binding of GAM680 RNA, herein designated GAM RNA, to target binding sites on GAM680 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM680 target RNA, herein designated GAM TARGET RNA, into GAM680 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10762] It is appreciated that GAM680 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM680 target genes. The mRNA of each one of this plurality of GAM680 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM680 RNA, herein designated GAM RNA, and which when bound by GAM680 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM680 target proteins.

[10763] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM680 gene, herein designated GAM GENE, on one or more GAM680 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10764] It is yet further appreciated that specific functions, and accordingly utilities, of GAM680 correlate with, and may be deduced from, the identity of the target genes which GAM680 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10765] Nucleotide sequences of the GAM680 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM680 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM680 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM680 are further described hereinbelow with reference to Table Table1.

[10766] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM680 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10767] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 681 (GAM681) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10768] GAM681 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM681 was detected is described hereinabove with reference to Figs. 2-8.

[10769] GAM681 gene, herein designated GAM GENE, and GAM681 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10770] GAM681 gene, herein designated GAM GENE, encodes a GAM681 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM681 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM681 precursor RNA is designated SEQ ID:654, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:654 is located at position 2206001 relative to contig NT_022135.11, on chromosome 2.

[10771] GAM681 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM681 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10772] An enzyme complex designated DICER COMPLEX, dices the GAM681 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM681 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM681 RNA is designated SEQ ID:2330, and is provided hereinbelow with reference to the sequence listing part.

[10773] GAM681 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM681 target RNA, herein designated GAM TARGET RNA.

GAM681 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10774] GAM681 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM681 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM681 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM681 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM681 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10775] The complementary binding of GAM681 RNA, herein designated GAM RNA, to target binding sites on GAM681 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM681 target RNA, herein designated GAM TARGET RNA, into GAM681 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10776] It is appreciated that GAM681 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM681 target genes. The mRNA of each one of this plurality of GAM681 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM681 RNA, herein designated GAM RNA, and which when bound by GAM681 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM681 target proteins.

[10777] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM681 gene, herein designated GAM GENE, on one or more GAM681 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10778] It is yet further appreciated that specific functions, and accordingly utilities, of GAM681 correlate with, and may be deduced from, the identity of the target genes which GAM681 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10779] Nucleotide sequences of the GAM681 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM681 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM681 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM681 are further described hereinbelow with reference to Table Table1.

[10780] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM681 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10781] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 682 (GAM682) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10782] GAM682 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM682 was detected is described hereinabove with reference to Figs. 2-8.

[10783] GAM682 gene, herein designated GAM GENE, and GAM682 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10784] GAM682 gene, herein designated GAM GENE, encodes a GAM682 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM682 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM682 precursor RNA is designated SEQ ID:655, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:655 is located at position 4851355 relative to contig NT_022517.13, on chromosome 3.

[10785] GAM682 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM682 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10786] An enzyme complex designated DICER COMPLEX, dices the GAM682 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM682 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM682 RNA is designated SEQ ID:2331, and is provided hereinbelow with reference to the sequence listing part.

[10787] GAM682 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM682 target RNA, herein designated GAM TARGET RNA. GAM682 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10788] GAM682 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM682 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM682 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM682 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM682 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10789] The complementary binding of GAM682 RNA, herein designated GAM RNA, to target binding sites on GAM682 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM682 target RNA, herein designated GAM TARGET RNA, into GAM682 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10790] It is appreciated that GAM682 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM682 target genes. The mRNA of each one of this plu-

rality of GAM682 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM682 RNA, herein designated GAM RNA, and which when bound by GAM682 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM682 target proteins.

[10791] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM682 gene, herein designated GAM GENE, on one or more GAM682 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10792] It is yet further appreciated that specific functions, and accordingly utilities, of GAM682 correlate with, and may be deduced from, the identity of the target genes which GAM682 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10793] Nucleotide sequences of the GAM682 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM682 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM682 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM682 are further described hereinbelow with reference to Table Table1.

[10794] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM682 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10795] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 683 (GAM683) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[10796] GAM683 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM683 was detected is described hereinabove with reference to Figs. 2-8.

[10797] GAM683 gene, herein designated GAM GENE, and GAM683 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10798] GAM683 gene, herein designated GAM GENE, encodes a GAM683 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM683 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM683 precursor RNA is designated SEQ ID:656, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:656 is located at position 7933233 relative to contig NT_033899.3, on chromosome 11.

[10799] GAM683 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:100319, which mouse homolog is detected in

mouse EST accession BI411194.1.

[10800] GAM683 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM683 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10801] An enzyme complex designated DICER COMPLEX, dices the GAM683 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM683 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM683 RNA is designated SEQ ID:2332, and is provided hereinbelow with reference to the sequence listing part.

[10802] GAM683 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM683 target RNA, herein designated GAM TARGET RNA.

GAM683 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10803] GAM683 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM683 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM683 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM683 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM683 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10804] The complementary binding of GAM683 RNA, herein designated GAM RNA, to target binding sites on GAM683 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM683 target RNA, herein designated GAM TARGET RNA, into GAM683 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10805] It is appreciated that GAM683 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM683 target genes. The mRNA of each one of this plurality of GAM683 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM683 RNA, herein designated GAM RNA, and which when bound by GAM683 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM683 target proteins.

[10806] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM683 gene, herein designated GAM GENE, on one or more GAM683 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10807] It is yet further appreciated that specific functions, and accordingly utilities, of GAM683 correlate with, and may be deduced from, the identity of the target genes which GAM683 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10808] Nucleotide sequences of the GAM683 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM683 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM683 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM683 are further described hereinbelow with reference to Table Table1.

[10809] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM683 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10810] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 684 (GAM684) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10811] GAM684 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM684 was detected is described hereinabove with reference to Figs. 2-8.

[10812] GAM684 gene, herein designated GAM GENE, and GAM684 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10813] GAM684 gene, herein designated GAM GENE, encodes a GAM684 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM684 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM684 precursor RNA is designated SEQ ID:657, and is provided hereinbelow with reference to the sequence listing part.

[10814] GAM684 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM684 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10815] An enzyme complex designated DICER COMPLEX, dices the GAM684 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM684 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM684 RNA is designated SEQ ID:2333, and is provided hereinbelow with reference to the sequence listing part.

[10816] GAM684 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM684 target RNA, herein designated GAM TARGET RNA. GAM684 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10817] GAM684 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM684 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM684 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM684 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM684 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10818] The complementary binding of GAM684 RNA, herein designated GAM RNA, to target binding sites on GAM684 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM684 target RNA, herein designated GAM TARGET RNA, into GAM684 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10819] It is appreciated that GAM684 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM684 target genes. The mRNA of each one of this plu-

rality of GAM684 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM684 RNA, herein designated GAM RNA, and which when bound by GAM684 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM684 target proteins.

[10820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM684 gene, herein designated GAM GENE, on one or more GAM684 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10821] It is yet further appreciated that specific functions, and accordingly utilities, of GAM684 correlate with, and may be deduced from, the identity of the target genes which GAM684 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10822] Nucleotide sequences of the GAM684 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM684 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM684 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM684 are further described hereinbelow with reference to Table Table1.

[10823] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM684 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10824] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 685 (GAM685) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[10825] GAM685 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM685 was detected is described hereinabove with reference to Figs. 2-8.

[10826] GAM685 gene, herein designated GAM GENE, and GAM685 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10827] GAM685 gene, herein designated GAM GENE, encodes a GAM685 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM685 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM685 precursor RNA is designated SEQ ID:658, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:658 is located at position 5750768 relative to contig NT_010966.11, on chromosome 18.

[10828] GAM685 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10829] An enzyme complex designated DICER COMPLEX, dices the GAM685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM685 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM685 RNA is designated SEQ ID:2334, and is provided hereinbelow with reference to the sequence listing part.

[10830] GAM685 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM685 target RNA, herein designated GAM TARGET RNA. GAM685 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10831] GAM685 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM685 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM685 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM685 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM685 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10832] The complementary binding of GAM685 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM685 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM685 target RNA, herein designated GAM TARGET RNA, into GAM685 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10833] It is appreciated that GAM685 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM685 target genes. The mRNA of each one of this plurality of GAM685 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM685 RNA, herein designated GAM RNA, and which when bound by GAM685 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM685 target proteins.

[10834] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM685 gene, herein designated GAM GENE, on one or more GAM685 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10835] It is yet further appreciated that specific functions, and accordingly utilities, of GAM685 correlate with, and may be deduced from, the identity of the target genes which GAM685 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10836] Nucleotide sequences of the GAM685 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM685 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM685 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM685 are further described hereinbelow with reference to Table Table1.

[10837] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM685 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10838] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 686 (GAM686) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10839] GAM686 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM686 was detected is described hereinabove with reference to Figs. 2-8.

[10840] GAM686 gene, herein designated GAM GENE, and GAM686 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10841] GAM686 gene, herein designated GAM GENE, encodes a GAM686 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM686 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM686 precursor RNA is designated SEQ ID:659, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:659 is located at position 2532028 relative to contig NT_011109.13, on chromosome 19.

[10842] GAM686 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[10843] SEQ ID:100140 detected in mouse EST Accession AA541834.1.

[10844] SEQ ID:100141 detected in mouse EST Accession AA606484.1.

[10845] SEQ ID:100142 detected in mouse EST Accession AA097502.1.

[10846] SEQ ID:100143 detected in mouse EST Accession BI111547.1.

[10847] GAM686 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM686 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10848] An enzyme complex designated DICER COMPLEX, dices the GAM686 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM686 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM686 RNA is designated SEQ ID:2335, and is provided hereinbelow with reference to the sequence listing part.

[10849] GAM686 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM686 target RNA, herein designated GAM TARGET RNA. GAM686 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10850] GAM686 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM686 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM686 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM686 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM686 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10851] The complementary binding of GAM686 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM686 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM686 target RNA, herein designated GAM TARGET RNA, into GAM686 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10852] It is appreciated that GAM686 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM686 target genes. The mRNA of each one of this plurality of GAM686 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM686 RNA, herein designated GAM RNA, and which when bound by GAM686 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM686 target proteins.

[10853] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM686 gene, herein designated GAM GENE, on one or more GAM686 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10854] It is yet further appreciated that specific functions, and accordingly utilities, of GAM686 correlate with, and may be deduced from, the identity of the target genes which GAM686 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10855] Nucleotide sequences of the GAM686 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM686 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM686 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM686 are further described hereinbelow with reference to Table Table1.

[10856] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM686 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10857] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 687 (GAM687) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10858] GAM687 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM687 was detected is described hereinabove with reference to Figs. 2-8.

[10859] GAM687 gene, herein designated GAM GENE, and GAM687 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10860] GAM687 gene, herein designated GAM GENE, encodes a GAM687 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM687 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM687 precursor RNA is designated SEQ ID:660, and is provided hereinbelow with reference to the sequence listing part.

[10861] GAM687 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM687 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10862] An enzyme complex designated DICER COMPLEX, dices the GAM687 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM687 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM687 RNA is designated SEQ ID:2336, and is provided hereinbelow with reference to the sequence listing part.

[10863] GAM687 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM687 target RNA, herein designated GAM TARGET RNA. GAM687 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10864] GAM687 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM687 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM687 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM687 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM687 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10865] The complementary binding of GAM687 RNA, herein designated GAM RNA, to target binding sites on GAM687 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM687 target RNA, herein designated GAM TARGET RNA, into GAM687 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10866] It is appreciated that GAM687 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM687 target genes. The mRNA of each one of this plurality of GAM687 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM687 RNA, herein designated GAM RNA, and which when bound by GAM687 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM687 target proteins.

[10867] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM687 gene, herein designated GAM GENE, on one or more GAM687 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10868] It is yet further appreciated that specific functions, and accordingly utilities, of GAM687 correlate with, and may be deduced from, the identity of the target genes which GAM687 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10869] Nucleotide sequences of the GAM687 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM687 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM687 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM687 are further described hereinbelow with reference to Table Table1.

[10870] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM687 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10871] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 688 (GAM688) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10872] GAM688 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM688 was detected is described hereinabove with reference to Figs. 2-8.

[10873] GAM688 gene, herein designated GAM GENE, and GAM688 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10874] GAM688 gene, herein designated GAM GENE, encodes a GAM688 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM688 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM688 precursor RNA is designated SEQ ID:661, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:661 is located at position 1235058 relative to contig NT_009526.11, on chromosome 12.

[10875] GAM688 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[10876] SEQ ID:99672 detected in mouse EST Accession BI965652.1.

[10877] SEQ ID:100217 detected in mouse EST Accession BI965972.1.

[10878] SEQ ID:100218 detected in mouse EST Accession AI326210.1.

[10879] GAM688 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM688 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10880] An enzyme complex designated DICER COMPLEX, dices the GAM688 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM688 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM688 RNA is designated SEQ ID:2337, and is provided hereinbelow with reference to the sequence listing part.

[10881] GAM688 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM688 target RNA, herein designated GAM TARGET RNA. GAM688 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10882] GAM688 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM688 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM688 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM688 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM688

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10883] The complementary binding of GAM688 RNA, herein designated GAM RNA, to target binding sites on GAM688 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM688 target RNA, herein designated GAM TARGET RNA, into GAM688 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10884] It is appreciated that GAM688 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM688 target genes. The mRNA of each one of this plurality of GAM688 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM688 RNA, herein designated GAM RNA, and which when bound by GAM688 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM688 target proteins.

[10885] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM688 gene, herein designated GAM GENE, on one or more GAM688 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10886] It is yet further appreciated that specific functions, and accordingly utilities, of GAM688 correlate with, and may be deduced from, the identity of the target genes which GAM688 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10887] Nucleotide sequences of the GAM688 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM688 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM688 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM688 are further described hereinbelow with reference to Table Table1.

[10888] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM688 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10889] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 689 (GAM689) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10890] GAM689 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM689 was detected is described hereinabove with reference to Figs. 2-8.

[10891] GAM689 gene, herein designated GAM GENE, and GAM689 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[10892] GAM689 gene, herein designated GAM GENE, encodes a GAM689 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM689 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM689 precursor RNA is designated SEQ ID:662, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:662 is located at position 3434860 relative to contig NT_009714.13, on chromosome 12.

[10893] GAM689 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98323, which mouse homolog is detected in mouse EST accession BG288438.1.

[10894] GAM689 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10895] An enzyme complex designated DICER COMPLEX, dices the GAM689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM689 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM689 RNA is designated SEQ ID:2338, and is provided hereinbelow with reference to the sequence listing part.

[10896] GAM689 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM689 target RNA, herein designated GAM TARGET RNA.
GAM689 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10897] GAM689 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM689 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM689 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM689 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM689 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10898] The complementary binding of GAM689 RNA, herein designated GAM RNA, to target binding sites on GAM689 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM689 target RNA, herein designated GAM TARGET RNA, into GAM689 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10899] It is appreciated that GAM689 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM689 target genes. The mRNA of each one of this plurality of GAM689 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM689 RNA, herein designated GAM RNA, and which when bound by GAM689 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM689 target proteins.

[10900] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM689 gene, herein designated GAM GENE, on one or more GAM689 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10901] It is yet further appreciated that specific functions, and accordingly utilities, of GAM689 correlate with, and may be deduced from, the identity of the target genes which GAM689 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10902] Nucleotide sequences of the GAM689 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM689 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM689 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM689 are further described hereinbelow with reference to Table Table1.

[10903] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM689 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10904] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 690 (GAM690) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10905] GAM690 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM690 was detected is described hereinabove with reference to Figs. 2-8.

[10906] GAM690 gene, herein designated GAM GENE, and GAM690 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10907] GAM690 gene, herein designated GAM GENE, encodes a GAM690 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM690 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM690 precursor RNA is desig-

nated SEQ ID:663, and is provided hereinbelow with reference to the sequence listing part.

[10908] GAM690 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10909] An enzyme complex designated DICER COMPLEX, dices the GAM690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM690 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM690 RNA is designated SEQ ID:2339, and is provided hereinbelow with reference to the sequence listing part.

[10910] GAM690 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM690 target RNA, herein designated GAM TARGET RNA. GAM690 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10911] GAM690 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM690 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM690 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM690 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM690

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10912] The complementary binding of GAM690 RNA, herein designated GAM RNA, to target binding sites on GAM690 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM690 target RNA, herein designated GAM TARGET RNA, into GAM690 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10913] It is appreciated that GAM690 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM690 target genes. The mRNA of each one of this plurality of GAM690 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM690 RNA, herein designated GAM RNA, and which when bound by GAM690 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM690 target proteins.

[10914] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM690 gene, herein designated GAM GENE, on one or more GAM690 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10915] It is yet further appreciated that specific functions, and accordingly utilities, of GAM690 correlate with, and may be deduced from, the identity of the target genes which GAM690 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10916] Nucleotide sequences of the GAM690 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM690 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM690 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM690 are further described hereinbelow with reference to Table Table1.

[10917] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM690 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10918] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 691 (GAM691) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10919] GAM691 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM691 was detected is described hereinabove with reference to Figs. 2-8.

[10920] GAM691 gene, herein designated GAM GENE, and GAM691 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[10921] GAM691 gene, herein designated GAM GENE, encodes a GAM691 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM691 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM691 precursor RNA is designated SEQ ID:664, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:664 is located at position 631526 relative to contig NT_011597.10, on chromosome X.

[10922] GAM691 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10923] An enzyme complex designated DICER COMPLEX, dices

the GAM691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM691 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM691 RNA is designated SEQ ID:2340, and is provided hereinbelow with reference to the sequence listing part.

[10924] GAM691 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM691 target RNA, herein designated GAM TARGET RNA. GAM691 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10925] GAM691 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM691 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM691

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM691 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM691 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10926] The complementary binding of GAM691 RNA, herein designated GAM RNA, to target binding sites on GAM691 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM691 target RNA, herein designated GAM TARGET RNA, into GAM691 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10927] It is appreciated that GAM691 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM691 target genes. The mRNA of each one of this plurality of GAM691 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM691 RNA, herein designated GAM RNA, and which when bound by GAM691 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM691 target proteins.

[10928] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM691 gene, herein designated GAM GENE, on one or more GAM691 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10929] It is yet further appreciated that specific functions, and accordingly utilities, of GAM691 correlate with, and may be deduced from, the identity of the target genes which GAM691 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10930] Nucleotide sequences of the GAM691 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM691 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM691 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM691 are further described hereinbelow with reference to Table Table1.

[10931] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM691 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10932] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 692 (GAM692) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10933] GAM692 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM692 was detected is described hereinabove with reference to Figs. 2-8.

[10934] GAM692 gene, herein designated GAM GENE, and GAM692 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10935] GAM692 gene, herein designated GAM GENE, encodes a GAM692 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM692 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM692 precursor RNA is designated SEQ ID:665, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:665 is located at position 11904824 relative to contig NT_017568.11, on chromosome 9.

[10936] GAM692 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM692 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10937] An enzyme complex designated DICER COMPLEX, dices the GAM692 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM692 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM692 RNA is designated SEQ ID:2341, and is provided hereinbelow with reference to the sequence listing part.

[10938] GAM692 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM692 target RNA, herein designated GAM TARGET RNA.

GAM692 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10939] GAM692 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM692 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM692 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM692 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM692 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10940] The complementary binding of GAM692 RNA, herein designated GAM RNA, to target binding sites on GAM692 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM692 target RNA, herein designated GAM TARGET RNA, into GAM692 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10941] It is appreciated that GAM692 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM692 target genes. The mRNA of each one of this plurality of GAM692 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM692 RNA, herein designated GAM RNA, and which when bound by GAM692 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM692 target proteins.

[10942] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM692 gene, herein designated GAM GENE, on one or more GAM692 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10943] It is yet further appreciated that specific functions, and accordingly utilities, of GAM692 correlate with, and may be deduced from, the identity of the target genes which GAM692 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10944] Nucleotide sequences of the GAM692 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM692 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM692 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM692 are further described hereinbelow with reference to Table Table1.

[10945] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM692 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10946] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 693 (GAM693) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10947] GAM693 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM693 was detected is described hereinabove with reference to Figs. 2-8.

[10948] GAM693 gene, herein designated GAM GENE, and GAM693 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10949] GAM693 gene, herein designated GAM GENE, encodes a GAM693 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM693 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM693 precursor RNA is designated SEQ ID:666, and is provided hereinbelow with reference to the sequence listing part.

[10950] GAM693 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM693 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10951] An enzyme complex designated DICER COMPLEX, dices the GAM693 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM693 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM693 RNA is designated SEQ ID:2342, and is provided hereinbelow with reference to the sequence listing part.

[10952] GAM693 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM693 target RNA, herein designated GAM TARGET RNA. GAM693 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10953] GAM693 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM693 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM693 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM693 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM693 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10954] The complementary binding of GAM693 RNA, herein designated GAM RNA, to target binding sites on GAM693 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM693 target RNA, herein designated GAM TARGET RNA, into GAM693 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10955] It is appreciated that GAM693 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM693 target genes. The mRNA of each one of this plurality of GAM693 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM693 RNA, herein designated GAM RNA, and which when bound by GAM693 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM693 target proteins.

[10956] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM693 gene, herein designated GAM GENE, on one or more GAM693 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10957] It is yet further appreciated that specific functions, and accordingly utilities, of GAM693 correlate with, and may

be deduced from, the identity of the target genes which GAM693 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10958] Nucleotide sequences of the GAM693 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM693 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM693 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM693 are further described hereinbelow with reference to Table Table1.

[10959] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM693 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10960] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 694 (GAM694) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10961] GAM694 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM694 was detected is described hereinabove with reference to Figs. 2-8.

[10962] GAM694 gene, herein designated GAM GENE, and GAM694 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10963] GAM694 gene, herein designated GAM GENE, encodes a GAM694 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM694 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM694 precursor RNA is designated SEQ ID:667, and is provided hereinbelow with reference to the sequence listing part.

[10964] GAM694 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM694 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[10965] An enzyme complex designated DICER COMPLEX, dices the GAM694 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM694 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM694 RNA is designated SEQ ID:2343, and is provided hereinbelow with reference to the sequence listing part.

[10966] GAM694 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM694 target RNA, herein designated GAM TARGET RNA.
GAM694 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10967] GAM694 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM694 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM694 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM694 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM694 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10968] The complementary binding of GAM694 RNA, herein designated GAM RNA, to target binding sites on GAM694 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM694 target RNA, herein desig-

nated GAM TARGET RNA, into GAM694 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10969] It is appreciated that GAM694 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM694 target genes. The mRNA of each one of this plurality of GAM694 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM694 RNA, herein designated GAM RNA, and which when bound by GAM694 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM694 target proteins.

[10970] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM694 gene, herein designated GAM GENE, on one or more GAM694 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10971] It is yet further appreciated that specific functions, and accordingly utilities, of GAM694 correlate with, and may be deduced from, the identity of the target genes which GAM694 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10972] Nucleotide sequences of the GAM694 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM694 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM694 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM694 are further described hereinbelow with reference to Table Table1.

[10973] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM694 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[10974] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 695 (GAM695) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10975] GAM695 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM695 was detected is described hereinabove with reference to Figs. 2-8.

[10976] GAM695 gene, herein designated GAM GENE, and GAM695 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[10977] GAM695 gene, herein designated GAM GENE, encodes a GAM695 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM695 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM695 precursor RNA is designated SEQ ID:668, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:668 is located at position 2037056 relative to contig NT_021907.13, on chromosome 1.

[10978] GAM695 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM695 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10979] An enzyme complex designated DICER COMPLEX, dices the GAM695 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM695 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM695 RNA is designated SEQ ID:2344, and is provided hereinbelow with reference to the sequence listing part.

[10980] GAM695 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM695 target RNA, herein designated GAM TARGET RNA. GAM695 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10981] GAM695 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM695 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM695 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM695 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM695

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10982] The complementary binding of GAM695 RNA, herein designated GAM RNA, to target binding sites on GAM695 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM695 target RNA, herein designated GAM TARGET RNA, into GAM695 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[10983] It is appreciated that GAM695 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM695 target genes. The mRNA of each one of this plurality of GAM695 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM695 RNA, herein designated GAM RNA, and which when bound by GAM695 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM695 target proteins.

[10984] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM695 gene, herein designated GAM GENE, on one or more GAM695 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[10985] It is yet further appreciated that specific functions, and accordingly utilities, of GAM695 correlate with, and may be deduced from, the identity of the target genes which GAM695 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[10986] Nucleotide sequences of the GAM695 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM695 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM695 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM695 are further described hereinbelow with reference to Table Table1.

[10987] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM695 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[10988] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 696 (GAM696) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[10989] GAM696 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM696 was detected is described hereinabove with reference to Figs. 2-8.

[10990] GAM696 gene, herein designated GAM GENE, and GAM696 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[10991] GAM696 gene, herein designated GAM GENE, encodes a GAM696 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM696 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM696 precursor RNA is designated SEQ ID:669, and is provided hereinbelow with reference to the sequence listing part.

[10992] GAM696 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[10993] SEQ ID:100216 detected in mouse EST Accession AW411769.1.

[10994] SEQ ID:98766 detected in mouse EST Accession AW411769.1.

[10995] GAM696 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM696 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[10996] An enzyme complex designated DICER COMPLEX, dices the GAM696 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM696 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM696 RNA is designated SEQ ID:2345, and is provided hereinbelow with reference to the sequence listing part.

[10997] GAM696 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM696 target RNA, herein designated GAM TARGET RNA. GAM696 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[10998] GAM696 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM696 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM696 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM696 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM696 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[10999] The complementary binding of GAM696 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM696 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM696 target RNA, herein designated GAM TARGET RNA, into GAM696 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11000] It is appreciated that GAM696 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM696 target genes. The mRNA of each one of this plurality of GAM696 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM696 RNA, herein designated GAM RNA, and which when bound by GAM696 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM696 target proteins.

[11001] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM696 gene, herein designated GAM GENE, on one or more GAM696 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11002] It is yet further appreciated that specific functions, and accordingly utilities, of GAM696 correlate with, and may be deduced from, the identity of the target genes which GAM696 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11003] Nucleotide sequences of the GAM696 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM696 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM696 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM696 are further described hereinbelow with reference to Table Table1.

[11004] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM696 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11005] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 697 (GAM697) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11006] GAM697 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM697 was detected is described hereinabove with reference to Figs. 2-8.

[11007] GAM697 gene, herein designated GAM GENE, and GAM697 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11008] GAM697 gene, herein designated GAM GENE, encodes a GAM697 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM697 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM697 precursor RNA is designated SEQ ID:670, and is provided hereinbelow with reference to the sequence listing part.

[11009] GAM697 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11010] An enzyme complex designated DICER COMPLEX, dices the GAM697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM697 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM697 RNA is designated SEQ ID:2346, and is provided hereinbelow with reference to the sequence listing part.

[11011] GAM697 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM697 target RNA, herein designated GAM TARGET RNA. GAM697 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11012] GAM697 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM697 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM697 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM697 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM697 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11013] The complementary binding of GAM697 RNA, herein designated GAM RNA, to target binding sites on GAM697 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM697 target RNA, herein designated GAM TARGET RNA, into GAM697 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11014] It is appreciated that GAM697 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM697 target genes. The mRNA of each one of this plurality of GAM697 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM697 RNA, herein designated GAM RNA, and which when bound by GAM697 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM697 target proteins.

[11015] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM697 gene, herein designated GAM GENE, on one or more GAM697 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11016] It is yet further appreciated that specific functions, and accordingly utilities, of GAM697 correlate with, and may be deduced from, the identity of the target genes which GAM697 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11017] Nucleotide sequences of the GAM697 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM697 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM697 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM697 are further described hereinbelow with reference to Table Table1.

[11018] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM697 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11019] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 698 (GAM698) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11020] GAM698 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM698 was detected is described hereinabove with reference to Figs. 2-8.

[11021] GAM698 gene, herein designated GAM GENE, and GAM698 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11022] GAM698 gene, herein designated GAM GENE, encodes a GAM698 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM698 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM698 precursor RNA is designated SEQ ID:671, and is provided hereinbelow with reference to the sequence listing part.

[11023] GAM698 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM698 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11024] An enzyme complex designated DICER COMPLEX, dices

the GAM698 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM698 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM698 RNA is designated SEQ ID:2347, and is provided hereinbelow with reference to the sequence listing part.

[11025] GAM698 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM698 target RNA, herein designated GAM TARGET RNA. GAM698 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11026] GAM698 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM698 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM698

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM698 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM698 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11027] The complementary binding of GAM698 RNA, herein designated GAM RNA, to target binding sites on GAM698 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM698 target RNA, herein designated GAM TARGET RNA, into GAM698 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11028] It is appreciated that GAM698 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM698 target genes. The mRNA of each one of this plurality of GAM698 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM698 RNA, herein designated GAM RNA, and which when bound by GAM698 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM698 target proteins.

[11029] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM698 gene, herein designated GAM GENE, on one or more GAM698 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11030] It is yet further appreciated that specific functions, and accordingly utilities, of GAM698 correlate with, and may be deduced from, the identity of the target genes which GAM698 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11031] Nucleotide sequences of the GAM698 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM698 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM698 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM698 are further described hereinbelow with reference to Table Table1.

[11032] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM698 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11033] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 699 (GAM699) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11034] GAM699 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM699 was detected is described hereinabove with reference to Figs. 2-8.

[11035] GAM699 gene, herein designated GAM GENE, and GAM699 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11036] GAM699 gene, herein designated GAM GENE, encodes a GAM699 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM699 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM699 precursor RNA is designated SEQ ID:672, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:672 is located at position 11259458 relative to contig NT_007592.11, on chromosome 6.

[11037] GAM699 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM699 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11038] An enzyme complex designated DICER COMPLEX, dices the GAM699 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM699 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM699 RNA is designated SEQ ID:2348, and is provided hereinbelow with reference to the sequence listing part.

[11039] GAM699 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM699 target RNA, herein designated GAM TARGET RNA.

GAM699 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11040] GAM699 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM699 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM699 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM699 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM699 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11041] The complementary binding of GAM699 RNA, herein designated GAM RNA, to target binding sites on GAM699 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM699 target RNA, herein designated GAM TARGET RNA, into GAM699 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11042] It is appreciated that GAM699 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM699 target genes. The mRNA of each one of this plurality of GAM699 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM699 RNA, herein designated GAM RNA, and which when bound by GAM699 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM699 target proteins.

[11043] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM699 gene, herein designated GAM GENE, on one or more GAM699 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11044] It is yet further appreciated that specific functions, and accordingly utilities, of GAM699 correlate with, and may be deduced from, the identity of the target genes which GAM699 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11045] Nucleotide sequences of the GAM699 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM699 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM699 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM699 are further described hereinbelow with reference to Table Table1.

[11046] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM699 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11047] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 700 (GAM700) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11048] GAM700 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM700 was detected is described hereinabove with reference to Figs. 2-8.

[11049] GAM700 gene, herein designated GAM GENE, and GAM700 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11050] GAM700 gene, herein designated GAM GENE, encodes a GAM700 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM700 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM700 precursor RNA is designated SEQ ID:673, and is provided hereinbelow with reference to the sequence listing part.

[11051] GAM700 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[11052] SEQ ID:98028 detected in mouse EST Accession BE631995.1.

[11053] SEQ ID:98029 detected in mouse EST Accession AA032944.1.

[11054] SEQ ID:98030 detected in mouse EST Accession BG974113.1.

[11055] SEQ ID:98031 detected in mouse EST Accession BG923775.1.

[11056] SEQ ID:98032 detected in mouse EST Accession AA011740.1.

[11057] SEQ ID:98033 detected in mouse EST Accession

AA413633.1.

[11058] SEQ ID:98034 detected in mouse EST Accession BI659868.1.

[11059] SEQ ID:98035 detected in mouse EST Accession BF134406.1.

[11060] GAM700 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11061] An enzyme complex designated DICER COMPLEX, dices the GAM700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM700 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM700 RNA is designated SEQ ID:2349, and is provided hereinbelow with reference to the sequence listing part.

[11062] GAM700 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM700 target RNA, herein designated GAM TARGET RNA. GAM700 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11063] GAM700 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM700 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM700 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM700 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM700 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11064] The complementary binding of GAM700 RNA, herein designated GAM RNA, to target binding sites on GAM700 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM700 target RNA, herein designated GAM TARGET RNA, into GAM700 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11065] It is appreciated that GAM700 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM700 target genes. The mRNA of each one of this plurality of GAM700 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM700 RNA, herein designated GAM RNA, and which when bound by

GAM700 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM700 target proteins.

[11066] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM700 gene, herein designated GAM GENE, on one or more GAM700 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11067] It is yet further appreciated that specific functions, and accordingly utilities, of GAM700 correlate with, and may be deduced from, the identity of the target genes which GAM700 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[11068] Nucleotide sequences of the GAM700 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM700 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM700 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM700 are further described hereinbelow with reference to Table Table1.

[11069] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM700 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11070] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 701 (GAM701) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11071] GAM701 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM701 was detected is described hereinabove

with reference to Figs. 2-8.

[11072] GAM701 gene, herein designated GAM GENE, and GAM701 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11073] GAM701 gene, herein designated GAM GENE, encodes a GAM701 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM701 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM701 precursor RNA is designated SEQ ID:674, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:674 is located at position 1917723 relative to contig NT_007914.10, on chromosome 7.

[11074] GAM701 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM701 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[11075] An enzyme complex designated DICER COMPLEX, dices the GAM701 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM701 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM701 RNA is designated SEQ ID:2350, and is provided hereinbelow with reference to the sequence listing part.

[11076] GAM701 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM701 target RNA, herein designated GAM TARGET RNA.
GAM701 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11077] GAM701 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM701 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM701 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM701 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM701 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11078] The complementary binding of GAM701 RNA, herein designated GAM RNA, to target binding sites on GAM701 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM701 target RNA, herein desig-

nated GAM TARGET RNA, into GAM701 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11079] It is appreciated that GAM701 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM701 target genes. The mRNA of each one of this plurality of GAM701 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM701 RNA, herein designated GAM RNA, and which when bound by GAM701 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM701 target proteins.

[11080] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM701 gene, herein designated GAM GENE, on one or more GAM701 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11081] It is yet further appreciated that specific functions, and accordingly utilities, of GAM701 correlate with, and may be deduced from, the identity of the target genes which GAM701 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11082] Nucleotide sequences of the GAM701 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM701 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM701 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM701 are further described hereinbelow with reference to Table Table1.

[11083] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM701 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[11084] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 702 (GAM702) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11085] GAM702 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM702 was detected is described hereinabove with reference to Figs. 2-8.

[11086] GAM702 gene, herein designated GAM GENE, and GAM702 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11087] GAM702 gene, herein designated GAM GENE, encodes a GAM702 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM702 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM702 precursor RNA is designated SEQ ID:675, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:675 is located at position 7678826 relative to contig NT_004852.13, on chromosome 1.

[11088] GAM702 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM702 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11089] An enzyme complex designated DICER COMPLEX, dices the GAM702 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM702 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM702 RNA is designated SEQ ID:2351, and is provided hereinbelow with reference to the sequence listing part.

[11090] GAM702 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM702 target RNA, herein designated GAM TARGET RNA. GAM702 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11091] GAM702 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM702 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM702 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM702 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM702

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11092] The complementary binding of GAM702 RNA, herein designated GAM RNA, to target binding sites on GAM702 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM702 target RNA, herein designated GAM TARGET RNA, into GAM702 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11093] It is appreciated that GAM702 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM702 target genes. The mRNA of each one of this plurality of GAM702 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM702 RNA, herein designated GAM RNA, and which when bound by GAM702 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM702 target proteins.

[11094] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM702 gene, herein designated GAM GENE, on one or more GAM702 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11095] It is yet further appreciated that specific functions, and accordingly utilities, of GAM702 correlate with, and may be deduced from, the identity of the target genes which GAM702 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11096] Nucleotide sequences of the GAM702 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM702 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM702 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM702 are further described hereinbelow with reference to Table Table1.

[11097] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM702 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11098] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 703 (GAM703) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11099] GAM703 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM703 was detected is described hereinabove with reference to Figs. 2-8.

[11100] GAM703 gene, herein designated GAM GENE, and GAM703 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[11101] GAM703 gene, herein designated GAM GENE, encodes a GAM703 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM703 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM703 precursor RNA is designated SEQ ID:676, and is provided hereinbelow with reference to the sequence listing part.

[11102] GAM703 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11103] An enzyme complex designated DICER COMPLEX, dices the GAM703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM703 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM703 RNA is designated SEQ ID:2352, and is provided hereinbelow with reference to the sequence listing part.

[11104] GAM703 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM703 target RNA, herein designated GAM TARGET RNA. GAM703 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11105] GAM703 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM703 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM703 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM703 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM703 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11106] The complementary binding of GAM703 RNA, herein designated GAM RNA, to target binding sites on GAM703 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM703 target RNA, herein designated GAM TARGET RNA, into GAM703 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11107] It is appreciated that GAM703 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM703 target genes. The mRNA of each one of this plurality of GAM703 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM703 RNA, herein designated GAM RNA, and which when bound by GAM703 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM703 target proteins.

[11108] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM703 gene, herein designated GAM GENE, on one or more GAM703 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[11109] It is yet further appreciated that specific functions, and accordingly utilities, of GAM703 correlate with, and may be deduced from, the identity of the target genes which GAM703 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11110] Nucleotide sequences of the GAM703 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM703 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM703 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM703 are further described hereinbelow with reference to Table Table1.

[11111] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM703 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11112] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 704 (GAM704) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[11113] GAM704 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM704 was detected is described hereinabove with reference to Figs. 2-8.

[11114] GAM704 gene, herein designated GAM GENE, and GAM704 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11115] GAM704 gene, herein designated GAM GENE, encodes a GAM704 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM704 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM704 precursor RNA is designated SEQ ID:677, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:677 is located at position 9200276 relative to contig NT_023974.13, on chromosome 9.

[11116] GAM704 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM704 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11117] An enzyme complex designated DICER COMPLEX, dices the GAM704 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM704 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM704 RNA is designated SEQ ID:2353, and is provided hereinbelow with reference to the sequence listing part.

[11118] GAM704 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM704 target RNA, herein designated GAM TARGET RNA. GAM704 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11119] GAM704 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM704 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM704 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM704 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM704 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11120] The complementary binding of GAM704 RNA, herein designated GAM RNA, to target binding sites on GAM704 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM704 target RNA, herein designated GAM TARGET RNA, into GAM704 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11121] It is appreciated that GAM704 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM704 target genes. The mRNA of each one of this plurality of GAM704 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM704 RNA, herein designated GAM RNA, and which when bound by GAM704 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM704 target proteins.

[11122] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM704 gene, herein designated GAM GENE, on one or more GAM704 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11123] It is yet further appreciated that specific functions, and accordingly utilities, of GAM704 correlate with, and may be deduced from, the identity of the target genes which GAM704 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11124] Nucleotide sequences of the GAM704 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM704 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM704 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM704 are further described hereinbelow with reference to Table Table1.

[11125] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM704 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11126] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 705 (GAM705) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11127] GAM705 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM705 was detected is described hereinabove with reference to Figs. 2-8.

[11128] GAM705 gene, herein designated GAM GENE, and GAM705 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11129] GAM705 gene, herein designated GAM GENE, encodes a GAM705 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM705 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM705 precursor RNA is designated SEQ ID:678, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:678 is located at position 4421892 relative to contig NT_022155.11, on chromosome 2.

[11130] GAM705 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM705 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11131] An enzyme complex designated DICER COMPLEX, dices the GAM705 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM705 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM705 RNA is designated SEQ ID:2354, and is provided hereinbelow with reference to the sequence listing part.

[11132] GAM705 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM705 target RNA, herein designated GAM TARGET RNA. GAM705 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11133] GAM705 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM705 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM705 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM705 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM705 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11134] The complementary binding of GAM705 RNA, herein designated GAM RNA, to target binding sites on GAM705 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM705 target RNA, herein designated GAM TARGET RNA, into GAM705 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11135] It is appreciated that GAM705 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM705 target genes. The mRNA of each one of this plurality of GAM705 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM705 RNA, herein designated GAM RNA, and which when bound by GAM705 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM705 target proteins.

[11136] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM705 gene, herein designated GAM GENE, on one or more GAM705 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11137] It is yet further appreciated that specific functions, and accordingly utilities, of GAM705 correlate with, and may

be deduced from, the identity of the target genes which GAM705 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11138] Nucleotide sequences of the GAM705 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM705 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM705 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM705 are further described hereinbelow with reference to Table Table1.

[11139] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM705 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11140] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 706 (GAM706) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11141] GAM706 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM706 was detected is described hereinabove with reference to Figs. 2-8.

[11142] GAM706 gene, herein designated GAM GENE, and GAM706 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11143] GAM706 gene, herein designated GAM GENE, encodes a GAM706 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM706 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM706 precursor RNA is designated SEQ ID:679, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:679 is located at position 4478014 relative to contig NT_023811.12, on chromosome 8.

[11144] GAM706 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM706 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11145] An enzyme complex designated DICER COMPLEX, dices the GAM706 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM706 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM706 RNA is designated SEQ ID:2355, and is provided hereinbelow with reference to the sequence listing part.

[11146] GAM706 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM706 target RNA, herein designated GAM TARGET RNA. GAM706 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11147] GAM706 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM706 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM706 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM706 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM706 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11148] The complementary binding of GAM706 RNA, herein designated GAM RNA, to target binding sites on GAM706 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM706 target RNA, herein designated GAM TARGET RNA, into GAM706 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11149] It is appreciated that GAM706 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM706 target genes. The mRNA of each one of this plurality of GAM706 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM706 RNA, herein designated GAM RNA, and which when bound by GAM706 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM706 target proteins.

[11150] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM706 gene, herein designated GAM GENE, on one or more GAM706 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11151] It is yet further appreciated that specific functions, and accordingly utilities, of GAM706 correlate with, and may be deduced from, the identity of the target genes which GAM706 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11152] Nucleotide sequences of the GAM706 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM706 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM706 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM706 are further described hereinbelow with reference to Table Table1.

[11153] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM706 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11154] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 707 (GAM707) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11155] GAM707 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM707 was detected is described hereinabove with reference to Figs. 2-8.

[11156] GAM707 gene, herein designated GAM GENE, and GAM707 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11157] GAM707 gene, herein designated GAM GENE, encodes a GAM707 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM707 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM707 precursor RNA is desig-

nated SEQ ID:680, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:680 is located at position 3102354 relative to contig NT_011109.13, on chromosome 19.

[11158] GAM707 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11159] An enzyme complex designated DICER COMPLEX, dices the GAM707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM707 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM707 RNA is designated SEQ ID:2356, and is provided hereinbelow with reference to the sequence listing part.

[11160] GAM707 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM707 target RNA, herein designated GAM TARGET RNA. GAM707 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11161] GAM707 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM707 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM707 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM707 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM707 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11162] The complementary binding of GAM707 RNA, herein designated GAM RNA, to target binding sites on GAM707 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM707 target RNA, herein designated GAM TARGET RNA, into GAM707 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11163] It is appreciated that GAM707 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM707 target genes. The mRNA of each one of this plurality of GAM707 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM707 RNA, herein designated GAM RNA, and which when bound by GAM707 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM707 target proteins.

[11164] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM707 gene, herein designated GAM GENE, on one or more GAM707 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11165] It is yet further appreciated that specific functions, and accordingly utilities, of GAM707 correlate with, and may be deduced from, the identity of the target genes which GAM707 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11166] Nucleotide sequences of the GAM707 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM707 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM707 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM707 are further described hereinbelow with reference to Table Table1.

[11167] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM707 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11168] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 708 (GAM708) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11169] GAM708 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM708 was detected is described hereinabove with reference to Figs. 2-8.

[11170] GAM708 gene, herein designated GAM GENE, and GAM708 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11171] GAM708 gene, herein designated GAM GENE, encodes a GAM708 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM708 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM708 precursor RNA is designated SEQ ID:681, and is provided hereinbelow with reference to the sequence listing part.

[11172] GAM708 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM708 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11173] An enzyme complex designated DICER COMPLEX, dices

the GAM708 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM708 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM708 RNA is designated SEQ ID:2357, and is provided hereinbelow with reference to the sequence listing part.

[11174] GAM708 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM708 target RNA, herein designated GAM TARGET RNA. GAM708 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11175] GAM708 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM708 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM708

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM708 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM708 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11176] The complementary binding of GAM708 RNA, herein designated GAM RNA, to target binding sites on GAM708 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM708 target RNA, herein designated GAM TARGET RNA, into GAM708 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11177] It is appreciated that GAM708 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM708 target genes. The mRNA of each one of this plurality of GAM708 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM708 RNA, herein designated GAM RNA, and which when bound by GAM708 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM708 target proteins.

[11178] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM708 gene, herein designated GAM GENE, on one or more GAM708 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11179] It is yet further appreciated that specific functions, and accordingly utilities, of GAM708 correlate with, and may be deduced from, the identity of the target genes which GAM708 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11180] Nucleotide sequences of the GAM708 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM708 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM708 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM708 are further described hereinbelow with reference to Table Table1.

[11181] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM708 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11182] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 709 (GAM709) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11183] GAM709 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM709 was detected is described hereinabove with reference to Figs. 2-8.

[11184] GAM709 gene, herein designated GAM GENE, and GAM709 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11185] GAM709 gene, herein designated GAM GENE, encodes a GAM709 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM709 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM709 precursor RNA is designated SEQ ID:682, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:682 is located at position 249248 relative to contig NT_035414.2, on chromosome 17.

[11186] GAM709 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM709 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11187] An enzyme complex designated DICER COMPLEX, dices the GAM709 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM709 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM709 RNA is designated SEQ ID:2358, and is provided hereinbelow with reference to the sequence listing part.

[11188] GAM709 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM709 target RNA, herein designated GAM TARGET RNA.

GAM709 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11189] GAM709 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM709 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM709 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM709 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM709 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11190] The complementary binding of GAM709 RNA, herein designated GAM RNA, to target binding sites on GAM709 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM709 target RNA, herein designated GAM TARGET RNA, into GAM709 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11191] It is appreciated that GAM709 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM709 target genes. The mRNA of each one of this plurality of GAM709 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM709 RNA, herein designated GAM RNA, and which when bound by GAM709 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM709 target proteins.

[11192] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM709 gene, herein designated GAM GENE, on one or more GAM709 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11193] It is yet further appreciated that specific functions, and accordingly utilities, of GAM709 correlate with, and may be deduced from, the identity of the target genes which GAM709 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11194] Nucleotide sequences of the GAM709 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM709 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM709 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM709 are further described hereinbelow with reference to Table Table1.

[11195] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM709 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11196] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 710 (GAM710) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11197] GAM710 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM710 was detected is described hereinabove with reference to Figs. 2-8.

[11198] GAM710 gene, herein designated GAM GENE, and GAM710 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11199] GAM710 gene, herein designated GAM GENE, encodes a GAM710 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM710 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM710 precursor RNA is designated SEQ ID:683, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:683 is located at position 4142955 relative to contig NT_035235.2, on chromosome 12.

[11200] GAM710 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM710 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11201] An enzyme complex designated DICER COMPLEX, dices the GAM710 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM710 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM710 RNA is designated SEQ ID:2359, and is provided hereinbelow with reference to the sequence listing part.

[11202] GAM710 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM710 target RNA, herein designated GAM TARGET RNA. GAM710 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11203] GAM710 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM710 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM710 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM710 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM710 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11204] The complementary binding of GAM710 RNA, herein designated GAM RNA, to target binding sites on GAM710 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM710 target RNA, herein designated GAM TARGET RNA, into GAM710 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11205] It is appreciated that GAM710 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM710 target genes. The mRNA of each one of this plu-

rality of GAM710 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM710 RNA, herein designated GAM RNA, and which when bound by GAM710 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM710 target proteins.

[11206] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM710 gene, herein designated GAM GENE, on one or more GAM710 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11207] It is yet further appreciated that specific functions, and accordingly utilities, of GAM710 correlate with, and may be deduced from, the identity of the target genes which GAM710 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11208] Nucleotide sequences of the GAM710 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM710 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM710 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM710 are further described hereinbelow with reference to Table Table1.

[11209] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM710 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11210] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 711 (GAM711) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[11211] GAM711 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM711 was detected is described hereinabove with reference to Figs. 2-8.

[11212] GAM711 gene, herein designated GAM GENE, and GAM711 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11213] GAM711 gene, herein designated GAM GENE, encodes a GAM711 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM711 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM711 precursor RNA is designated SEQ ID:684, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:684 is located at position 963313 relative to contig NT_010755.11, on chromosome 17.

[11214] GAM711 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM711 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11215] An enzyme complex designated DICER COMPLEX, dices the GAM711 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM711 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM711 RNA is designated SEQ ID:2360, and is provided hereinbelow with reference to the sequence listing part.

[11216] GAM711 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM711 target RNA, herein designated GAM TARGET RNA. GAM711 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11217] GAM711 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM711 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM711 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM711 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM711 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11218] The complementary binding of GAM711 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM711 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM711 target RNA, herein designated GAM TARGET RNA, into GAM711 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11219] It is appreciated that GAM711 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM711 target genes. The mRNA of each one of this plurality of GAM711 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM711 RNA, herein designated GAM RNA, and which when bound by GAM711 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM711 target proteins.

[11220] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM711 gene, herein designated GAM GENE, on one or more GAM711 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11221] It is yet further appreciated that specific functions, and accordingly utilities, of GAM711 correlate with, and may be deduced from, the identity of the target genes which GAM711 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11222] Nucleotide sequences of the GAM711 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM711 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM711 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM711 are further described hereinbelow with reference to Table Table1.

[11223] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM711 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11224] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 712 (GAM712) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11225] GAM712 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM712 was detected is described hereinabove with reference to Figs. 2-8.

[11226] GAM712 gene, herein designated GAM GENE, and GAM712 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11227] GAM712 gene, herein designated GAM GENE, encodes a GAM712 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM712 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM712 precursor RNA is designated SEQ ID:685, and is provided hereinbelow with reference to the sequence listing part.

[11228] GAM712 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM712 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11229] An enzyme complex designated DICER COMPLEX, dices the GAM712 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM712 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM712 RNA is designated SEQ ID:2361, and is provided hereinbelow with reference to the sequence listing part.

[11230] GAM712 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM712 target RNA, herein designated GAM TARGET RNA. GAM712 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11231] GAM712 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM712 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM712 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM712 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM712 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11232] The complementary binding of GAM712 RNA, herein designated GAM RNA, to target binding sites on GAM712 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM712 target RNA, herein designated GAM TARGET RNA, into GAM712 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11233] It is appreciated that GAM712 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM712 target genes. The mRNA of each one of this plurality of GAM712 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM712 RNA, herein designated GAM RNA, and which when bound by GAM712 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM712 target proteins.

[11234] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM712 gene, herein designated GAM GENE, on one or more GAM712 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11235] It is yet further appreciated that specific functions, and accordingly utilities, of GAM712 correlate with, and may be deduced from, the identity of the target genes which GAM712 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11236] Nucleotide sequences of the GAM712 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM712 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM712 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM712 are further described hereinbelow with reference to Table Table1.

[11237] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM712 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11238] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 713 (GAM713) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11239] GAM713 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM713 was detected is described hereinabove with reference to Figs. 2-8.

[11240] GAM713 gene, herein designated GAM GENE, and GAM713 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11241] GAM713 gene, herein designated GAM GENE, encodes a GAM713 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM713 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM713 precursor RNA is designated SEQ ID:686, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:686 is located at position 249251 relative to contig NT_035414.2, on chromosome 17.

[11242] GAM713 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM713 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[11243] An enzyme complex designated DICER COMPLEX, dices the GAM713 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM713 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM713 RNA is designated SEQ ID:2362, and is provided hereinbelow with reference to the sequence listing part.

[11244] GAM713 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM713 target RNA, herein designated GAM TARGET RNA. GAM713 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11245] GAM713 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM713 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM713 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM713 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM713 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11246] The complementary binding of GAM713 RNA, herein designated GAM RNA, to target binding sites on GAM713 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM713 target RNA, herein designated GAM TARGET RNA, into GAM713 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11247] It is appreciated that GAM713 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM713 target genes. The mRNA of each one of this plurality of GAM713 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM713 RNA, herein designated GAM RNA, and which when bound by GAM713 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM713 target proteins.

[11248] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM713 gene, herein designated GAM GENE, on one or more GAM713 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11249] It is yet further appreciated that specific functions, and accordingly utilities, of GAM713 correlate with, and may be deduced from, the identity of the target genes which GAM713 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11250] Nucleotide sequences of the GAM713 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM713 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM713 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM713 are further described hereinbelow with reference to Table Table1.

[11251] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM713 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11252] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 714 (GAM714) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11253] GAM714 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM714 was detected is described hereinabove with reference to Figs. 2-8.

[11254] GAM714 gene, herein designated GAM GENE, and GAM714 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11255] GAM714 gene, herein designated GAM GENE, encodes a GAM714 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM714 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM714 precursor RNA is designated SEQ ID:687, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:687 is located at position 4531567 relative to con-

tig NT_011657.11, on chromosome X.

[11256] GAM714 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM714 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11257] An enzyme complex designated DICER COMPLEX, dices the GAM714 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM714 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM714 RNA is designated SEQ ID:2363, and is provided hereinbelow with reference to the sequence listing part.

[11258] GAM714 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM714 target RNA, herein designated GAM TARGET RNA.

GAM714 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11259] GAM714 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM714 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM714 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM714 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM714 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11260] The complementary binding of GAM714 RNA, herein designated GAM RNA, to target binding sites on GAM714 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM714 target RNA, herein designated GAM TARGET RNA, into GAM714 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11261] It is appreciated that GAM714 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM714 target genes. The mRNA of each one of this plurality of GAM714 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM714 RNA, herein designated GAM RNA, and which when bound by GAM714 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM714 target proteins.

[11262] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM714 gene, herein designated GAM GENE, on one or more GAM714 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11263] It is yet further appreciated that specific functions, and accordingly utilities, of GAM714 correlate with, and may be deduced from, the identity of the target genes which GAM714 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11264] Nucleotide sequences of the GAM714 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM714 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM714 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM714 are further described hereinbelow with reference to Table Table1.

[11265] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM714 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11266] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 715 (GAM715) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11267] GAM715 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM715 was detected is described hereinabove with reference to Figs. 2-8.

[11268] GAM715 gene, herein designated GAM GENE, and GAM715 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11269] GAM715 gene, herein designated GAM GENE, encodes a GAM715 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM715 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM715 precursor RNA is designated SEQ ID:688, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:688 is located at position 7678826 relative to contig NT_004852.13, on chromosome 1.

[11270] GAM715 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM715 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11271] An enzyme complex designated DICER COMPLEX, dices the GAM715 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM715 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM715 RNA is designated SEQ ID:2364, and is provided hereinbelow with reference to the sequence listing part.

[11272] GAM715 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM715 target RNA, herein designated GAM TARGET RNA. GAM715 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11273] GAM715 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM715 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM715 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM715 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM715 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11274] The complementary binding of GAM715 RNA, herein designated GAM RNA, to target binding sites on GAM715 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM715 target RNA, herein designated GAM TARGET RNA, into GAM715 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11275] It is appreciated that GAM715 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM715 target genes. The mRNA of each one of this plurality of GAM715 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM715 RNA, herein designated GAM RNA, and which when bound by GAM715 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM715 target proteins.

[11276] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM715 gene, herein designated GAM GENE, on one or more GAM715 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11277] It is yet further appreciated that specific functions, and accordingly utilities, of GAM715 correlate with, and may be deduced from, the identity of the target genes which GAM715 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11278] Nucleotide sequences of the GAM715 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM715 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM715 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM715 are further described hereinbelow with reference to Table Table1.

[11279] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM715 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11280] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

716 (GAM716) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11281] GAM716 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM716 was detected is described hereinabove with reference to Figs. 2-8.

[11282] GAM716 gene, herein designated GAM GENE, and GAM716 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11283] GAM716 gene, herein designated GAM GENE, encodes a GAM716 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM716 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM716 precursor RNA is designated SEQ ID:689, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:689 is located at position 2349689 relative to contig NT_021907.13, on chromosome 1.

[11284] GAM716 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM716 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11285] An enzyme complex designated DICER COMPLEX, dices the GAM716 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM716 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM716 RNA is designated SEQ ID:2365, and is provided hereinbelow with reference to the sequence listing part.

[11286] GAM716 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM716 target RNA, herein designated GAM TARGET RNA. GAM716 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11287] GAM716 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM716 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM716 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM716 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM716 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[11288] The complementary binding of GAM716 RNA, herein designated GAM RNA, to target binding sites on GAM716 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM716 target RNA, herein designated GAM TARGET RNA, into GAM716 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11289] It is appreciated that GAM716 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM716 target genes. The mRNA of each one of this plurality of GAM716 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM716 RNA, herein designated GAM RNA, and which when bound by GAM716 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM716 target proteins.

[11290] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM716 gene, herein designated GAM GENE, on one or

more GAM716 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11291] It is yet further appreciated that specific functions, and accordingly utilities, of GAM716 correlate with, and may be deduced from, the identity of the target genes which GAM716 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11292] Nucleotide sequences of the GAM716 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM716 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM716 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM716 are further de-

scribed hereinbelow with reference to Table Table1.

[11293] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM716 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11294] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 717 (GAM717) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11295] GAM717 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM717 was detected is described hereinabove with reference to Figs. 2-8.

[11296] GAM717 gene, herein designated GAM GENE, and GAM717 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11297] GAM717 gene, herein designated GAM GENE, encodes a GAM717 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM717 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM717 precursor RNA is designated SEQ ID:690, and is provided hereinbelow with reference to the sequence listing part.

[11298] GAM717 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM717 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11299] An enzyme complex designated DICER COMPLEX, dices the GAM717 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM717 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM717 RNA is designated SEQ ID:2366, and is provided hereinbelow with reference to the sequence listing part.

[11300] GAM717 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM717 target RNA, herein designated GAM TARGET RNA. GAM717 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11301] GAM717 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM717 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM717 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM717 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM717 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11302] The complementary binding of GAM717 RNA, herein designated GAM RNA, to target binding sites on GAM717 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM717 target RNA, herein designated GAM TARGET RNA, into GAM717 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11303] It is appreciated that GAM717 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM717 target genes. The mRNA of each one of this plurality of GAM717 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM717 RNA,

herein designated GAM RNA, and which when bound by GAM717 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM717 target proteins.

[11304] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM717 gene, herein designated GAM GENE, on one or more GAM717 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11305] It is yet further appreciated that specific functions, and accordingly utilities, of GAM717 correlate with, and may be deduced from, the identity of the target genes which

GAM717 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11306] Nucleotide sequences of the GAM717 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM717 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM717 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM717 are further described hereinbelow with reference to Table Table1.

[11307] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM717 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11308] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 718 (GAM718) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11309] GAM718 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM718 was detected is described hereinabove with reference to Figs. 2-8.

[11310] GAM718 gene, herein designated GAM GENE, and GAM718 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11311] GAM718 gene, herein designated GAM GENE, encodes a GAM718 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM718 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM718 precursor RNA is designated SEQ ID:691, and is provided hereinbelow with reference to the sequence listing part.

[11312] GAM718 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM718 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[11313] An enzyme complex designated DICER COMPLEX, dices the GAM718 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM718 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM718 RNA is designated SEQ ID:2367, and is provided hereinbelow with reference to the sequence listing part.

[11314] GAM718 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM718 target RNA, herein designated GAM TARGET RNA. GAM718 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11315] GAM718 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM718 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM718 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM718 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM718 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11316] The complementary binding of GAM718 RNA, herein designated GAM RNA, to target binding sites on GAM718 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM718 target RNA, herein designated GAM TARGET RNA, into GAM718 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11317] It is appreciated that GAM718 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM718 target genes. The mRNA of each one of this plurality of GAM718 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM718 RNA, herein designated GAM RNA, and which when bound by GAM718 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM718 target proteins.

[11318] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM718 gene, herein designated GAM GENE, on one or more GAM718 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11319] It is yet further appreciated that specific functions, and accordingly utilities, of GAM718 correlate with, and may be deduced from, the identity of the target genes which GAM718 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11320] Nucleotide sequences of the GAM718 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM718 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM718 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM718 are further described hereinbelow with reference to Table Table1.

[11321] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM718 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11322] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 719 (GAM719) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11323] GAM719 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM719 was detected is described hereinabove with reference to Figs. 2-8.

[11324] GAM719 gene, herein designated GAM GENE, and GAM719 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11325] GAM719 gene, herein designated GAM GENE, encodes a GAM719 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM719 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM719 precursor RNA is designated SEQ ID:692, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:692 is located at position 22520512 relative to

contig NT_008705.13, on chromosome 10.

[11326] GAM719 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM719 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11327] An enzyme complex designated DICER COMPLEX, dices the GAM719 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM719 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM719 RNA is designated SEQ ID:2368, and is provided hereinbelow with reference to the sequence listing part.

[11328] GAM719 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM719 target RNA, herein designated GAM TARGET RNA.

GAM719 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11329] GAM719 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM719 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM719 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM719 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM719 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11330] The complementary binding of GAM719 RNA, herein designated GAM RNA, to target binding sites on GAM719 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM719 target RNA, herein designated GAM TARGET RNA, into GAM719 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11331] It is appreciated that GAM719 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM719 target genes. The mRNA of each one of this plurality of GAM719 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM719 RNA, herein designated GAM RNA, and which when bound by GAM719 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM719 target proteins.

[11332] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM719 gene, herein designated GAM GENE, on one or more GAM719 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11333] It is yet further appreciated that specific functions, and accordingly utilities, of GAM719 correlate with, and may be deduced from, the identity of the target genes which GAM719 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11334] Nucleotide sequences of the GAM719 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM719 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM719 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM719 are further described hereinbelow with reference to Table Table1.

[11335] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM719 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11336] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 720 (GAM720) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11337] GAM720 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM720 was detected is described hereinabove with reference to Figs. 2-8.

[11338] GAM720 gene, herein designated GAM GENE, and GAM720 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11339] GAM720 gene, herein designated GAM GENE, encodes a GAM720 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM720 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM720 precursor RNA is designated SEQ ID:693, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:693 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[11340] GAM720 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM720 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11341] An enzyme complex designated DICER COMPLEX, dices the GAM720 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM720 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM720 RNA is designated SEQ ID:2369, and is provided hereinbelow with reference to the sequence listing part.

[11342] GAM720 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM720 target RNA, herein designated GAM TARGET RNA. GAM720 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11343] GAM720 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM720 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM720 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM720 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM720 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11344] The complementary binding of GAM720 RNA, herein designated GAM RNA, to target binding sites on GAM720 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM720 target RNA, herein designated GAM TARGET RNA, into GAM720 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11345] It is appreciated that GAM720 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM720 target genes. The mRNA of each one of this plurality of GAM720 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM720 RNA, herein designated GAM RNA, and which when bound by GAM720 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM720 target proteins.

[11346] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM720 gene, herein designated GAM GENE, on one or more GAM720 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11347] It is yet further appreciated that specific functions, and accordingly utilities, of GAM720 correlate with, and may be deduced from, the identity of the target genes which GAM720 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11348] Nucleotide sequences of the GAM720 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM720 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM720 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM720 are further described hereinbelow with reference to Table Table1.

[11349] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM720 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11350] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

721 (GAM721) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11351] GAM721 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM721 was detected is described hereinabove with reference to Figs. 2-8.

[11352] GAM721 gene, herein designated GAM GENE, and GAM721 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11353] GAM721 gene, herein designated GAM GENE, encodes a GAM721 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM721 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM721 precursor RNA is designated SEQ ID:694, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:694 is located at position 3263790 relative to contig NT_028392.4, on chromosome 20.

[11354] GAM721 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM721 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11355] An enzyme complex designated DICER COMPLEX, dices the GAM721 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM721 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM721 RNA is designated SEQ ID:2370, and is provided hereinbelow with reference to the sequence listing part.

[11356] GAM721 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM721 target RNA, herein designated GAM TARGET RNA. GAM721 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11357] GAM721 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM721 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM721 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM721 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM721 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[11358] The complementary binding of GAM721 RNA, herein designated GAM RNA, to target binding sites on GAM721 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM721 target RNA, herein designated GAM TARGET RNA, into GAM721 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11359] It is appreciated that GAM721 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM721 target genes. The mRNA of each one of this plurality of GAM721 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM721 RNA, herein designated GAM RNA, and which when bound by GAM721 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM721 target proteins.

[11360] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM721 gene, herein designated GAM GENE, on one or

more GAM721 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11361] It is yet further appreciated that specific functions, and accordingly utilities, of GAM721 correlate with, and may be deduced from, the identity of the target genes which GAM721 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11362] Nucleotide sequences of the GAM721 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM721 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM721 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM721 are further de-

scribed hereinbelow with reference to Table Table1.

[11363] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM721 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11364] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 722 (GAM722) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11365] GAM722 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM722 was detected is described hereinabove with reference to Figs. 2-8.

[11366] GAM722 gene, herein designated GAM GENE, and GAM722 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11367] GAM722 gene, herein designated GAM GENE, encodes a GAM722 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM722 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM722 precursor RNA is designated SEQ ID:695, and is provided hereinbelow with reference to the sequence listing part.

[11368] GAM722 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[11369] SEQ ID:99495 detected in mouse EST Accession BG174226.1.

[11370] SEQ ID:99496 detected in mouse EST Accession BI112519.1.

[11371] GAM722 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM722 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[11372] An enzyme complex designated DICER COMPLEX, dices the GAM722 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM722 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM722 RNA is designated SEQ ID:2371, and is provided hereinbelow with reference to the sequence listing part.

[11373] GAM722 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM722 target RNA, herein designated GAM TARGET RNA.
GAM722 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11374] GAM722 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM722 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM722 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM722 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM722 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11375] The complementary binding of GAM722 RNA, herein designated GAM RNA, to target binding sites on GAM722 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM722 target RNA, herein desig-

nated GAM TARGET RNA, into GAM722 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11376] It is appreciated that GAM722 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM722 target genes. The mRNA of each one of this plurality of GAM722 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM722 RNA, herein designated GAM RNA, and which when bound by GAM722 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM722 target proteins.

[11377] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM722 gene, herein designated GAM GENE, on one or more GAM722 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11378] It is yet further appreciated that specific functions, and accordingly utilities, of GAM722 correlate with, and may be deduced from, the identity of the target genes which GAM722 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11379] Nucleotide sequences of the GAM722 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM722 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM722 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM722 are further described hereinbelow with reference to Table Table1.

[11380] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM722 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[11381] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 723 (GAM723) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11382] GAM723 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM723 was detected is described hereinabove with reference to Figs. 2-8.

[11383] GAM723 gene, herein designated GAM GENE, and GAM723 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11384] GAM723 gene, herein designated GAM GENE, encodes a GAM723 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM723 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM723 precursor RNA is designated SEQ ID:696, and is provided hereinbelow with reference to the sequence listing part.

[11385] GAM723 has 11 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[11386] SEQ ID:99790 detected in mouse EST Accession AI157515.1.

[11387] SEQ ID:99792 detected in mouse EST Accession AA034667.1.

[11388] SEQ ID:99793 detected in mouse EST Accession W54339.1.

[11389] SEQ ID:99801 detected in mouse EST Accession BE625355.1.

[11390] SEQ ID:99802 detected in mouse EST Accession W65790.1.

[11391] SEQ ID:99803 detected in mouse EST Accession BI145910.1.

[11392] SEQ ID:99804 detected in mouse EST Accession AI613817.1.

[11393] SEQ ID:99805 detected in mouse EST Accession BE861499.1.

[11394] SEQ ID:99809 detected in mouse EST Accession AA051691.1.

[11395] SEQ ID:99810 detected in mouse EST Accession BB667583.1.

[11396] SEQ ID:99812 detected in mouse EST Accession BI101177.1.

[11397] GAM723 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM723 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11398] An enzyme complex designated DICER COMPLEX, dices the GAM723 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM723 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM723 RNA is designated SEQ ID:2372, and is provided hereinbelow with reference to the sequence listing part.

[11399] GAM723 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM723 target RNA, herein designated GAM TARGET RNA. GAM723 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11400] GAM723 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM723 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM723 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM723 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM723 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11401] The complementary binding of GAM723 RNA, herein designated GAM RNA, to target binding sites on GAM723 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM723 target RNA, herein designated GAM TARGET RNA, into GAM723 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11402] It is appreciated that GAM723 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM723 target genes. The mRNA of each one of this plurality of GAM723 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM723 RNA, herein designated GAM RNA, and which when bound by GAM723 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM723 target proteins.

[11403] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM723 gene, herein designated GAM GENE, on one or more GAM723 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11404] It is yet further appreciated that specific functions, and accordingly utilities, of GAM723 correlate with, and may be deduced from, the identity of the target genes which GAM723 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11405] Nucleotide sequences of the GAM723 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM723 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM723 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM723 are further described hereinbelow with reference to Table Table1.

[11406] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM723 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11407] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 724 (GAM724) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11408] GAM724 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM724 was detected is described hereinabove with reference to Figs. 2-8.

[11409] GAM724 gene, herein designated GAM GENE, and GAM724 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11410] GAM724 gene, herein designated GAM GENE, encodes a GAM724 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM724 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM724 precursor RNA is designated SEQ ID:697, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:697 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[11411] GAM724 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM724 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[11412] An enzyme complex designated DICER COMPLEX, dices the GAM724 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM724 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM724 RNA is designated SEQ ID:2373, and is provided hereinbelow with reference to the sequence listing part.

[11413] GAM724 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM724 target RNA, herein designated GAM TARGET RNA. GAM724 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11414] GAM724 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM724 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM724 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM724 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM724 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11415] The complementary binding of GAM724 RNA, herein designated GAM RNA, to target binding sites on GAM724 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM724 target RNA, herein designated GAM TARGET RNA, into GAM724 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11416] It is appreciated that GAM724 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM724 target genes. The mRNA of each one of this plurality of GAM724 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM724 RNA, herein designated GAM RNA, and which when bound by GAM724 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM724 target proteins.

[11417] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM724 gene, herein designated GAM GENE, on one or more GAM724 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11418] It is yet further appreciated that specific functions, and accordingly utilities, of GAM724 correlate with, and may be deduced from, the identity of the target genes which GAM724 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11419] Nucleotide sequences of the GAM724 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM724 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM724 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM724 are further described hereinbelow with reference to Table Table1.

[11420] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM724 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11421] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 725 (GAM725) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11422] GAM725 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM725 was detected is described hereinabove with reference to Figs. 2-8.

[11423] GAM725 gene, herein designated GAM GENE, and GAM725 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11424] GAM725 gene, herein designated GAM GENE, encodes a GAM725 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM725 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM725 precursor RNA is designated SEQ ID:698, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:698 is located at position 33703762 relative to

contig NT_007592.11, on chromosome 6.

[11425] GAM725 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM725 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11426] An enzyme complex designated DICER COMPLEX, dices the GAM725 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM725 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM725 RNA is designated SEQ ID:2374, and is provided hereinbelow with reference to the sequence listing part.

[11427] GAM725 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM725 target RNA, herein designated GAM TARGET RNA.

GAM725 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11428] GAM725 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM725 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM725 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM725 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM725 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11429] The complementary binding of GAM725 RNA, herein designated GAM RNA, to target binding sites on GAM725 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM725 target RNA, herein designated GAM TARGET RNA, into GAM725 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11430] It is appreciated that GAM725 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM725 target genes. The mRNA of each one of this plurality of GAM725 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM725 RNA, herein designated GAM RNA, and which when bound by GAM725 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM725 target proteins.

[11431] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM725 gene, herein designated GAM GENE, on one or more GAM725 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11432] It is yet further appreciated that specific functions, and accordingly utilities, of GAM725 correlate with, and may be deduced from, the identity of the target genes which GAM725 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11433] Nucleotide sequences of the GAM725 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM725 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM725 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM725 are further described hereinbelow with reference to Table Table1.

[11434] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM725 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11435] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 726 (GAM726) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11436] GAM726 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM726 was detected is described hereinabove with reference to Figs. 2-8.

[11437] GAM726 gene, herein designated GAM GENE, and GAM726 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11438] GAM726 gene, herein designated GAM GENE, encodes a GAM726 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM726 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM726 precursor RNA is designated SEQ ID:699, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:699 is located at position 4740562 relative to contig NT_011109.13, on chromosome 19.

[11439] GAM726 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM726 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11440] An enzyme complex designated DICER COMPLEX, dices the GAM726 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM726 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM726 RNA is designated SEQ ID:2375, and is provided hereinbelow with reference to the sequence listing part.

[11441] GAM726 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM726 target RNA, herein designated GAM TARGET RNA. GAM726 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11442] GAM726 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM726 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM726 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM726 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM726 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11443] The complementary binding of GAM726 RNA, herein designated GAM RNA, to target binding sites on GAM726 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM726 target RNA, herein designated GAM TARGET RNA, into GAM726 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11444] It is appreciated that GAM726 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM726 target genes. The mRNA of each one of this plurality of GAM726 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM726 RNA, herein designated GAM RNA, and which when bound by GAM726 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM726 target proteins.

[11445] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM726 gene, herein designated GAM GENE, on one or more GAM726 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11446] It is yet further appreciated that specific functions, and accordingly utilities, of GAM726 correlate with, and may be deduced from, the identity of the target genes which GAM726 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11447] Nucleotide sequences of the GAM726 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM726 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM726 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM726 are further described hereinbelow with reference to Table Table1.

[11448] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM726 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11449] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

727 (GAM727) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11450] GAM727 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM727 was detected is described hereinabove with reference to Figs. 2-8.

[11451] GAM727 gene, herein designated GAM GENE, and GAM727 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11452] GAM727 gene, herein designated GAM GENE, encodes a GAM727 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM727 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM727 precursor RNA is designated SEQ ID:700, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:700 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[11453] GAM727 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM727 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11454] An enzyme complex designated DICER COMPLEX, dices the GAM727 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM727 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM727 RNA is designated SEQ ID:2376, and is provided hereinbelow with reference to the sequence listing part.

[11455] GAM727 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM727 target RNA, herein designated GAM TARGET RNA. GAM727 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11456] GAM727 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM727 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM727 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM727 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM727 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[11457] The complementary binding of GAM727 RNA, herein designated GAM RNA, to target binding sites on GAM727 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM727 target RNA, herein designated GAM TARGET RNA, into GAM727 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11458] It is appreciated that GAM727 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM727 target genes. The mRNA of each one of this plurality of GAM727 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM727 RNA, herein designated GAM RNA, and which when bound by GAM727 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM727 target proteins.

[11459] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM727 gene, herein designated GAM GENE, on one or

more GAM727 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11460] It is yet further appreciated that specific functions, and accordingly utilities, of GAM727 correlate with, and may be deduced from, the identity of the target genes which GAM727 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11461] Nucleotide sequences of the GAM727 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM727 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM727 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM727 are further de-

scribed hereinbelow with reference to Table Table1.

[11462] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM727 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11463] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 728 (GAM728) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11464] GAM728 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM728 was detected is described hereinabove with reference to Figs. 2-8.

[11465] GAM728 gene, herein designated GAM GENE, and GAM728 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11466] GAM728 gene, herein designated GAM GENE, encodes a GAM728 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM728 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM728 precursor RNA is designated SEQ ID:701, and is provided hereinbelow with reference to the sequence listing part.

[11467] GAM728 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11468] An enzyme complex designated DICER COMPLEX, dices the GAM728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM728 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM728 RNA is designated SEQ ID:2377, and is provided hereinbelow with reference to the sequence listing part.

[11469] GAM728 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM728 target RNA, herein designated GAM TARGET RNA. GAM728 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11470] GAM728 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM728 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM728 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM728 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM728 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11471] The complementary binding of GAM728 RNA, herein designated GAM RNA, to target binding sites on GAM728 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM728 target RNA, herein designated GAM TARGET RNA, into GAM728 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11472] It is appreciated that GAM728 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM728 target genes. The mRNA of each one of this plurality of GAM728 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM728 RNA,

herein designated GAM RNA, and which when bound by GAM728 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM728 target proteins.

[11473] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM728 gene, herein designated GAM GENE, on one or more GAM728 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11474] It is yet further appreciated that specific functions, and accordingly utilities, of GAM728 correlate with, and may be deduced from, the identity of the target genes which

GAM728 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11475] Nucleotide sequences of the GAM728 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM728 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM728 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM728 are further described hereinbelow with reference to Table Table1.

[11476] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM728 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11477] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 729 (GAM729) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11478] GAM729 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM729 was detected is described hereinabove with reference to Figs. 2-8.

[11479] GAM729 gene, herein designated GAM GENE, and GAM729 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11480] GAM729 gene, herein designated GAM GENE, encodes a GAM729 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM729 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM729 precursor RNA is designated SEQ ID:702, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:702 is located at position 2934168 relative to contig NT_009458.12, on chromosome 12.

[11481] GAM729 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[11482] SEQ ID:98412 detected in mouse EST Accession BI202421.1.

[11483] SEQ ID:98413 detected in mouse EST Accession AA692083.1.

[11484] GAM729 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11485] An enzyme complex designated DICER COMPLEX, dices the GAM729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM729 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM729 RNA is designated SEQ ID:2378, and is provided hereinbelow with reference to the sequence listing part.

[11486] GAM729 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM729 target RNA, herein designated GAM TARGET RNA. GAM729 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11487] GAM729 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM729 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM729 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM729 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM729

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11488] The complementary binding of GAM729 RNA, herein designated GAM RNA, to target binding sites on GAM729 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM729 target RNA, herein designated GAM TARGET RNA, into GAM729 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11489] It is appreciated that GAM729 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM729 target genes. The mRNA of each one of this plurality of GAM729 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM729 RNA, herein designated GAM RNA, and which when bound by GAM729 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM729 target proteins.

[11490] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM729 gene, herein designated GAM GENE, on one or more GAM729 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11491] It is yet further appreciated that specific functions, and accordingly utilities, of GAM729 correlate with, and may be deduced from, the identity of the target genes which GAM729 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11492] Nucleotide sequences of the GAM729 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM729 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM729 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM729 are further described hereinbelow with reference to Table Table1.

[11493] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM729 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11494] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 730 (GAM730) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11495] GAM730 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM730 was detected is described hereinabove with reference to Figs. 2-8.

[11496] GAM730 gene, herein designated GAM GENE, and GAM730 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[11497] GAM730 gene, herein designated GAM GENE, encodes a GAM730 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM730 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM730 precursor RNA is designated SEQ ID:703, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:703 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[11498] GAM730 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM730 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11499] An enzyme complex designated DICER COMPLEX, dices

the GAM730 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM730 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM730 RNA is designated SEQ ID:2379, and is provided hereinbelow with reference to the sequence listing part.

[11500] GAM730 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM730 target RNA, herein designated GAM TARGET RNA.

GAM730 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11501] GAM730 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM730 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM730

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM730 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM730 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11502] The complementary binding of GAM730 RNA, herein designated GAM RNA, to target binding sites on GAM730 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM730 target RNA, herein designated GAM TARGET RNA, into GAM730 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11503] It is appreciated that GAM730 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM730 target genes. The mRNA of each one of this plurality of GAM730 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM730 RNA, herein designated GAM RNA, and which when bound by GAM730 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM730 target proteins.

[11504] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM730 gene, herein designated GAM GENE, on one or more GAM730 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11505] It is yet further appreciated that specific functions, and accordingly utilities, of GAM730 correlate with, and may be deduced from, the identity of the target genes which GAM730 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11506] Nucleotide sequences of the GAM730 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM730 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM730 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM730 are further described hereinbelow with reference to Table Table1.

[11507] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM730 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11508] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 731 (GAM731) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11509] GAM731 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM731 was detected is described hereinabove with reference to Figs. 2-8.

[11510] GAM731 gene, herein designated GAM GENE, and GAM731 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11511] GAM731 gene, herein designated GAM GENE, encodes a GAM731 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM731 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM731 precursor RNA is designated SEQ ID:704, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:704 is located at position 408142 relative to contig NT_005825.13, on chromosome 3.

[11512] GAM731 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM731 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11513] An enzyme complex designated DICER COMPLEX, dices the GAM731 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM731 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM731 RNA is designated SEQ ID:2380, and is provided hereinbelow with reference to the sequence listing part.

[11514] GAM731 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM731 target RNA, herein designated GAM TARGET RNA.

GAM731 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11515] GAM731 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM731 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM731 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM731 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM731 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11516] The complementary binding of GAM731 RNA, herein designated GAM RNA, to target binding sites on GAM731 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM731 target RNA, herein designated GAM TARGET RNA, into GAM731 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11517] It is appreciated that GAM731 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM731 target genes. The mRNA of each one of this plurality of GAM731 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM731 RNA, herein designated GAM RNA, and which when bound by GAM731 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM731 target proteins.

[11518] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM731 gene, herein designated GAM GENE, on one or more GAM731 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11519] It is yet further appreciated that specific functions, and accordingly utilities, of GAM731 correlate with, and may be deduced from, the identity of the target genes which GAM731 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11520] Nucleotide sequences of the GAM731 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM731 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM731 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM731 are further described hereinbelow with reference to Table Table1.

[11521] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM731 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11522] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 732 (GAM732) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11523] GAM732 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM732 was detected is described hereinabove with reference to Figs. 2-8.

[11524] GAM732 gene, herein designated GAM GENE, and GAM732 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11525] GAM732 gene, herein designated GAM GENE, encodes a GAM732 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM732 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM732 precursor RNA is designated SEQ ID:705, and is provided hereinbelow with reference to the sequence listing part.

[11526] GAM732 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11527] An enzyme complex designated DICER COMPLEX, dices the GAM732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM732 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM732 RNA is designated SEQ ID:2381, and is provided hereinbelow with reference to the sequence listing part.

[11528] GAM732 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM732 target RNA, herein designated GAM TARGET RNA. GAM732 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11529] GAM732 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM732 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM732 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM732 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM732 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11530] The complementary binding of GAM732 RNA, herein designated GAM RNA, to target binding sites on GAM732 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM732 target RNA, herein designated GAM TARGET RNA, into GAM732 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11531] It is appreciated that GAM732 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM732 target genes. The mRNA of each one of this plurality of GAM732 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM732 RNA, herein designated GAM RNA, and which when bound by GAM732 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM732 target proteins.

[11532] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM732 gene, herein designated GAM GENE, on one or more GAM732 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11533] It is yet further appreciated that specific functions, and accordingly utilities, of GAM732 correlate with, and may

be deduced from, the identity of the target genes which GAM732 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11534] Nucleotide sequences of the GAM732 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM732 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM732 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM732 are further described hereinbelow with reference to Table Table1.

[11535] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM732 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11536] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 733 (GAM733) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11537] GAM733 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM733 was detected is described hereinabove with reference to Figs. 2-8.

[11538] GAM733 gene, herein designated GAM GENE, and GAM733 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11539] GAM733 gene, herein designated GAM GENE, encodes a GAM733 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM733 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM733 precursor RNA is designated SEQ ID:706, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:706 is located at position 13875414 relative to contig NT_017568.11, on chromosome 9.

[11540] GAM733 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM733 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11541] An enzyme complex designated DICER COMPLEX, dices the GAM733 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM733 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM733 RNA is designated SEQ ID:2382, and is provided hereinbelow with reference to the sequence listing part.

[11542] GAM733 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM733 target RNA, herein designated GAM TARGET RNA. GAM733 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11543] GAM733 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM733 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM733 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM733 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM733 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11544] The complementary binding of GAM733 RNA, herein designated GAM RNA, to target binding sites on GAM733 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM733 target RNA, herein designated GAM TARGET RNA, into GAM733 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11545] It is appreciated that GAM733 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM733 target genes. The mRNA of each one of this plurality of GAM733 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM733 RNA, herein designated GAM RNA, and which when bound by GAM733 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM733 target proteins.

[11546] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM733 gene, herein designated GAM GENE, on one or more GAM733 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11547] It is yet further appreciated that specific functions, and accordingly utilities, of GAM733 correlate with, and may be deduced from, the identity of the target genes which GAM733 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11548] Nucleotide sequences of the GAM733 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM733 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM733 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM733 are further described hereinbelow with reference to Table Table1.

[11549] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM733 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11550] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 734 (GAM734) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11551] GAM734 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM734 was detected is described hereinabove with reference to Figs. 2-8.

[11552] GAM734 gene, herein designated GAM GENE, and GAM734 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11553] GAM734 gene, herein designated GAM GENE, encodes a GAM734 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM734 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM734 precursor RNA is desig-

nated SEQ ID:707, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:707 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[11554] GAM734 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM734 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11555] An enzyme complex designated DICER COMPLEX, dices the GAM734 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM734 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM734 RNA is designated SEQ ID:2383, and is provided hereinbelow with reference to the sequence listing part.

[11556] GAM734 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM734 target RNA, herein designated GAM TARGET RNA. GAM734 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11557] GAM734 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM734 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM734 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM734 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM734 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11558] The complementary binding of GAM734 RNA, herein designated GAM RNA, to target binding sites on GAM734 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM734 target RNA, herein designated GAM TARGET RNA, into GAM734 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11559] It is appreciated that GAM734 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM734 target genes. The mRNA of each one of this plurality of GAM734 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM734 RNA, herein designated GAM RNA, and which when bound by GAM734 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM734 target proteins.

[11560] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM734 gene, herein designated GAM GENE, on one or more GAM734 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11561] It is yet further appreciated that specific functions, and accordingly utilities, of GAM734 correlate with, and may be deduced from, the identity of the target genes which GAM734 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11562] Nucleotide sequences of the GAM734 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM734 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM734 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM734 are further described hereinbelow with reference to Table Table1.

[11563] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM734 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11564] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 735 (GAM735) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11565] GAM735 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM735 was detected is described hereinabove with reference to Figs. 2-8.

[11566] GAM735 gene, herein designated GAM GENE, and GAM735 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11567] GAM735 gene, herein designated GAM GENE, encodes a GAM735 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM735 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM735 precursor RNA is designated SEQ ID:708, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:708 is located at position 3991141 relative to contig NT_033944.3, on chromosome 6.

[11568] GAM735 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM735 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[11569] An enzyme complex designated DICER COMPLEX, dices the GAM735 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM735 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM735 RNA is designated SEQ ID:2384, and is provided hereinbelow with reference to the sequence listing part.

[11570] GAM735 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM735 target RNA, herein designated GAM TARGET RNA. GAM735 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11571] GAM735 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM735 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM735 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM735 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM735 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11572] The complementary binding of GAM735 RNA, herein designated GAM RNA, to target binding sites on GAM735 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM735 target RNA, herein designated GAM TARGET RNA, into GAM735 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11573] It is appreciated that GAM735 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM735 target genes. The mRNA of each one of this plurality of GAM735 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM735 RNA, herein designated GAM RNA, and which when bound by GAM735 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM735 target proteins.

[11574] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM735 gene, herein designated GAM GENE, on one or more GAM735 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11575] It is yet further appreciated that specific functions, and accordingly utilities, of GAM735 correlate with, and may be deduced from, the identity of the target genes which GAM735 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11576] Nucleotide sequences of the GAM735 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM735 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM735 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM735 are further described hereinbelow with reference to Table Table1.

[11577] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM735 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11578] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 736 (GAM736) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11579] GAM736 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM736 was detected is described hereinabove with reference to Figs. 2-8.

[11580] GAM736 gene, herein designated GAM GENE, and GAM736 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11581] GAM736 gene, herein designated GAM GENE, encodes a GAM736 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM736 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM736 precursor RNA is designated SEQ ID:709, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:709 is located at position 2472455 relative to con-

tig NT_022760.12, on chromosome 4.

[11582] GAM736 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM736 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11583] An enzyme complex designated DICER COMPLEX, dices the GAM736 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM736 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM736 RNA is designated SEQ ID:2385, and is provided hereinbelow with reference to the sequence listing part.

[11584] GAM736 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM736 target RNA, herein designated GAM TARGET RNA.

GAM736 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11585] GAM736 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM736 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM736 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM736 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM736 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11586] The complementary binding of GAM736 RNA, herein designated GAM RNA, to target binding sites on GAM736 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM736 target RNA, herein designated GAM TARGET RNA, into GAM736 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11587] It is appreciated that GAM736 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM736 target genes. The mRNA of each one of this plurality of GAM736 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM736 RNA, herein designated GAM RNA, and which when bound by GAM736 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM736 target proteins.

[11588] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM736 gene, herein designated GAM GENE, on one or more GAM736 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11589] It is yet further appreciated that specific functions, and accordingly utilities, of GAM736 correlate with, and may be deduced from, the identity of the target genes which GAM736 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11590] Nucleotide sequences of the GAM736 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM736 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM736 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM736 are further described hereinbelow with reference to Table Table1.

[11591] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM736 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11592] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 737 (GAM737) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11593] GAM737 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM737 was detected is described hereinabove with reference to Figs. 2-8.

[11594] GAM737 gene, herein designated GAM GENE, and GAM737 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11595] GAM737 gene, herein designated GAM GENE, encodes a GAM737 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM737 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM737 precursor RNA is designated SEQ ID:710, and is provided hereinbelow with reference to the sequence listing part.

[11596] GAM737 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM737 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11597] An enzyme complex designated DICER COMPLEX, dices the GAM737 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM737 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM737 RNA is designated SEQ ID:2386, and is provided hereinbelow with reference to the sequence listing part.

[11598] GAM737 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM737 target RNA, herein designated GAM TARGET RNA. GAM737 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11599] GAM737 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM737 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM737 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM737 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM737 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11600] The complementary binding of GAM737 RNA, herein designated GAM RNA, to target binding sites on GAM737 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM737 target RNA, herein designated GAM TARGET RNA, into GAM737 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11601] It is appreciated that GAM737 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM737 target genes. The mRNA of each one of this plu-

rality of GAM737 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM737 RNA, herein designated GAM RNA, and which when bound by GAM737 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM737 target proteins.

[11602] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM737 gene, herein designated GAM GENE, on one or more GAM737 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11603] It is yet further appreciated that specific functions, and accordingly utilities, of GAM737 correlate with, and may be deduced from, the identity of the target genes which GAM737 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11604] Nucleotide sequences of the GAM737 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM737 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM737 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM737 are further described hereinbelow with reference to Table Table1.

[11605] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM737 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11606] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 738 (GAM738) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[11607] GAM738 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM738 was detected is described hereinabove with reference to Figs. 2-8.

[11608] GAM738 gene, herein designated GAM GENE, and GAM738 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11609] GAM738 gene, herein designated GAM GENE, encodes a GAM738 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM738 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM738 precursor RNA is designated SEQ ID:711, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:711 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[11610] GAM738 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11611] An enzyme complex designated DICER COMPLEX, dices the GAM738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM738 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM738 RNA is designated SEQ ID:2387, and is provided hereinbelow with reference to the sequence listing part.

[11612] GAM738 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM738 target RNA, herein designated GAM TARGET RNA. GAM738 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11613] GAM738 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM738 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM738 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM738 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM738 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11614] The complementary binding of GAM738 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM738 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM738 target RNA, herein designated GAM TARGET RNA, into GAM738 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11615] It is appreciated that GAM738 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM738 target genes. The mRNA of each one of this plurality of GAM738 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM738 RNA, herein designated GAM RNA, and which when bound by GAM738 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM738 target proteins.

[11616] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM738 gene, herein designated GAM GENE, on one or more GAM738 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11617] It is yet further appreciated that specific functions, and accordingly utilities, of GAM738 correlate with, and may be deduced from, the identity of the target genes which GAM738 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11618] Nucleotide sequences of the GAM738 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM738 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM738 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM738 are further described hereinbelow with reference to Table Table1.

[11619] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM738 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11620] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 739 (GAM739) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11621] GAM739 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM739 was detected is described hereinabove with reference to Figs. 2-8.

[11622] GAM739 gene, herein designated GAM GENE, and GAM739 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11623] GAM739 gene, herein designated GAM GENE, encodes a GAM739 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM739 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM739 precursor RNA is designated SEQ ID:712, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:712 is located at position 1698742 relative to contig NT_028309.8, on chromosome 11.

[11624] GAM739 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM739 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11625] An enzyme complex designated DICER COMPLEX, dices the GAM739 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM739 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM739 RNA is designated SEQ ID:2388, and is provided hereinbelow with reference to the sequence listing part.

[11626] GAM739 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM739 target RNA, herein designated GAM TARGET RNA. GAM739 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11627] GAM739 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM739 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM739 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM739 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM739 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11628] The complementary binding of GAM739 RNA, herein designated GAM RNA, to target binding sites on GAM739 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM739 target RNA, herein designated GAM TARGET RNA, into GAM739 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11629] It is appreciated that GAM739 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM739 target genes. The mRNA of each one of this plurality of GAM739 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM739 RNA,

herein designated GAM RNA, and which when bound by GAM739 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM739 target proteins.

[11630] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM739 gene, herein designated GAM GENE, on one or more GAM739 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11631] It is yet further appreciated that specific functions, and accordingly utilities, of GAM739 correlate with, and may be deduced from, the identity of the target genes which

GAM739 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11632] Nucleotide sequences of the GAM739 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM739 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM739 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM739 are further described hereinbelow with reference to Table Table1.

[11633] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM739 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11634] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 740 (GAM740) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11635] GAM740 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM740 was detected is described hereinabove with reference to Figs. 2-8.

[11636] GAM740 gene, herein designated GAM GENE, and GAM740 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11637] GAM740 gene, herein designated GAM GENE, encodes a GAM740 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM740 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM740 precursor RNA is designated SEQ ID:713, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:713 is located at position 8666475 relative to contig NT_026437.9, on chromosome 14.

[11638] GAM740 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM740 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11639] An enzyme complex designated DICER COMPLEX, dices the GAM740 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM740 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM740 RNA is designated SEQ ID:2389, and is provided hereinbelow with reference to the sequence listing part.

[11640] GAM740 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM740 target RNA, herein designated GAM TARGET RNA. GAM740 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11641] GAM740 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM740 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM740 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM740 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM740 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11642] The complementary binding of GAM740 RNA, herein designated GAM RNA, to target binding sites on GAM740 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM740 target RNA, herein designated GAM TARGET RNA, into GAM740 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11643] It is appreciated that GAM740 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM740 target genes. The mRNA of each one of this plurality of GAM740 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM740 RNA, herein designated GAM RNA, and which when bound by GAM740 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM740 target proteins.

[11644] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM740 gene, herein designated GAM GENE, on one or more GAM740 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11645] It is yet further appreciated that specific functions, and accordingly utilities, of GAM740 correlate with, and may be deduced from, the identity of the target genes which GAM740 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11646] Nucleotide sequences of the GAM740 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM740 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM740 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM740 are further described hereinbelow with reference to Table Table1.

[11647] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM740 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11648] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 741 (GAM741) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11649] GAM741 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM741 was detected is described hereinabove with reference to Figs. 2-8.

[11650] GAM741 gene, herein designated GAM GENE, and GAM741 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11651] GAM741 gene, herein designated GAM GENE, encodes a GAM741 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM741 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM741 precursor RNA is designated SEQ ID:714, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:714 is located at position 6027489 relative to contig NT_016755.11, on chromosome 5.

[11652] GAM741 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM741 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11653] An enzyme complex designated DICER COMPLEX, dices the GAM741 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM741 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM741 RNA is designated SEQ ID:2390, and is provided

hereinbelow with reference to the sequence listing part.

[11654] GAM741 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM741 target RNA, herein designated GAM TARGET RNA.

GAM741 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11655] GAM741 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM741 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM741 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM741 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM741 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11656] The complementary binding of GAM741 RNA, herein designated GAM RNA, to target binding sites on GAM741 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM741 target RNA, herein designated GAM TARGET RNA, into GAM741 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11657] It is appreciated that GAM741 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM741 target genes. The mRNA of each one of this plurality of GAM741 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM741 RNA, herein designated GAM RNA, and which when bound by GAM741 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM741 tar-

get proteins.

[11658] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM741 gene, herein designated GAM GENE, on one or more GAM741 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11659] It is yet further appreciated that specific functions, and accordingly utilities, of GAM741 correlate with, and may be deduced from, the identity of the target genes which GAM741 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11660] Nucleotide sequences of the GAM741 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM741 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM741 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM741 are further described hereinbelow with reference to Table Table1.

[11661] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM741 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11662] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 742 (GAM742) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11663] GAM742 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM742 was detected is described hereinabove with reference to Figs. 2-8.

[11664] GAM742 gene, herein designated GAM GENE, and

GAM742 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11665] GAM742 gene, herein designated GAM GENE, encodes a GAM742 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM742 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM742 precursor RNA is designated SEQ ID:715, and is provided hereinbelow with reference to the sequence listing part.

[11666] GAM742 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[11667] SEQ ID:98026 detected in mouse EST Accession BF141022.1.

[11668] SEQ ID:98027 detected in mouse EST Accession BG174833.1.

[11669] GAM742 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM742 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11670] An enzyme complex designated DICER COMPLEX, dices the GAM742 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM742 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM742 RNA is designated SEQ ID:2391, and is provided hereinbelow with reference to the sequence listing part.

[11671] GAM742 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM742 target RNA, herein designated GAM TARGET RNA. GAM742 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11672] GAM742 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM742 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM742 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM742 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM742 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11673] The complementary binding of GAM742 RNA, herein designated GAM RNA, to target binding sites on GAM742 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM742 target RNA, herein designated GAM TARGET RNA, into GAM742 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11674] It is appreciated that GAM742 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM742 target genes. The mRNA of each one of this plurality of GAM742 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM742 RNA, herein designated GAM RNA, and which when bound by GAM742 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM742 target proteins.

[11675] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM742 gene, herein designated GAM GENE, on one or more GAM742 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11676] It is yet further appreciated that specific functions, and accordingly utilities, of GAM742 correlate with, and may be deduced from, the identity of the target genes which GAM742 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11677] Nucleotide sequences of the GAM742 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM742 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM742 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM742 are further described hereinbelow with reference to Table Table1.

[11678] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM742 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11679] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 743 (GAM743) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11680] GAM743 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM743 was detected is described hereinabove with reference to Figs. 2-8.

[11681] GAM743 gene, herein designated GAM GENE, and GAM743 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11682] GAM743 gene, herein designated GAM GENE, encodes a GAM743 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM743 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM743 precursor RNA is designated SEQ ID:716, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:716 is located at position 4650509 relative to contig NT_010641.11, on chromosome 17.

[11683] GAM743 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99046, which mouse homolog is detected in mouse EST accession BI083272.1.

[11684] GAM743 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM743 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11685] An enzyme complex designated DICER COMPLEX, dices

the GAM743 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM743 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM743 RNA is designated SEQ ID:2392, and is provided hereinbelow with reference to the sequence listing part.

[11686] GAM743 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM743 target RNA, herein designated GAM TARGET RNA.

GAM743 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11687] GAM743 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM743 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM743

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM743 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM743 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11688] The complementary binding of GAM743 RNA, herein designated GAM RNA, to target binding sites on GAM743 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM743 target RNA, herein designated GAM TARGET RNA, into GAM743 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11689] It is appreciated that GAM743 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM743 target genes. The mRNA of each one of this plurality of GAM743 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM743 RNA, herein designated GAM RNA, and which when bound by GAM743 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM743 target proteins.

[11690] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM743 gene, herein designated GAM GENE, on one or more GAM743 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11691] It is yet further appreciated that specific functions, and accordingly utilities, of GAM743 correlate with, and may be deduced from, the identity of the target genes which GAM743 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11692] Nucleotide sequences of the GAM743 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM743 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM743 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM743 are further described hereinbelow with reference to Table Table1.

[11693] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM743 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11694] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 744 (GAM744) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11695] GAM744 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM744 was detected is described hereinabove with reference to Figs. 2-8.

[11696] GAM744 gene, herein designated GAM GENE, and GAM744 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11697] GAM744 gene, herein designated GAM GENE, encodes a GAM744 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM744 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM744 precursor RNA is designated SEQ ID:717, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:717 is located at position 12165377 relative to contig NT_009952.11, on chromosome 13.

[11698] GAM744 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11699] An enzyme complex designated DICER COMPLEX, dices the GAM744 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM744 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM744 RNA is designated SEQ ID:2393, and is provided hereinbelow with reference to the sequence listing part.

[11700] GAM744 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM744 target RNA, herein designated GAM TARGET RNA.

GAM744 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11701] GAM744 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM744 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM744 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM744 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM744 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11702] The complementary binding of GAM744 RNA, herein designated GAM RNA, to target binding sites on GAM744 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM744 target RNA, herein designated GAM TARGET RNA, into GAM744 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11703] It is appreciated that GAM744 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM744 target genes. The mRNA of each one of this plurality of GAM744 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM744 RNA, herein designated GAM RNA, and which when bound by GAM744 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM744 target proteins.

[11704] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM744 gene, herein designated GAM GENE, on one or more GAM744 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11705] It is yet further appreciated that specific functions, and accordingly utilities, of GAM744 correlate with, and may be deduced from, the identity of the target genes which GAM744 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11706] Nucleotide sequences of the GAM744 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM744 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM744 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM744 are further described hereinbelow with reference to Table Table1.

[11707] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM744 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11708] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 745 (GAM745) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11709] GAM745 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM745 was detected is described hereinabove with reference to Figs. 2-8.

[11710] GAM745 gene, herein designated GAM GENE, and GAM745 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11711] GAM745 gene, herein designated GAM GENE, encodes a GAM745 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM745 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM745 precursor RNA is designated SEQ ID:718, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:718 is located at position 2156517 relative to contig NT_007592.11, on chromosome 6.

[11712] GAM745 has 9 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[11713] SEQ ID:99771 detected in mouse EST Accession W98814.1.

[11714] SEQ ID:99772 detected in mouse EST Accession AA839842.1.

[11715] SEQ ID:99773 detected in mouse EST Accession BE448900.1.

[11716] SEQ ID:99774 detected in mouse EST Accession AW761921.1.

[11717] SEQ ID:99775 detected in mouse EST Accession

BF584264.1.

[11718] SEQ ID:99776 detected in mouse EST Accession BG920670.1.

[11719] SEQ ID:99777 detected in mouse EST Accession BI554717.1.

[11720] SEQ ID:98321 detected in mouse EST Accession AA086501.1.

[11721] SEQ ID:98322 detected in mouse EST Accession AA637831.1.

[11722] GAM745 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM745 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11723] An enzyme complex designated DICER COMPLEX, dices the GAM745 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM745 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM745 RNA is designated SEQ ID:2394, and is provided hereinbelow with reference to the sequence listing part.

[11724] GAM745 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM745 target RNA, herein designated GAM TARGET RNA. GAM745 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11725] GAM745 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM745 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM745 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM745 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM745 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11726] The complementary binding of GAM745 RNA, herein designated GAM RNA, to target binding sites on GAM745 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM745 target RNA, herein designated GAM TARGET RNA, into GAM745 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11727] It is appreciated that GAM745 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM745 target genes. The mRNA of each one of this plu-

rality of GAM745 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM745 RNA, herein designated GAM RNA, and which when bound by GAM745 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM745 target proteins.

[11728] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM745 gene, herein designated GAM GENE, on one or more GAM745 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11729] It is yet further appreciated that specific functions, and accordingly utilities, of GAM745 correlate with, and may be deduced from, the identity of the target genes which GAM745 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11730] Nucleotide sequences of the GAM745 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM745 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM745 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM745 are further described hereinbelow with reference to Table Table1.

[11731] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM745 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11732] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 746 (GAM746) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[11733] GAM746 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM746 was detected is described hereinabove with reference to Figs. 2-8.

[11734] GAM746 gene, herein designated GAM GENE, and GAM746 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11735] GAM746 gene, herein designated GAM GENE, encodes a GAM746 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM746 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM746 precursor RNA is designated SEQ ID:719, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:719 is located at position 1235053 relative to contig NT_009526.11, on chromosome 12.

[11736] GAM746 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse

EST's in which these homologs were detected are:

[11737] SEQ ID:98490 detected in mouse EST Accession BI965972.1.

[11738] SEQ ID:98491 detected in mouse EST Accession AI326210.1.

[11739] SEQ ID:98492 detected in mouse EST Accession BI965652.1.

[11740] GAM746 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM746 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11741] An enzyme complex designated DICER COMPLEX, dices the GAM746 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM746 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM746 RNA is designated SEQ ID:2395, and is provided hereinbelow with reference to the sequence listing part.

[11742] GAM746 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM746 target RNA, herein designated GAM TARGET RNA. GAM746 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11743] GAM746 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM746 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM746 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM746 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM746 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11744] The complementary binding of GAM746 RNA, herein designated GAM RNA, to target binding sites on GAM746 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM746 target RNA, herein designated GAM TARGET RNA, into GAM746 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11745] It is appreciated that GAM746 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM746 target genes. The mRNA of each one of this plurality of GAM746 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM746 RNA, herein designated GAM RNA, and which when bound by GAM746 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM746 target proteins.

[11746] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM746 gene, herein designated GAM GENE, on one or more GAM746 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11747] It is yet further appreciated that specific functions, and accordingly utilities, of GAM746 correlate with, and may

be deduced from, the identity of the target genes which GAM746 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11748] Nucleotide sequences of the GAM746 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM746 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM746 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM746 are further described hereinbelow with reference to Table Table1.

[11749] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM746 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11750] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 747 (GAM747) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11751] GAM747 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM747 was detected is described hereinabove with reference to Figs. 2-8.

[11752] GAM747 gene, herein designated GAM GENE, and GAM747 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11753] GAM747 gene, herein designated GAM GENE, encodes a GAM747 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM747 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM747 precursor RNA is designated SEQ ID:720, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:720 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[11754] GAM747 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11755] An enzyme complex designated DICER COMPLEX, dices the GAM747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM747 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM747 RNA is designated SEQ ID:2396, and is provided hereinbelow with reference to the sequence listing part.

[11756] GAM747 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM747 target RNA, herein designated GAM TARGET RNA. GAM747 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11757] GAM747 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM747 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM747 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM747 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM747 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11758] The complementary binding of GAM747 RNA, herein designated GAM RNA, to target binding sites on GAM747 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM747 target RNA, herein designated GAM TARGET RNA, into GAM747 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11759] It is appreciated that GAM747 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM747 target genes. The mRNA of each one of this plurality of GAM747 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM747 RNA, herein designated GAM RNA, and which when bound by GAM747 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM747 target proteins.

[11760] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM747 gene, herein designated GAM GENE, on one or more GAM747 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11761] It is yet further appreciated that specific functions, and accordingly utilities, of GAM747 correlate with, and may be deduced from, the identity of the target genes which GAM747 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11762] Nucleotide sequences of the GAM747 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM747 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM747 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM747 are further described hereinbelow with reference to Table Table1.

[11763] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM747 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11764] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 748 (GAM748) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11765] GAM748 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM748 was detected is described hereinabove with reference to Figs. 2-8.

[11766] GAM748 gene, herein designated GAM GENE, and GAM748 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11767] GAM748 gene, herein designated GAM GENE, encodes a GAM748 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM748 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM748 precursor RNA is desig-

nated SEQ ID:721, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:721 is located at position 8666480 relative to contig NT_026437.9, on chromosome 14.

[11768] GAM748 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM748 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11769] An enzyme complex designated DICER COMPLEX, dices the GAM748 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM748 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM748 RNA is designated SEQ ID:2397, and is provided hereinbelow with reference to the sequence listing part.

[11770] GAM748 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM748 target RNA, herein designated GAM TARGET RNA. GAM748 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11771] GAM748 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM748 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM748 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM748 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM748 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11772] The complementary binding of GAM748 RNA, herein designated GAM RNA, to target binding sites on GAM748 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM748 target RNA, herein designated GAM TARGET RNA, into GAM748 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11773] It is appreciated that GAM748 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM748 target genes. The mRNA of each one of this plurality of GAM748 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM748 RNA, herein designated GAM RNA, and which when bound by GAM748 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM748 target proteins.

[11774] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM748 gene, herein designated GAM GENE, on one or more GAM748 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11775] It is yet further appreciated that specific functions, and accordingly utilities, of GAM748 correlate with, and may be deduced from, the identity of the target genes which GAM748 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11776] Nucleotide sequences of the GAM748 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM748 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM748 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM748 are further described hereinbelow with reference to Table Table1.

[11777] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM748 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11778] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 749 (GAM749) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11779] GAM749 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM749 was detected is described hereinabove with reference to Figs. 2-8.

[11780] GAM749 gene, herein designated GAM GENE, and GAM749 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11781] GAM749 gene, herein designated GAM GENE, encodes a GAM749 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM749 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM749 precursor RNA is designated SEQ ID:722, and is provided hereinbelow with reference to the sequence listing part.

[11782] GAM749 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11783] An enzyme complex designated DICER COMPLEX, dices

the GAM749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM749 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM749 RNA is designated SEQ ID:2398, and is provided hereinbelow with reference to the sequence listing part.

[11784] GAM749 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM749 target RNA, herein designated GAM TARGET RNA. GAM749 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11785] GAM749 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM749 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM749

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM749 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM749 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11786] The complementary binding of GAM749 RNA, herein designated GAM RNA, to target binding sites on GAM749 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM749 target RNA, herein designated GAM TARGET RNA, into GAM749 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11787] It is appreciated that GAM749 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM749 target genes. The mRNA of each one of this plurality of GAM749 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM749 RNA, herein designated GAM RNA, and which when bound by GAM749 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM749 target proteins.

[11788] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM749 gene, herein designated GAM GENE, on one or more GAM749 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11789] It is yet further appreciated that specific functions, and accordingly utilities, of GAM749 correlate with, and may be deduced from, the identity of the target genes which GAM749 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11790] Nucleotide sequences of the GAM749 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM749 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM749 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM749 are further described hereinbelow with reference to Table Table1.

[11791] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM749 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11792] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 750 (GAM750) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11793] GAM750 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM750 was detected is described hereinabove with reference to Figs. 2-8.

[11794] GAM750 gene, herein designated GAM GENE, and GAM750 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11795] GAM750 gene, herein designated GAM GENE, encodes a GAM750 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM750 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM750 precursor RNA is designated SEQ ID:723, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:723 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[11796] GAM750 has 15 highly conserved, expressed mouse ho-

mologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[11797] SEQ ID:99365 detected in mouse EST Accession AA144533.1.

[11798] SEQ ID:99366 detected in mouse EST Accession AW824753.1.

[11799] SEQ ID:99367 detected in mouse EST Accession BE691413.1.

[11800] SEQ ID:99368 detected in mouse EST Accession BG808025.1.

[11801] SEQ ID:99369 detected in mouse EST Accession AA671455.1.

[11802] SEQ ID:99370 detected in mouse EST Accession BG808010.1.

[11803] SEQ ID:99371 detected in mouse EST Accession BG807850.1.

[11804] SEQ ID:99372 detected in mouse EST Accession BG805970.1.

[11805] SEQ ID:99373 detected in mouse EST Accession AW208601.1.

[11806] SEQ ID:99374 detected in mouse EST Accession

BB610842.1.

[11807] SEQ ID:99375 detected in mouse EST Accession BB609859.1.

[11808] SEQ ID:99377 detected in mouse EST Accession BE691447.1.

[11809] SEQ ID:99382 detected in mouse EST Accession BE943987.1.

[11810] SEQ ID:99383 detected in mouse EST Accession BG145596.1.

[11811] SEQ ID:99384 detected in mouse EST Accession BE692802.1.

[11812] GAM750 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM750 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11813] An enzyme complex designated DICER COMPLEX, dices the GAM750 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM750 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM750 RNA is designated SEQ ID:2399, and is provided hereinbelow with reference to the sequence listing part.

[11814] GAM750 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM750 target RNA, herein designated GAM TARGET RNA. GAM750 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11815] GAM750 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM750 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM750 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM750 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM750 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11816] The complementary binding of GAM750 RNA, herein designated GAM RNA, to target binding sites on GAM750 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM750 target RNA, herein designated GAM TARGET RNA, into GAM750 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11817] It is appreciated that GAM750 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM750 target genes. The mRNA of each one of this plurality of GAM750 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM750 RNA, herein designated GAM RNA, and which when bound by GAM750 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM750 target proteins.

[11818] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM750 gene, herein designated GAM GENE, on one or more GAM750 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11819] It is yet further appreciated that specific functions, and accordingly utilities, of GAM750 correlate with, and may be deduced from, the identity of the target genes which GAM750 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11820] Nucleotide sequences of the GAM750 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM750 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM750 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM750 are further described hereinbelow with reference to Table Table1.

[11821] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM750 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11822] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

751 (GAM751) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11823] GAM751 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM751 was detected is described hereinabove with reference to Figs. 2-8.

[11824] GAM751 gene, herein designated GAM GENE, and GAM751 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11825] GAM751 gene, herein designated GAM GENE, encodes a GAM751 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM751 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM751 precursor RNA is designated SEQ ID:724, and is provided hereinbelow with reference to the sequence listing part.

[11826] GAM751 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM751 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11827] An enzyme complex designated DICER COMPLEX, dices the GAM751 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM751 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM751 RNA is designated SEQ ID:2400, and is provided hereinbelow with reference to the sequence listing part.

[11828] GAM751 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM751 target RNA, herein designated GAM TARGET RNA. GAM751 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11829] GAM751 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM751 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM751 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM751 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM751 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11830] The complementary binding of GAM751 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM751 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM751 target RNA, herein designated GAM TARGET RNA, into GAM751 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11831] It is appreciated that GAM751 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM751 target genes. The mRNA of each one of this plurality of GAM751 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM751 RNA, herein designated GAM RNA, and which when bound by GAM751 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM751 target proteins.

[11832] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM751 gene, herein designated GAM GENE, on one or more GAM751 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11833] It is yet further appreciated that specific functions, and accordingly utilities, of GAM751 correlate with, and may be deduced from, the identity of the target genes which GAM751 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11834] Nucleotide sequences of the GAM751 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM751 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM751 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM751 are further described hereinbelow with reference to Table Table1.

[11835] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM751 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11836] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 752 (GAM752) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11837] GAM752 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM752 was detected is described hereinabove with reference to Figs. 2-8.

[11838] GAM752 gene, herein designated GAM GENE, and GAM752 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11839] GAM752 gene, herein designated GAM GENE, encodes a GAM752 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM752 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM752 precursor RNA is designated SEQ ID:725, and is provided hereinbelow with reference to the sequence listing part.

[11840] GAM752 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM752 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11841] An enzyme complex designated DICER COMPLEX, dices the GAM752 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM752 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM752 RNA is designated SEQ ID:2401, and is provided hereinbelow with reference to the sequence listing part.

[11842] GAM752 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM752 target RNA, herein designated GAM TARGET RNA.

GAM752 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11843] GAM752 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM752 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM752 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM752 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM752 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11844] The complementary binding of GAM752 RNA, herein designated GAM RNA, to target binding sites on GAM752 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM752 target RNA, herein designated GAM TARGET RNA, into GAM752 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11845] It is appreciated that GAM752 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM752 target genes. The mRNA of each one of this plurality of GAM752 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM752 RNA, herein designated GAM RNA, and which when bound by GAM752 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM752 target proteins.

[11846] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM752 gene, herein designated GAM GENE, on one or more GAM752 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11847] It is yet further appreciated that specific functions, and accordingly utilities, of GAM752 correlate with, and may be deduced from, the identity of the target genes which GAM752 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11848] Nucleotide sequences of the GAM752 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM752 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM752 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM752 are further described hereinbelow with reference to Table Table1.

[11849] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM752 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11850] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 753 (GAM753) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11851] GAM753 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM753 was detected is described hereinabove with reference to Figs. 2-8.

[11852] GAM753 gene, herein designated GAM GENE, and GAM753 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11853] GAM753 gene, herein designated GAM GENE, encodes a GAM753 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM753 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM753 precursor RNA is designated SEQ ID:726, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:726 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[11854] GAM753 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM753 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[11855] An enzyme complex designated DICER COMPLEX, dices the GAM753 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM753 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM753 RNA is designated SEQ ID:2402, and is provided hereinbelow with reference to the sequence listing part.

[11856] GAM753 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM753 target RNA, herein designated GAM TARGET RNA. GAM753 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11857] GAM753 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM753 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM753 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM753 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM753 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11858] The complementary binding of GAM753 RNA, herein designated GAM RNA, to target binding sites on GAM753 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM753 target RNA, herein designated GAM TARGET RNA, into GAM753 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11859] It is appreciated that GAM753 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM753 target genes. The mRNA of each one of this plurality of GAM753 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM753 RNA, herein designated GAM RNA, and which when bound by GAM753 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM753 target proteins.

[11860] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM753 gene, herein designated GAM GENE, on one or more GAM753 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11861] It is yet further appreciated that specific functions, and accordingly utilities, of GAM753 correlate with, and may be deduced from, the identity of the target genes which GAM753 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11862] Nucleotide sequences of the GAM753 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM753 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM753 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM753 are further described hereinbelow with reference to Table Table1.

[11863] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM753 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11864] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 754 (GAM754) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11865] GAM754 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM754 was detected is described hereinabove with reference to Figs. 2-8.

[11866] GAM754 gene, herein designated GAM GENE, and GAM754 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11867] GAM754 gene, herein designated GAM GENE, encodes a GAM754 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM754 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM754 precursor RNA is designated SEQ ID:727, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:727 is located at position 2349674 relative to con-

tig NT_021907.13, on chromosome 1.

[11868] GAM754 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM754 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11869] An enzyme complex designated DICER COMPLEX, dices the GAM754 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM754 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM754 RNA is designated SEQ ID:2403, and is provided hereinbelow with reference to the sequence listing part.

[11870] GAM754 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM754 target RNA, herein designated GAM TARGET RNA.

GAM754 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11871] GAM754 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM754 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM754 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM754 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM754 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11872] The complementary binding of GAM754 RNA, herein designated GAM RNA, to target binding sites on GAM754 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM754 target RNA, herein designated GAM TARGET RNA, into GAM754 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11873] It is appreciated that GAM754 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM754 target genes. The mRNA of each one of this plurality of GAM754 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM754 RNA, herein designated GAM RNA, and which when bound by GAM754 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM754 target proteins.

[11874] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM754 gene, herein designated GAM GENE, on one or more GAM754 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11875] It is yet further appreciated that specific functions, and accordingly utilities, of GAM754 correlate with, and may be deduced from, the identity of the target genes which GAM754 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11876] Nucleotide sequences of the GAM754 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM754 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM754 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM754 are further described hereinbelow with reference to Table Table1.

[11877] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM754 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11878] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 755 (GAM755) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11879] GAM755 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM755 was detected is described hereinabove with reference to Figs. 2-8.

[11880] GAM755 gene, herein designated GAM GENE, and GAM755 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11881] GAM755 gene, herein designated GAM GENE, encodes a GAM755 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM755 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM755 precursor RNA is designated SEQ ID:728, and is provided hereinbelow with reference to the sequence listing part.

[11882] GAM755 has 12 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[11883] SEQ ID:99386 detected in mouse EST Accession AA120179.1.

[11884] SEQ ID:99387 detected in mouse EST Accession AA067809.1.

[11885] SEQ ID:99388 detected in mouse EST Accession AI325803.1.

[11886] SEQ ID:99389 detected in mouse EST Accession AA571769.1.

[11887] SEQ ID:99390 detected in mouse EST Accession

BE288419.1.

[11888] SEQ ID:99391 detected in mouse EST Accession AI892495.1.

[11889] SEQ ID:99392 detected in mouse EST Accession AI314077.1.

[11890] SEQ ID:99393 detected in mouse EST Accession BI102267.1.

[11891] SEQ ID:99394 detected in mouse EST Accession AI226829.1.

[11892] SEQ ID:99415 detected in mouse EST Accession BE309522.1.

[11893] SEQ ID:99416 detected in mouse EST Accession AW682208.1.

[11894] SEQ ID:99417 detected in mouse EST Accession BE915479.1.

[11895] GAM755 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM755 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[11896] An enzyme complex designated DICER COMPLEX, dices the GAM755 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM755 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM755 RNA is designated SEQ ID:2404, and is provided hereinbelow with reference to the sequence listing part.

[11897] GAM755 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM755 target RNA, herein designated GAM TARGET RNA.
GAM755 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11898] GAM755 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM755 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM755 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM755 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM755 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11899] The complementary binding of GAM755 RNA, herein designated GAM RNA, to target binding sites on GAM755 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM755 target RNA, herein desig-

nated GAM TARGET RNA, into GAM755 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11900] It is appreciated that GAM755 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM755 target genes. The mRNA of each one of this plurality of GAM755 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM755 RNA, herein designated GAM RNA, and which when bound by GAM755 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM755 target proteins.

[11901] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM755 gene, herein designated GAM GENE, on one or more GAM755 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11902] It is yet further appreciated that specific functions, and accordingly utilities, of GAM755 correlate with, and may be deduced from, the identity of the target genes which GAM755 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11903] Nucleotide sequences of the GAM755 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM755 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM755 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM755 are further described hereinbelow with reference to Table Table1.

[11904] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM755 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[11905] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 756 (GAM756) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11906] GAM756 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM756 was detected is described hereinabove with reference to Figs. 2-8.

[11907] GAM756 gene, herein designated GAM GENE, and GAM756 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11908] GAM756 gene, herein designated GAM GENE, encodes a GAM756 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM756 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM756 precursor RNA is designated SEQ ID:729, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:729 is located at position 371098 relative to contig NT_029253.8, on chromosome 3.

[11909] GAM756 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM756 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11910] An enzyme complex designated DICER COMPLEX, dices the GAM756 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM756 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM756 RNA is designated SEQ ID:2405, and is provided hereinbelow with reference to the sequence listing part.

[11911] GAM756 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM756 target RNA, herein designated GAM TARGET RNA. GAM756 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11912] GAM756 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM756 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM756 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM756 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM756

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11913] The complementary binding of GAM756 RNA, herein designated GAM RNA, to target binding sites on GAM756 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM756 target RNA, herein designated GAM TARGET RNA, into GAM756 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11914] It is appreciated that GAM756 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM756 target genes. The mRNA of each one of this plurality of GAM756 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM756 RNA, herein designated GAM RNA, and which when bound by GAM756 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM756 target proteins.

[11915] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM756 gene, herein designated GAM GENE, on one or more GAM756 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11916] It is yet further appreciated that specific functions, and accordingly utilities, of GAM756 correlate with, and may be deduced from, the identity of the target genes which GAM756 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11917] Nucleotide sequences of the GAM756 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM756 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM756 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM756 are further described hereinbelow with reference to Table Table1.

[11918] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM756 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11919] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 757 (GAM757) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11920] GAM757 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM757 was detected is described hereinabove with reference to Figs. 2-8.

[11921] GAM757 gene, herein designated GAM GENE, and GAM757 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[11922] GAM757 gene, herein designated GAM GENE, encodes a GAM757 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM757 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM757 precursor RNA is designated SEQ ID:730, and is provided hereinbelow with reference to the sequence listing part.

[11923] GAM757 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM757 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11924] An enzyme complex designated DICER COMPLEX, dices the GAM757 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM757 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM757 RNA is designated SEQ ID:2406, and is provided hereinbelow with reference to the sequence listing part.

[11925] GAM757 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM757 target RNA, herein designated GAM TARGET RNA. GAM757 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11926] GAM757 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM757 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM757 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM757 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM757 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11927] The complementary binding of GAM757 RNA, herein designated GAM RNA, to target binding sites on GAM757 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM757 target RNA, herein designated GAM TARGET RNA, into GAM757 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11928] It is appreciated that GAM757 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM757 target genes. The mRNA of each one of this plurality of GAM757 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM757 RNA, herein designated GAM RNA, and which when bound by GAM757 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM757 target proteins.

[11929] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM757 gene, herein designated GAM GENE, on one or more GAM757 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[11930] It is yet further appreciated that specific functions, and accordingly utilities, of GAM757 correlate with, and may be deduced from, the identity of the target genes which GAM757 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11931] Nucleotide sequences of the GAM757 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM757 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM757 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM757 are further described hereinbelow with reference to Table Table1.

[11932] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM757 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11933] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 758 (GAM758) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[11934] GAM758 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM758 was detected is described hereinabove with reference to Figs. 2-8.

[11935] GAM758 gene, herein designated GAM GENE, and GAM758 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11936] GAM758 gene, herein designated GAM GENE, encodes a GAM758 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM758 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM758 precursor RNA is designated SEQ ID:731, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:731 is located at position 10031168 relative to contig NT_006431.11, on chromosome 5.

[11937] GAM758 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM758 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11938] An enzyme complex designated DICER COMPLEX, dices the GAM758 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM758 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM758 RNA is designated SEQ ID:2407, and is provided hereinbelow with reference to the sequence listing part.

[11939] GAM758 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM758 target RNA, herein designated GAM TARGET RNA. GAM758 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11940] GAM758 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM758 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM758 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM758 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM758 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11941] The complementary binding of GAM758 RNA, herein designated GAM RNA, to target binding sites on GAM758 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM758 target RNA, herein designated GAM TARGET RNA, into GAM758 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11942] It is appreciated that GAM758 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM758 target genes. The mRNA of each one of this plurality of GAM758 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM758 RNA, herein designated GAM RNA, and which when bound by GAM758 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM758 target proteins.

[11943] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM758 gene, herein designated GAM GENE, on one or more GAM758 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11944] It is yet further appreciated that specific functions, and accordingly utilities, of GAM758 correlate with, and may be deduced from, the identity of the target genes which GAM758 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11945] Nucleotide sequences of the GAM758 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM758 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM758 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM758 are further described hereinbelow with reference to Table Table1.

[11946] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM758 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11947] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 759 (GAM759) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11948] GAM759 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM759 was detected is described hereinabove with reference to Figs. 2-8.

[11949] GAM759 gene, herein designated GAM GENE, and GAM759 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11950] GAM759 gene, herein designated GAM GENE, encodes a GAM759 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM759 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM759 precursor RNA is designated SEQ ID:732, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:732 is located at position 1235053 relative to contig NT_009526.11, on chromosome 12.

[11951] GAM759 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[11952] SEQ ID:98073 detected in mouse EST Accession BI965972.1.

[11953] SEQ ID:98074 detected in mouse EST Accession AI326210.1.

[11954] SEQ ID:98075 detected in mouse EST Accession BI965652.1.

[11955] GAM759 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM759 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11956] An enzyme complex designated DICER COMPLEX, dices the GAM759 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM759 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM759 RNA is designated SEQ ID:2408, and is provided hereinbelow with reference to the sequence listing part.

[11957] GAM759 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM759 target RNA, herein designated GAM TARGET RNA.
GAM759 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[11958] GAM759 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM759 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM759 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM759 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM759 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11959] The complementary binding of GAM759 RNA, herein designated GAM RNA, to target binding sites on GAM759 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM759 target RNA, herein designated GAM TARGET RNA, into GAM759 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11960] It is appreciated that GAM759 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM759 target genes. The mRNA of each one of this plurality of GAM759 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM759 RNA, herein designated GAM RNA, and which when bound by GAM759 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM759 target proteins.

[11961] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM759 gene, herein designated GAM GENE, on one or more GAM759 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11962] It is yet further appreciated that specific functions, and accordingly utilities, of GAM759 correlate with, and may be deduced from, the identity of the target genes which GAM759 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11963] Nucleotide sequences of the GAM759 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM759 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM759 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM759 are further described hereinbelow with reference to Table Table1.

[11964] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM759 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11965] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 760 (GAM760) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11966] GAM760 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM760 was detected is described hereinabove with reference to Figs. 2-8.

[11967] GAM760 gene, herein designated GAM GENE, and GAM760 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11968] GAM760 gene, herein designated GAM GENE, encodes a GAM760 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM760 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM760 precursor RNA is designated SEQ ID:733, and is provided hereinbelow with reference to the sequence listing part.

[11969] GAM760 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM760 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11970] An enzyme complex designated DICER COMPLEX, dices the GAM760 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM760 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM760 RNA is designated SEQ ID:2409, and is provided

hereinbelow with reference to the sequence listing part.

[11971] GAM760 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM760 target RNA, herein designated GAM TARGET RNA.

GAM760 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11972] GAM760 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM760 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM760 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM760 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM760 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11973] The complementary binding of GAM760 RNA, herein designated GAM RNA, to target binding sites on GAM760 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM760 target RNA, herein designated GAM TARGET RNA, into GAM760 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11974] It is appreciated that GAM760 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM760 target genes. The mRNA of each one of this plurality of GAM760 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM760 RNA, herein designated GAM RNA, and which when bound by GAM760 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM760 tar-

get proteins.

[11975] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM760 gene, herein designated GAM GENE, on one or more GAM760 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11976] It is yet further appreciated that specific functions, and accordingly utilities, of GAM760 correlate with, and may be deduced from, the identity of the target genes which GAM760 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11977] Nucleotide sequences of the GAM760 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM760 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM760 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM760 are further described hereinbelow with reference to Table Table1.

[11978] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM760 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11979] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 761 (GAM761) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11980] GAM761 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM761 was detected is described hereinabove with reference to Figs. 2-8.

[11981] GAM761 gene, herein designated GAM GENE, and

GAM761 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11982] GAM761 gene, herein designated GAM GENE, encodes a GAM761 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM761 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM761 precursor RNA is designated SEQ ID:734, and is provided hereinbelow with reference to the sequence listing part.

[11983] GAM761 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM761 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11984] An enzyme complex designated DICER COMPLEX, dices the GAM761 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM761 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM761 RNA is designated SEQ ID:2410, and is provided hereinbelow with reference to the sequence listing part.

[11985] GAM761 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM761 target RNA, herein designated GAM TARGET RNA. GAM761 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[11986] GAM761 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM761 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM761 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM761 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM761 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[11987] The complementary binding of GAM761 RNA, herein designated GAM RNA, to target binding sites on GAM761 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM761 target RNA, herein designated GAM TARGET RNA, into GAM761 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[11988] It is appreciated that GAM761 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM761 target genes. The mRNA of each one of this plurality of GAM761 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM761 RNA, herein designated GAM RNA, and which when bound by GAM761 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM761 target proteins.

[11989] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM761 gene, herein designated GAM GENE, on one or more GAM761 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[11990] It is yet further appreciated that specific functions, and accordingly utilities, of GAM761 correlate with, and may be deduced from, the identity of the target genes which GAM761 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[11991] Nucleotide sequences of the GAM761 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM761 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM761 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM761 are further described hereinbelow with reference to Table Table1.

[11992] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM761 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[11993] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

762 (GAM762) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[11994] GAM762 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM762 was detected is described hereinabove with reference to Figs. 2-8.

[11995] GAM762 gene, herein designated GAM GENE, and GAM762 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[11996] GAM762 gene, herein designated GAM GENE, encodes a GAM762 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM762 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM762 precursor RNA is designated SEQ ID:735, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:735 is located at position 2349693 relative to contig NT_021907.13, on chromosome 1.

[11997] GAM762 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM762 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[11998] An enzyme complex designated DICER COMPLEX, dices the GAM762 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM762 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM762 RNA is designated SEQ ID:2411, and is provided hereinbelow with reference to the sequence listing part.

[11999] GAM762 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM762 target RNA, herein designated GAM TARGET RNA. GAM762 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12000] GAM762 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM762 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM762 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM762 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM762 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[12001] The complementary binding of GAM762 RNA, herein designated GAM RNA, to target binding sites on GAM762 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM762 target RNA, herein designated GAM TARGET RNA, into GAM762 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12002] It is appreciated that GAM762 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM762 target genes. The mRNA of each one of this plurality of GAM762 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM762 RNA, herein designated GAM RNA, and which when bound by GAM762 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM762 target proteins.

[12003] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM762 gene, herein designated GAM GENE, on one or

more GAM762 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12004] It is yet further appreciated that specific functions, and accordingly utilities, of GAM762 correlate with, and may be deduced from, the identity of the target genes which GAM762 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12005] Nucleotide sequences of the GAM762 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM762 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM762 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM762 are further de-

scribed hereinbelow with reference to Table Table1.

[12006] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM762 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12007] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 763 (GAM763) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12008] GAM763 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM763 was detected is described hereinabove with reference to Figs. 2-8.

[12009] GAM763 gene, herein designated GAM GENE, and GAM763 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12010] GAM763 gene, herein designated GAM GENE, encodes a GAM763 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM763 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM763 precursor RNA is designated SEQ ID:736, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:736 is located at position 65225 relative to contig NT_024901.11, on chromosome 17.

[12011] GAM763 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM763 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12012] An enzyme complex designated DICER COMPLEX, dices the GAM763 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM763 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM763 RNA is designated SEQ ID:2412, and is provided hereinbelow with reference to the sequence listing part.

[12013] GAM763 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM763 target RNA, herein designated GAM TARGET RNA. GAM763 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12014] GAM763 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM763 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM763 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM763 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM763 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12015] The complementary binding of GAM763 RNA, herein designated GAM RNA, to target binding sites on GAM763 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM763 target RNA, herein designated GAM TARGET RNA, into GAM763 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12016] It is appreciated that GAM763 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM763 target genes. The mRNA of each one of this plurality of GAM763 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM763 RNA, herein designated GAM RNA, and which when bound by GAM763 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM763 target proteins.

[12017] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM763 gene, herein designated GAM GENE, on one or more GAM763 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12018] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM763 correlate with, and may be deduced from, the identity of the target genes which GAM763 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12019] Nucleotide sequences of the GAM763 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM763 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM763 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM763 are further described hereinbelow with reference to Table Table1.

[12020] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM763 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12021] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 764 (GAM764) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12022] GAM764 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM764 was detected is described hereinabove with reference to Figs. 2-8.

[12023] GAM764 gene, herein designated GAM GENE, and GAM764 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12024] GAM764 gene, herein designated GAM GENE, encodes a GAM764 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM764 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM764 precursor RNA is designated SEQ ID:737, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:737 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[12025] GAM764 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12026] An enzyme complex designated DICER COMPLEX, dices the GAM764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM764 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM764 RNA is designated SEQ ID:2413, and is provided hereinbelow with reference to the sequence listing part.

[12027] GAM764 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM764 target RNA, herein designated GAM TARGET RNA.
GAM764 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[12028] GAM764 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM764 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM764 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM764 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM764 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12029] The complementary binding of GAM764 RNA, herein designated GAM RNA, to target binding sites on GAM764 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM764 target RNA, herein designated GAM TARGET RNA, into GAM764 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12030] It is appreciated that GAM764 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM764 target genes. The mRNA of each one of this plurality of GAM764 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM764 RNA, herein designated GAM RNA, and which when bound by GAM764 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM764 target proteins.

[12031] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM764 gene, herein designated GAM GENE, on one or more GAM764 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12032] It is yet further appreciated that specific functions, and accordingly utilities, of GAM764 correlate with, and may be deduced from, the identity of the target genes which GAM764 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12033] Nucleotide sequences of the GAM764 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM764 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM764 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM764 are further described hereinbelow with reference to Table Table1.

[12034] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM764 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12035] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 765 (GAM765) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12036] GAM765 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM765 was detected is described hereinabove with reference to Figs. 2-8.

[12037] GAM765 gene, herein designated GAM GENE, and GAM765 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12038] GAM765 gene, herein designated GAM GENE, encodes a GAM765 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM765 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM765 precursor RNA is designated SEQ ID:738, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:738 is located at position 14253451 relative to contig NT_011362.7, on chromosome 20.

[12039] GAM765 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM765 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12040] An enzyme complex designated DICER COMPLEX, dices the GAM765 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM765 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM765 RNA is designated SEQ ID:2414, and is provided hereinbelow with reference to the sequence listing part.

[12041] GAM765 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM765 target RNA, herein designated GAM TARGET RNA. GAM765 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12042] GAM765 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM765 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM765 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM765 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM765 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12043] The complementary binding of GAM765 RNA, herein designated GAM RNA, to target binding sites on GAM765 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM765 target RNA, herein designated GAM TARGET RNA, into GAM765 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12044] It is appreciated that GAM765 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM765 target genes. The mRNA of each one of this plurality of GAM765 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM765 RNA, herein designated GAM RNA, and which when bound by

GAM765 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM765 target proteins.

[12045] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM765 gene, herein designated GAM GENE, on one or more GAM765 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12046] It is yet further appreciated that specific functions, and accordingly utilities, of GAM765 correlate with, and may be deduced from, the identity of the target genes which GAM765 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[12047] Nucleotide sequences of the GAM765 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM765 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM765 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM765 are further described hereinbelow with reference to Table Table1.

[12048] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM765 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12049] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 766 (GAM766) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12050] GAM766 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM766 was detected is described hereinabove

with reference to Figs. 2-8.

[12051] GAM766 gene, herein designated GAM GENE, and GAM766 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12052] GAM766 gene, herein designated GAM GENE, encodes a GAM766 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM766 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM766 precursor RNA is designated SEQ ID:739, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:739 is located at position 1475289 relative to contig NT_007422.11, on chromosome 6.

[12053] GAM766 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[12054] SEQ ID:99488 detected in mouse EST Accession AA002466.1.

[12055] SEQ ID:99489 detected in mouse EST Accession

AW824224.1.

[12056] SEQ ID:99490 detected in mouse EST Accession BG145815.1.

[12057] SEQ ID:99491 detected in mouse EST Accession BI157250.1.

[12058] SEQ ID:99492 detected in mouse EST Accession BE915757.1.

[12059] SEQ ID:99493 detected in mouse EST Accession AA068733.1.

[12060] SEQ ID:99494 detected in mouse EST Accession W64380.1.

[12061] SEQ ID:99498 detected in mouse EST Accession BI083270.1.

[12062] SEQ ID:99499 detected in mouse EST Accession BF578597.1.

[12063] SEQ ID:99500 detected in mouse EST Accession BF135474.1.

[12064] SEQ ID:99501 detected in mouse EST Accession BI555255.1.

[12065] SEQ ID:99503 detected in mouse EST Accession AA423494.1.

[12066] SEQ ID:99504 detected in mouse EST Accession AW824782.1.

[12067] SEQ ID:99505 detected in mouse EST Accession BE375055.1.

[12068] SEQ ID:99506 detected in mouse EST Accession BI107509.1.

[12069] GAM766 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM766 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12070] An enzyme complex designated DICER COMPLEX, dices the GAM766 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM766 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of

GAM766 RNA is designated SEQ ID:2415, and is provided hereinbelow with reference to the sequence listing part.

[12071] GAM766 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM766 target RNA, herein designated GAM TARGET RNA.

GAM766 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12072] GAM766 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM766 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM766 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM766 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM766 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12073] The complementary binding of GAM766 RNA, herein designated GAM RNA, to target binding sites on GAM766 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM766 target RNA, herein designated GAM TARGET RNA, into GAM766 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12074] It is appreciated that GAM766 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM766 target genes. The mRNA of each one of this plurality of GAM766 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM766 RNA, herein designated GAM RNA, and which when bound by GAM766 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM766 target proteins.

[12075] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM766 gene, herein designated GAM GENE, on one or more GAM766 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12076] It is yet further appreciated that specific functions, and accordingly utilities, of GAM766 correlate with, and may be deduced from, the identity of the target genes which GAM766 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12077] Nucleotide sequences of the GAM766 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM766 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM766 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM766 are further described hereinbelow with reference to Table Table1.

[12078] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM766 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12079] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 767 (GAM767) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12080] GAM767 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM767 was detected is described hereinabove with reference to Figs. 2-8.

[12081] GAM767 gene, herein designated GAM GENE, and GAM767 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12082] GAM767 gene, herein designated GAM GENE, encodes a GAM767 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM767 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM767 precursor RNA is designated SEQ ID:740, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:740 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[12083] GAM767 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM767 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[12084] An enzyme complex designated DICER COMPLEX, dices the GAM767 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM767 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM767 RNA is designated SEQ ID:2416, and is provided hereinbelow with reference to the sequence listing part.

[12085] GAM767 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM767 target RNA, herein designated GAM TARGET RNA. GAM767 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12086] GAM767 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM767 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM767 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM767 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM767 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12087] The complementary binding of GAM767 RNA, herein designated GAM RNA, to target binding sites on GAM767 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM767 target RNA, herein designated GAM TARGET RNA, into GAM767 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12088] It is appreciated that GAM767 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM767 target genes. The mRNA of each one of this plurality of GAM767 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM767 RNA, herein designated GAM RNA, and which when bound by GAM767 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM767 target proteins.

[12089] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM767 gene, herein designated GAM GENE, on one or more GAM767 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12090] It is yet further appreciated that specific functions, and accordingly utilities, of GAM767 correlate with, and may be deduced from, the identity of the target genes which GAM767 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12091] Nucleotide sequences of the GAM767 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM767 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM767 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM767 are further described hereinbelow with reference to Table Table1.

[12092] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM767 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12093] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 768 (GAM768) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12094] GAM768 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM768 was detected is described hereinabove with reference to Figs. 2-8.

[12095] GAM768 gene, herein designated GAM GENE, and GAM768 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12096] GAM768 gene, herein designated GAM GENE, encodes a GAM768 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM768 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM768 precursor RNA is designated SEQ ID:741, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:741 is located at position 5359482 relative to con-

tig NT_007819.11, on chromosome 7.

[12097] GAM768 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12098] An enzyme complex designated DICER COMPLEX, dices the GAM768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM768 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM768 RNA is designated SEQ ID:2417, and is provided hereinbelow with reference to the sequence listing part.

[12099] GAM768 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM768 target RNA, herein designated GAM TARGET RNA.

GAM768 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12100] GAM768 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM768 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM768 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM768 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM768 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12101] The complementary binding of GAM768 RNA, herein designated GAM RNA, to target binding sites on GAM768 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM768 target RNA, herein designated GAM TARGET RNA, into GAM768 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12102] It is appreciated that GAM768 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM768 target genes. The mRNA of each one of this plurality of GAM768 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM768 RNA, herein designated GAM RNA, and which when bound by GAM768 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM768 target proteins.

[12103] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM768 gene, herein designated GAM GENE, on one or more GAM768 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12104] It is yet further appreciated that specific functions, and accordingly utilities, of GAM768 correlate with, and may be deduced from, the identity of the target genes which GAM768 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12105] Nucleotide sequences of the GAM768 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM768 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM768 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM768 are further described hereinbelow with reference to Table Table1.

[12106] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM768 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12107] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 769 (GAM769) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12108] GAM769 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM769 was detected is described hereinabove with reference to Figs. 2-8.

[12109] GAM769 gene, herein designated GAM GENE, and GAM769 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12110] GAM769 gene, herein designated GAM GENE, encodes a GAM769 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM769 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM769 precursor RNA is designated SEQ ID:742, and is provided hereinbelow with reference to the sequence listing part.

[12111] GAM769 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM769 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12112] An enzyme complex designated DICER COMPLEX, dices the GAM769 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM769 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM769 RNA is designated SEQ ID:2418, and is provided hereinbelow with reference to the sequence listing part.

[12113] GAM769 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM769 target RNA, herein designated GAM TARGET RNA. GAM769 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12114] GAM769 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM769 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM769 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM769 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM769 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12115] The complementary binding of GAM769 RNA, herein designated GAM RNA, to target binding sites on GAM769 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM769 target RNA, herein designated GAM TARGET RNA, into GAM769 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12116] It is appreciated that GAM769 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM769 target genes. The mRNA of each one of this plu-

rality of GAM769 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM769 RNA, herein designated GAM RNA, and which when bound by GAM769 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM769 target proteins.

[12117] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM769 gene, herein designated GAM GENE, on one or more GAM769 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12118] It is yet further appreciated that specific functions, and accordingly utilities, of GAM769 correlate with, and may be deduced from, the identity of the target genes which GAM769 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12119] Nucleotide sequences of the GAM769 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM769 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM769 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM769 are further described hereinbelow with reference to Table Table1.

[12120] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM769 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12121] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 770 (GAM770) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[12122] GAM770 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM770 was detected is described hereinabove with reference to Figs. 2-8.

[12123] GAM770 gene, herein designated GAM GENE, and GAM770 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12124] GAM770 gene, herein designated GAM GENE, encodes a GAM770 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM770 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM770 precursor RNA is designated SEQ ID:743, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:743 is located at position 1822711 relative to contig NT_022423.12, on chromosome 3.

[12125] GAM770 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12126] An enzyme complex designated DICER COMPLEX, dices the GAM770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM770 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM770 RNA is designated SEQ ID:2419, and is provided hereinbelow with reference to the sequence listing part.

[12127] GAM770 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM770 target RNA, herein designated GAM TARGET RNA. GAM770 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12128] GAM770 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM770 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM770 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM770 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM770 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12129] The complementary binding of GAM770 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM770 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM770 target RNA, herein designated GAM TARGET RNA, into GAM770 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12130] It is appreciated that GAM770 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM770 target genes. The mRNA of each one of this plurality of GAM770 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM770 RNA, herein designated GAM RNA, and which when bound by GAM770 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM770 target proteins.

[12131] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM770 gene, herein designated GAM GENE, on one or more GAM770 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12132] It is yet further appreciated that specific functions, and accordingly utilities, of GAM770 correlate with, and may be deduced from, the identity of the target genes which GAM770 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12133] Nucleotide sequences of the GAM770 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM770 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM770 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM770 are further described hereinbelow with reference to Table Table1.

[12134] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM770 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12135] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 771 (GAM771) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12136] GAM771 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM771 was detected is described hereinabove with reference to Figs. 2-8.

[12137] GAM771 gene, herein designated GAM GENE, and GAM771 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12138] GAM771 gene, herein designated GAM GENE, encodes a GAM771 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM771 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM771 precursor RNA is designated SEQ ID:744, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:744 is located at position 452835 relative to contig NT_005526.12, on chromosome 3.

[12139] GAM771 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM771 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12140] An enzyme complex designated DICER COMPLEX, dices the GAM771 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM771 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM771 RNA is designated SEQ ID:2420, and is provided hereinbelow with reference to the sequence listing part.

[12141] GAM771 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM771 target RNA, herein designated GAM TARGET RNA. GAM771 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12142] GAM771 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM771 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM771 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM771 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM771 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12143] The complementary binding of GAM771 RNA, herein designated GAM RNA, to target binding sites on GAM771 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM771 target RNA, herein designated GAM TARGET RNA, into GAM771 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12144] It is appreciated that GAM771 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM771 target genes. The mRNA of each one of this plurality of GAM771 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM771 RNA,

herein designated GAM RNA, and which when bound by GAM771 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM771 target proteins.

[12145] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM771 gene, herein designated GAM GENE, on one or more GAM771 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12146] It is yet further appreciated that specific functions, and accordingly utilities, of GAM771 correlate with, and may be deduced from, the identity of the target genes which

GAM771 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12147] Nucleotide sequences of the GAM771 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM771 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM771 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM771 are further described hereinbelow with reference to Table Table1.

[12148] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM771 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12149] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 772 (GAM772) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12150] GAM772 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM772 was detected is described hereinabove with reference to Figs. 2-8.

[12151] GAM772 gene, herein designated GAM GENE, and GAM772 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12152] GAM772 gene, herein designated GAM GENE, encodes a GAM772 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM772 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM772 precursor RNA is designated SEQ ID:745, and is provided hereinbelow with reference to the sequence listing part.

[12153] GAM772 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[12154] An enzyme complex designated DICER COMPLEX, dices the GAM772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM772 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM772 RNA is designated SEQ ID:2421, and is provided hereinbelow with reference to the sequence listing part.

[12155] GAM772 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM772 target RNA, herein designated GAM TARGET RNA. GAM772 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12156] GAM772 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM772 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM772 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM772 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM772 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12157] The complementary binding of GAM772 RNA, herein designated GAM RNA, to target binding sites on GAM772 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM772 target RNA, herein designated GAM TARGET RNA, into GAM772 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12158] It is appreciated that GAM772 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM772 target genes. The mRNA of each one of this plurality of GAM772 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM772 RNA, herein designated GAM RNA, and which when bound by GAM772 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM772 target proteins.

[12159] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM772 gene, herein designated GAM GENE, on one or more GAM772 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12160] It is yet further appreciated that specific functions, and accordingly utilities, of GAM772 correlate with, and may be deduced from, the identity of the target genes which GAM772 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12161] Nucleotide sequences of the GAM772 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM772 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM772 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM772 are further described hereinbelow with reference to Table Table1.

[12162] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM772 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12163] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 773 (GAM773) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12164] GAM773 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM773 was detected is described hereinabove with reference to Figs. 2-8.

[12165] GAM773 gene, herein designated GAM GENE, and GAM773 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12166] GAM773 gene, herein designated GAM GENE, encodes a GAM773 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM773 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM773 precursor RNA is designated SEQ ID:746, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:746 is located at position 2349674 relative to con-

tig NT_021907.13, on chromosome 1.

[12167] GAM773 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12168] An enzyme complex designated DICER COMPLEX, dices the GAM773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM773 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM773 RNA is designated SEQ ID:2422, and is provided hereinbelow with reference to the sequence listing part.

[12169] GAM773 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM773 target RNA, herein designated GAM TARGET RNA.

GAM773 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12170] GAM773 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM773 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM773 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM773 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM773 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12171] The complementary binding of GAM773 RNA, herein designated GAM RNA, to target binding sites on GAM773 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM773 target RNA, herein designated GAM TARGET RNA, into GAM773 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12172] It is appreciated that GAM773 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM773 target genes. The mRNA of each one of this plurality of GAM773 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM773 RNA, herein designated GAM RNA, and which when bound by GAM773 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM773 target proteins.

[12173] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM773 gene, herein designated GAM GENE, on one or more GAM773 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12174] It is yet further appreciated that specific functions, and accordingly utilities, of GAM773 correlate with, and may be deduced from, the identity of the target genes which GAM773 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12175] Nucleotide sequences of the GAM773 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM773 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM773 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM773 are further described hereinbelow with reference to Table Table1.

[12176] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM773 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12177] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 774 (GAM774) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12178] GAM774 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM774 was detected is described hereinabove with reference to Figs. 2-8.

[12179] GAM774 gene, herein designated GAM GENE, and GAM774 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12180] GAM774 gene, herein designated GAM GENE, encodes a GAM774 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM774 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM774 precursor RNA is designated SEQ ID:747, and is provided hereinbelow with reference to the sequence listing part.

[12181] GAM774 has 11 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[12182] SEQ ID:99463 detected in mouse EST Accession AI613817.1.

[12183] SEQ ID:99464 detected in mouse EST Accession BE625355.1.

[12184] SEQ ID:99465 detected in mouse EST Accession AI157515.1.

[12185] SEQ ID:99466 detected in mouse EST Accession W65790.1.

[12186] SEQ ID:99467 detected in mouse EST Accession

AA051691.1.

[12187] SEQ ID:99468 detected in mouse EST Accession AA034667.1.

[12188] SEQ ID:99469 detected in mouse EST Accession W54339.1.

[12189] SEQ ID:99470 detected in mouse EST Accession BI101177.1.

[12190] SEQ ID:99471 detected in mouse EST Accession BE861499.1.

[12191] SEQ ID:99472 detected in mouse EST Accession BB667583.1.

[12192] SEQ ID:99473 detected in mouse EST Accession BI145910.1.

[12193] GAM774 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM774 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12194] An enzyme complex designated DICER COMPLEX, dices the GAM774 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM774 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM774 RNA is designated SEQ ID:2423, and is provided hereinbelow with reference to the sequence listing part.

[12195] GAM774 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM774 target RNA, herein designated GAM TARGET RNA. GAM774 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12196] GAM774 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM774 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM774 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM774 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM774 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12197] The complementary binding of GAM774 RNA, herein designated GAM RNA, to target binding sites on GAM774 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM774 target RNA, herein designated GAM TARGET RNA, into GAM774 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[12198] It is appreciated that GAM774 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM774 target genes. The mRNA of each one of this plurality of GAM774 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM774 RNA, herein designated GAM RNA, and which when bound by GAM774 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM774 target proteins.

[12199] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM774 gene, herein designated GAM GENE, on one or more GAM774 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12200] It is yet further appreciated that specific functions, and accordingly utilities, of GAM774 correlate with, and may be deduced from, the identity of the target genes which GAM774 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12201] Nucleotide sequences of the GAM774 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM774 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM774 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM774 are further described hereinbelow with reference to Table Table1.

[12202] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM774 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12203] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 775 (GAM775) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12204] GAM775 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM775 was detected is described hereinabove with reference to Figs. 2-8.

[12205] GAM775 gene, herein designated GAM GENE, and GAM775 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12206] GAM775 gene, herein designated GAM GENE, encodes a GAM775 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM775 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM775 precursor RNA is designated SEQ ID:748, and is provided hereinbelow with reference to the sequence listing part.

[12207] GAM775 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM775 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12208] An enzyme complex designated DICER COMPLEX, dices the GAM775 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM775 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM775 RNA is designated SEQ ID:2424, and is provided hereinbelow with reference to the sequence listing part.

[12209] GAM775 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM775 target RNA, herein designated GAM TARGET RNA. GAM775 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12210] GAM775 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM775 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM775 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM775 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM775 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[12211] The complementary binding of GAM775 RNA, herein designated GAM RNA, to target binding sites on GAM775 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM775 target RNA, herein designated GAM TARGET RNA, into GAM775 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12212] It is appreciated that GAM775 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM775 target genes. The mRNA of each one of this plurality of GAM775 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM775 RNA, herein designated GAM RNA, and which when bound by GAM775 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM775 target proteins.

[12213] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM775 gene, herein designated GAM GENE, on one or

more GAM775 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12214] It is yet further appreciated that specific functions, and accordingly utilities, of GAM775 correlate with, and may be deduced from, the identity of the target genes which GAM775 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12215] Nucleotide sequences of the GAM775 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM775 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM775 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM775 are further de-

scribed hereinbelow with reference to Table Table1.

[12216] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM775 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12217] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 776 (GAM776) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12218] GAM776 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM776 was detected is described hereinabove with reference to Figs. 2-8.

[12219] GAM776 gene, herein designated GAM GENE, and GAM776 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12220] GAM776 gene, herein designated GAM GENE, encodes a GAM776 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM776 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM776 precursor RNA is designated SEQ ID:749, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:749 is located at position 4851354 relative to contig NT_022517.13, on chromosome 3.

[12221] GAM776 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12222] An enzyme complex designated DICER COMPLEX, dices the GAM776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM776 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM776 RNA is designated SEQ ID:2425, and is provided hereinbelow with reference to the sequence listing part.

[12223] GAM776 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM776 target RNA, herein designated GAM TARGET RNA. GAM776 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12224] GAM776 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM776 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM776 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM776 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM776 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12225] The complementary binding of GAM776 RNA, herein designated GAM RNA, to target binding sites on GAM776 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM776 target RNA, herein designated GAM TARGET RNA, into GAM776 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12226] It is appreciated that GAM776 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM776 target genes. The mRNA of each one of this plurality of GAM776 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM776 RNA, herein designated GAM RNA, and which when bound by GAM776 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM776 target proteins.

[12227] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM776 gene, herein designated GAM GENE, on one or more GAM776 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12228] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM776 correlate with, and may be deduced from, the identity of the target genes which GAM776 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12229] Nucleotide sequences of the GAM776 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM776 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM776 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM776 are further described hereinbelow with reference to Table Table1.

[12230] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM776 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12231] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 777 (GAM777) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12232] GAM777 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM777 was detected is described hereinabove with reference to Figs. 2-8.

[12233] GAM777 gene, herein designated GAM GENE, and GAM777 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12234] GAM777 gene, herein designated GAM GENE, encodes a GAM777 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM777 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM777 precursor RNA is designated SEQ ID:750, and is provided hereinbelow with reference to the sequence listing part.

[12235] GAM777 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12236] An enzyme complex designated DICER COMPLEX, dices the GAM777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM777 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM777 RNA is designated SEQ ID:2426, and is provided hereinbelow with reference to the sequence listing part.

[12237] GAM777 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM777 target RNA, herein designated GAM TARGET RNA. GAM777 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12238] GAM777 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM777 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM777 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM777 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM777 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12239] The complementary binding of GAM777 RNA, herein designated GAM RNA, to target binding sites on GAM777 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM777 target RNA, herein designated GAM TARGET RNA, into GAM777 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12240] It is appreciated that GAM777 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM777 target genes. The mRNA of each one of this plurality of GAM777 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM777 RNA, herein designated GAM RNA, and which when bound by GAM777 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM777 target proteins.

[12241] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM777 gene, herein designated GAM GENE, on one or more GAM777 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12242] It is yet further appreciated that specific functions, and accordingly utilities, of GAM777 correlate with, and may be deduced from, the identity of the target genes which GAM777 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12243] Nucleotide sequences of the GAM777 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM777 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM777 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM777 are further described hereinbelow with reference to Table Table1.

[12244] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM777 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12245] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 778 (GAM778) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12246] GAM778 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM778 was detected is described hereinabove with reference to Figs. 2-8.

[12247] GAM778 gene, herein designated GAM GENE, and GAM778 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12248] GAM778 gene, herein designated GAM GENE, encodes a GAM778 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM778 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM778 precursor RNA is designated SEQ ID:751, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:751 is located at position 19308883 relative to contig NT_033899.3, on chromosome 11.

[12249] GAM778 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM778 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12250] An enzyme complex designated DICER COMPLEX, dices the GAM778 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM778 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM778 RNA is designated SEQ ID:2427, and is provided

hereinbelow with reference to the sequence listing part.

[12251] GAM778 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM778 target RNA, herein designated GAM TARGET RNA.

GAM778 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12252] GAM778 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM778 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM778 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM778 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM778 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12253] The complementary binding of GAM778 RNA, herein designated GAM RNA, to target binding sites on GAM778 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM778 target RNA, herein designated GAM TARGET RNA, into GAM778 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12254] It is appreciated that GAM778 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM778 target genes. The mRNA of each one of this plurality of GAM778 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM778 RNA, herein designated GAM RNA, and which when bound by GAM778 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM778 tar-

get proteins.

[12255] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM778 gene, herein designated GAM GENE, on one or more GAM778 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12256] It is yet further appreciated that specific functions, and accordingly utilities, of GAM778 correlate with, and may be deduced from, the identity of the target genes which GAM778 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12257] Nucleotide sequences of the GAM778 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM778 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM778 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM778 are further described hereinbelow with reference to Table Table1.

[12258] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM778 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12259] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 779 (GAM779) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12260] GAM779 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM779 was detected is described hereinabove with reference to Figs. 2-8.

[12261] GAM779 gene, herein designated GAM GENE, and GAM779 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[12262] GAM779 gene, herein designated GAM GENE, encodes a GAM779 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM779 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM779 precursor RNA is designated SEQ ID:752, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:752 is located at position 7933233 relative to contig NT_033899.3, on chromosome 11.

[12263] GAM779 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99344, which mouse homolog is detected in mouse EST accession BI411194.1.

[12264] GAM779 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM779 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12265] An enzyme complex designated DICER COMPLEX, dices the GAM779 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM779 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM779 RNA is designated SEQ ID:2428, and is provided hereinbelow with reference to the sequence listing part.

[12266] GAM779 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM779 target RNA, herein designated GAM TARGET RNA.
GAM779 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12267] GAM779 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM779 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM779 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM779 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM779 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12268] The complementary binding of GAM779 RNA, herein designated GAM RNA, to target binding sites on GAM779 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM779 target RNA, herein designated GAM TARGET RNA, into GAM779 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12269] It is appreciated that GAM779 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM779 target genes. The mRNA of each one of this plurality of GAM779 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM779 RNA, herein designated GAM RNA, and which when bound by GAM779 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM779 target proteins.

[12270] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM779 gene, herein designated GAM GENE, on one or more GAM779 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12271] It is yet further appreciated that specific functions, and accordingly utilities, of GAM779 correlate with, and may be deduced from, the identity of the target genes which GAM779 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12272] Nucleotide sequences of the GAM779 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM779 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM779 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM779 are further described hereinbelow with reference to Table Table1.

[12273] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM779 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12274] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 780 (GAM780) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12275] GAM780 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM780 was detected is described hereinabove with reference to Figs. 2-8.

[12276] GAM780 gene, herein designated GAM GENE, and GAM780 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12277] GAM780 gene, herein designated GAM GENE, encodes a GAM780 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM780 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM780 precursor RNA is desig-

nated SEQ ID:753, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:753 is located at position 365826 relative to contig NT_010799.11, on chromosome 17.

[12278] GAM780 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12279] An enzyme complex designated DICER COMPLEX, dices the GAM780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM780 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM780 RNA is designated SEQ ID:2429, and is provided hereinbelow with reference to the sequence listing part.

[12280] GAM780 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM780 target RNA, herein designated GAM TARGET RNA.

GAM780 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12281] GAM780 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM780 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM780 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM780 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM780 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12282] The complementary binding of GAM780 RNA, herein designated GAM RNA, to target binding sites on GAM780 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM780 target RNA, herein designated GAM TARGET RNA, into GAM780 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12283] It is appreciated that GAM780 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM780 target genes. The mRNA of each one of this plurality of GAM780 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM780 RNA, herein designated GAM RNA, and which when bound by GAM780 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM780 target proteins.

[12284] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM780 gene, herein designated GAM GENE, on one or more GAM780 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12285] It is yet further appreciated that specific functions, and accordingly utilities, of GAM780 correlate with, and may be deduced from, the identity of the target genes which GAM780 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12286] Nucleotide sequences of the GAM780 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM780 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM780 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM780 are further described hereinbelow with reference to Table Table1.

[12287] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM780 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12288] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 781 (GAM781) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12289] GAM781 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM781 was detected is described hereinabove with reference to Figs. 2-8.

[12290] GAM781 gene, herein designated GAM GENE, and GAM781 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12291] GAM781 gene, herein designated GAM GENE, encodes a GAM781 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM781 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM781 precursor RNA is designated SEQ ID:754, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:754 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[12292] GAM781 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[12293] An enzyme complex designated DICER COMPLEX, dices the GAM781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM781 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM781 RNA is designated SEQ ID:2430, and is provided hereinbelow with reference to the sequence listing part.

[12294] GAM781 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM781 target RNA, herein designated GAM TARGET RNA. GAM781 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12295] GAM781 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM781 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM781 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM781 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM781 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12296] The complementary binding of GAM781 RNA, herein designated GAM RNA, to target binding sites on GAM781 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM781 target RNA, herein designated GAM TARGET RNA, into GAM781 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12297] It is appreciated that GAM781 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM781 target genes. The mRNA of each one of this plurality of GAM781 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM781 RNA, herein designated GAM RNA, and which when bound by GAM781 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM781 target proteins.

[12298] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM781 gene, herein designated GAM GENE, on one or more GAM781 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12299] It is yet further appreciated that specific functions, and accordingly utilities, of GAM781 correlate with, and may be deduced from, the identity of the target genes which GAM781 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12300] Nucleotide sequences of the GAM781 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM781 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM781 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM781 are further described hereinbelow with reference to Table Table1.

[12301] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM781 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12302] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 782 (GAM782) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12303] GAM782 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM782 was detected is described hereinabove with reference to Figs. 2-8.

[12304] GAM782 gene, herein designated GAM GENE, and GAM782 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12305] GAM782 gene, herein designated GAM GENE, encodes a GAM782 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM782 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM782 precursor RNA is designated SEQ ID:755, and is provided hereinbelow with reference to the sequence listing part.

[12306] GAM782 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM782 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12307] An enzyme complex designated DICER COMPLEX, dices the GAM782 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM782 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM782 RNA is designated SEQ ID:2431, and is provided hereinbelow with reference to the sequence listing part.

[12308] GAM782 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM782 target RNA, herein designated GAM TARGET RNA.

GAM782 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12309] GAM782 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM782 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM782 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM782 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM782 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12310] The complementary binding of GAM782 RNA, herein designated GAM RNA, to target binding sites on GAM782 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM782 target RNA, herein designated GAM TARGET RNA, into GAM782 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12311] It is appreciated that GAM782 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM782 target genes. The mRNA of each one of this plurality of GAM782 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM782 RNA, herein designated GAM RNA, and which when bound by GAM782 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM782 target proteins.

[12312] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM782 gene, herein designated GAM GENE, on one or more GAM782 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12313] It is yet further appreciated that specific functions, and accordingly utilities, of GAM782 correlate with, and may be deduced from, the identity of the target genes which GAM782 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12314] Nucleotide sequences of the GAM782 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM782 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM782 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM782 are further described hereinbelow with reference to Table Table1.

[12315] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM782 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12316] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 783 (GAM783) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12317] GAM783 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM783 was detected is described hereinabove with reference to Figs. 2-8.

[12318] GAM783 gene, herein designated GAM GENE, and GAM783 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12319] GAM783 gene, herein designated GAM GENE, encodes a GAM783 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM783 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM783 precursor RNA is designated SEQ ID:756, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:756 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[12320] GAM783 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM783 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12321] An enzyme complex designated DICER COMPLEX, dices the GAM783 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM783 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM783 RNA is designated SEQ ID:2432, and is provided hereinbelow with reference to the sequence listing part.

[12322] GAM783 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM783 target RNA, herein designated GAM TARGET RNA. GAM783 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12323] GAM783 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM783 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM783 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM783 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM783 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12324] The complementary binding of GAM783 RNA, herein designated GAM RNA, to target binding sites on GAM783 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM783 target RNA, herein designated GAM TARGET RNA, into GAM783 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12325] It is appreciated that GAM783 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM783 target genes. The mRNA of each one of this plu-

rality of GAM783 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM783 RNA, herein designated GAM RNA, and which when bound by GAM783 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM783 target proteins.

[12326] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM783 gene, herein designated GAM GENE, on one or more GAM783 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12327] It is yet further appreciated that specific functions, and accordingly utilities, of GAM783 correlate with, and may be deduced from, the identity of the target genes which GAM783 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12328] Nucleotide sequences of the GAM783 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM783 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM783 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM783 are further described hereinbelow with reference to Table Table1.

[12329] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM783 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12330] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 784 (GAM784) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[12331] GAM784 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM784 was detected is described hereinabove with reference to Figs. 2-8.

[12332] GAM784 gene, herein designated GAM GENE, and GAM784 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12333] GAM784 gene, herein designated GAM GENE, encodes a GAM784 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM784 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM784 precursor RNA is designated SEQ ID:757, and is provided hereinbelow with reference to the sequence listing part.

[12334] GAM784 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM784 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12335] An enzyme complex designated DICER COMPLEX, dices the GAM784 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM784 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM784 RNA is designated SEQ ID:2433, and is provided hereinbelow with reference to the sequence listing part.

[12336] GAM784 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM784 target RNA, herein designated GAM TARGET RNA. GAM784 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12337] GAM784 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM784 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM784 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM784 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM784 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12338] The complementary binding of GAM784 RNA, herein designated GAM RNA, to target binding sites on GAM784 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM784 target RNA, herein designated GAM TARGET RNA, into GAM784 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12339] It is appreciated that GAM784 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM784 target genes. The mRNA of each one of this plurality of GAM784 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM784 RNA, herein designated GAM RNA, and which when bound by GAM784 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM784 target proteins.

[12340] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM784 gene, herein designated GAM GENE, on one or more GAM784 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12341] It is yet further appreciated that specific functions, and accordingly utilities, of GAM784 correlate with, and may be deduced from, the identity of the target genes which GAM784 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12342] Nucleotide sequences of the GAM784 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM784 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM784 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM784 are further described hereinbelow with reference to Table Table1.

[12343] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM784 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12344] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 785 (GAM785) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12345] GAM785 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM785 was detected is described hereinabove with reference to Figs. 2-8.

[12346] GAM785 gene, herein designated GAM GENE, and GAM785 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12347] GAM785 gene, herein designated GAM GENE, encodes a GAM785 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM785 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM785 precursor RNA is desig-

nated SEQ ID:758, and is provided hereinbelow with reference to the sequence listing part.

[12348] GAM785 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12349] An enzyme complex designated DICER COMPLEX, dices the GAM785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM785 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM785 RNA is designated SEQ ID:2434, and is provided hereinbelow with reference to the sequence listing part.

[12350] GAM785 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM785 target RNA, herein designated GAM TARGET RNA. GAM785 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12351] GAM785 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM785 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM785 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM785 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM785

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12352] The complementary binding of GAM785 RNA, herein designated GAM RNA, to target binding sites on GAM785 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM785 target RNA, herein designated GAM TARGET RNA, into GAM785 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12353] It is appreciated that GAM785 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM785 target genes. The mRNA of each one of this plurality of GAM785 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM785 RNA, herein designated GAM RNA, and which when bound by GAM785 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM785 target proteins.

[12354] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM785 gene, herein designated GAM GENE, on one or more GAM785 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12355] It is yet further appreciated that specific functions, and accordingly utilities, of GAM785 correlate with, and may be deduced from, the identity of the target genes which GAM785 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12356] Nucleotide sequences of the GAM785 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM785 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM785 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM785 are further described hereinbelow with reference to Table Table1.

[12357] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM785 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12358] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 786 (GAM786) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12359] GAM786 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM786 was detected is described hereinabove with reference to Figs. 2-8.

[12360] GAM786 gene, herein designated GAM GENE, and GAM786 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[12361] GAM786 gene, herein designated GAM GENE, encodes a GAM786 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM786 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM786 precursor RNA is designated SEQ ID:759, and is provided hereinbelow with reference to the sequence listing part.

[12362] GAM786 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM786 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12363] An enzyme complex designated DICER COMPLEX, dices the GAM786 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM786 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM786 RNA is designated SEQ ID:2435, and is provided hereinbelow with reference to the sequence listing part.

[12364] GAM786 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM786 target RNA, herein designated GAM TARGET RNA. GAM786 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12365] GAM786 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM786 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM786 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM786 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM786 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12366] The complementary binding of GAM786 RNA, herein designated GAM RNA, to target binding sites on GAM786 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM786 target RNA, herein designated GAM TARGET RNA, into GAM786 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12367] It is appreciated that GAM786 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM786 target genes. The mRNA of each one of this plurality of GAM786 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM786 RNA, herein designated GAM RNA, and which when bound by GAM786 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM786 target proteins.

[12368] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM786 gene, herein designated GAM GENE, on one or more GAM786 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[12369] It is yet further appreciated that specific functions, and accordingly utilities, of GAM786 correlate with, and may be deduced from, the identity of the target genes which GAM786 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12370] Nucleotide sequences of the GAM786 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM786 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM786 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM786 are further described hereinbelow with reference to Table Table1.

[12371] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM786 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12372] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 787 (GAM787) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[12373] GAM787 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM787 was detected is described hereinabove with reference to Figs. 2-8.

[12374] GAM787 gene, herein designated GAM GENE, and GAM787 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12375] GAM787 gene, herein designated GAM GENE, encodes a GAM787 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM787 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM787 precursor RNA is designated SEQ ID:760, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:760 is located at position 4851355 relative to contig NT_022517.13, on chromosome 3.

[12376] GAM787 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM787 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12377] An enzyme complex designated DICER COMPLEX, dices the GAM787 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM787 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM787 RNA is designated SEQ ID:2436, and is provided hereinbelow with reference to the sequence listing part.

[12378] GAM787 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM787 target RNA, herein designated GAM TARGET RNA. GAM787 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12379] GAM787 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM787 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM787 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM787 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM787 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12380] The complementary binding of GAM787 RNA, herein designated GAM RNA, to target binding sites on GAM787 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM787 target RNA, herein designated GAM TARGET RNA, into GAM787 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12381] It is appreciated that GAM787 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM787 target genes. The mRNA of each one of this plurality of GAM787 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM787 RNA, herein designated GAM RNA, and which when bound by GAM787 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM787 target proteins.

[12382] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM787 gene, herein designated GAM GENE, on one or more GAM787 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12383] It is yet further appreciated that specific functions, and accordingly utilities, of GAM787 correlate with, and may be deduced from, the identity of the target genes which GAM787 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12384] Nucleotide sequences of the GAM787 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM787 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM787 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM787 are further described hereinbelow with reference to Table Table1.

[12385] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM787 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12386] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 788 (GAM788) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12387] GAM788 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM788 was detected is described hereinabove with reference to Figs. 2-8.

[12388] GAM788 gene, herein designated GAM GENE, and GAM788 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12389] GAM788 gene, herein designated GAM GENE, encodes a GAM788 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM788 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM788 precursor RNA is designated SEQ ID:761, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:761 is located at position 8487472 relative to contig NT_011520.8, on chromosome 22.

[12390] GAM788 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12391] An enzyme complex designated DICER COMPLEX, dices the GAM788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM788 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM788 RNA is designated SEQ ID:2437, and is provided hereinbelow with reference to the sequence listing part.

[12392] GAM788 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM788 target RNA, herein designated GAM TARGET RNA. GAM788 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12393] GAM788 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM788 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM788 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM788 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM788 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12394] The complementary binding of GAM788 RNA, herein designated GAM RNA, to target binding sites on GAM788 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM788 target RNA, herein designated GAM TARGET RNA, into GAM788 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12395] It is appreciated that GAM788 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM788 target genes. The mRNA of each one of this plurality of GAM788 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM788 RNA, herein designated GAM RNA, and which when bound by GAM788 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM788 target proteins.

[12396] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM788 gene, herein designated GAM GENE, on one or more GAM788 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12397] It is yet further appreciated that specific functions, and accordingly utilities, of GAM788 correlate with, and may

be deduced from, the identity of the target genes which GAM788 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12398] Nucleotide sequences of the GAM788 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM788 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM788 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM788 are further described hereinbelow with reference to Table Table1.

[12399] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM788 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12400] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 789 (GAM789) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12401] GAM789 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM789 was detected is described hereinabove with reference to Figs. 2-8.

[12402] GAM789 gene, herein designated GAM GENE, and GAM789 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12403] GAM789 gene, herein designated GAM GENE, encodes a GAM789 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM789 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM789 precursor RNA is designated SEQ ID:762, and is provided hereinbelow with reference to the sequence listing part.

[12404] GAM789 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM789 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[12405] An enzyme complex designated DICER COMPLEX, dices the GAM789 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM789 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM789 RNA is designated SEQ ID:2438, and is provided hereinbelow with reference to the sequence listing part.

[12406] GAM789 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM789 target RNA, herein designated GAM TARGET RNA.
GAM789 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12407] GAM789 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM789 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM789 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM789 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM789 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12408] The complementary binding of GAM789 RNA, herein designated GAM RNA, to target binding sites on GAM789 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM789 target RNA, herein desig-

nated GAM TARGET RNA, into GAM789 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12409] It is appreciated that GAM789 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM789 target genes. The mRNA of each one of this plurality of GAM789 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM789 RNA, herein designated GAM RNA, and which when bound by GAM789 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM789 target proteins.

[12410] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM789 gene, herein designated GAM GENE, on one or more GAM789 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12411] It is yet further appreciated that specific functions, and accordingly utilities, of GAM789 correlate with, and may be deduced from, the identity of the target genes which GAM789 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12412] Nucleotide sequences of the GAM789 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM789 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM789 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM789 are further described hereinbelow with reference to Table Table1.

[12413] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM789 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[12414] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 790 (GAM790) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12415] GAM790 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM790 was detected is described hereinabove with reference to Figs. 2-8.

[12416] GAM790 gene, herein designated GAM GENE, and GAM790 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12417] GAM790 gene, herein designated GAM GENE, encodes a GAM790 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM790 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM790 precursor RNA is designated SEQ ID:763, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:763 is located at position 1692390 relative to contig NT_030737.5, on chromosome 8.

[12418] GAM790 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM790 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12419] An enzyme complex designated DICER COMPLEX, dices the GAM790 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM790 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM790 RNA is designated SEQ ID:2439, and is provided hereinbelow with reference to the sequence listing part.

[12420] GAM790 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM790 target RNA, herein designated GAM TARGET RNA. GAM790 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12421] GAM790 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM790 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM790 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM790 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM790

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12422] The complementary binding of GAM790 RNA, herein designated GAM RNA, to target binding sites on GAM790 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM790 target RNA, herein designated GAM TARGET RNA, into GAM790 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12423] It is appreciated that GAM790 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM790 target genes. The mRNA of each one of this plurality of GAM790 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM790 RNA, herein designated GAM RNA, and which when bound by GAM790 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM790 target proteins.

[12424] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM790 gene, herein designated GAM GENE, on one or more GAM790 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12425] It is yet further appreciated that specific functions, and accordingly utilities, of GAM790 correlate with, and may be deduced from, the identity of the target genes which GAM790 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12426] Nucleotide sequences of the GAM790 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM790 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM790 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM790 are further described hereinbelow with reference to Table Table1.

[12427] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM790 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12428] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 791 (GAM791) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12429] GAM791 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM791 was detected is described hereinabove with reference to Figs. 2-8.

[12430] GAM791 gene, herein designated GAM GENE, and GAM791 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[12431] GAM791 gene, herein designated GAM GENE, encodes a GAM791 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM791 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM791 precursor RNA is designated SEQ ID:764, and is provided hereinbelow with reference to the sequence listing part.

[12432] GAM791 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM791 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12433] An enzyme complex designated DICER COMPLEX, dices the GAM791 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM791 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM791 RNA is designated SEQ ID:2440, and is provided hereinbelow with reference to the sequence listing part.

[12434] GAM791 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM791 target RNA, herein designated GAM TARGET RNA. GAM791 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12435] GAM791 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM791 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM791 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM791 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM791 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12436] The complementary binding of GAM791 RNA, herein designated GAM RNA, to target binding sites on GAM791 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM791 target RNA, herein designated GAM TARGET RNA, into GAM791 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12437] It is appreciated that GAM791 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM791 target genes. The mRNA of each one of this plurality of GAM791 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM791 RNA, herein designated GAM RNA, and which when bound by GAM791 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM791 target proteins.

[12438] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM791 gene, herein designated GAM GENE, on one or more GAM791 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[12439] It is yet further appreciated that specific functions, and accordingly utilities, of GAM791 correlate with, and may be deduced from, the identity of the target genes which GAM791 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12440] Nucleotide sequences of the GAM791 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM791 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM791 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM791 are further described hereinbelow with reference to Table Table1.

[12441] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM791 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12442] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 792 (GAM792) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[12443] GAM792 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM792 was detected is described hereinabove with reference to Figs. 2-8.

[12444] GAM792 gene, herein designated GAM GENE, and GAM792 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12445] GAM792 gene, herein designated GAM GENE, encodes a GAM792 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM792 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM792 precursor RNA is designated SEQ ID:765, and is provided hereinbelow with reference to the sequence listing part.

[12446] GAM792 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM792 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12447] An enzyme complex designated DICER COMPLEX, dices the GAM792 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM792 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM792 RNA is designated SEQ ID:2441, and is provided hereinbelow with reference to the sequence listing part.

[12448] GAM792 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM792 target RNA, herein designated GAM TARGET RNA.
GAM792 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[12449] GAM792 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM792 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM792 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM792 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM792 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12450] The complementary binding of GAM792 RNA, herein designated GAM RNA, to target binding sites on GAM792 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM792 target RNA, herein designated GAM TARGET RNA, into GAM792 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12451] It is appreciated that GAM792 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM792 target genes. The mRNA of each one of this plurality of GAM792 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM792 RNA, herein designated GAM RNA, and which when bound by GAM792 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM792 target proteins.

[12452] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM792 gene, herein designated GAM GENE, on one or more GAM792 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12453] It is yet further appreciated that specific functions, and accordingly utilities, of GAM792 correlate with, and may be deduced from, the identity of the target genes which GAM792 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12454] Nucleotide sequences of the GAM792 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM792 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM792 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM792 are further described hereinbelow with reference to Table Table1.

[12455] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM792 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12456] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 793 (GAM793) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12457] GAM793 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM793 was detected is described hereinabove with reference to Figs. 2-8.

[12458] GAM793 gene, herein designated GAM GENE, and GAM793 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12459] GAM793 gene, herein designated GAM GENE, encodes a GAM793 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM793 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM793 precursor RNA is designated SEQ ID:766, and is provided hereinbelow with reference to the sequence listing part.

[12460] GAM793 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM793 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12461] An enzyme complex designated DICER COMPLEX, dices the GAM793 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM793 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM793 RNA is designated SEQ ID:2442, and is provided

hereinbelow with reference to the sequence listing part.

[12462] GAM793 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM793 target RNA, herein designated GAM TARGET RNA.

GAM793 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12463] GAM793 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM793 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM793 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM793 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM793 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12464] The complementary binding of GAM793 RNA, herein designated GAM RNA, to target binding sites on GAM793 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM793 target RNA, herein designated GAM TARGET RNA, into GAM793 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12465] It is appreciated that GAM793 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM793 target genes. The mRNA of each one of this plurality of GAM793 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM793 RNA, herein designated GAM RNA, and which when bound by GAM793 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM793 tar-

get proteins.

[12466] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM793 gene, herein designated GAM GENE, on one or more GAM793 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12467] It is yet further appreciated that specific functions, and accordingly utilities, of GAM793 correlate with, and may be deduced from, the identity of the target genes which GAM793 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12468] Nucleotide sequences of the GAM793 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM793 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM793 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM793 are further described hereinbelow with reference to Table Table1.

[12469] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM793 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12470] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 794 (GAM794) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12471] GAM794 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM794 was detected is described hereinabove with reference to Figs. 2-8.

[12472] GAM794 gene, herein designated GAM GENE, and

GAM794 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12473] GAM794 gene, herein designated GAM GENE, encodes a GAM794 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM794 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM794 precursor RNA is designated SEQ ID:767, and is provided hereinbelow with reference to the sequence listing part.

[12474] GAM794 has 17 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[12475] SEQ ID:98470 detected in mouse EST Accession AA960473.1.

[12476] SEQ ID:98471 detected in mouse EST Accession AA276264.1.

[12477] SEQ ID:98472 detected in mouse EST Accession BE198843.1.

[12478] SEQ ID:98473 detected in mouse EST Accession

BE198903.1.

[12479] SEQ ID:98474 detected in mouse EST Accession AV134799.2.

[12480] SEQ ID:98475 detected in mouse EST Accession BB378194.2.

[12481] SEQ ID:98476 detected in mouse EST Accession BI734803.1.

[12482] SEQ ID:98477 detected in mouse EST Accession BG295767.1.

[12483] SEQ ID:98480 detected in mouse EST Accession AI463499.1.

[12484] SEQ ID:98482 detected in mouse EST Accession AI607799.1.

[12485] SEQ ID:98483 detected in mouse EST Accession AI790711.1.

[12486] SEQ ID:98484 detected in mouse EST Accession AW987347.1.

[12487] SEQ ID:98485 detected in mouse EST Accession AA288520.1.

[12488] SEQ ID:98486 detected in mouse EST Accession BI652128.1.

[12489] SEQ ID:98487 detected in mouse EST Accession BI152789.1.

[12490] SEQ ID:98488 detected in mouse EST Accession AI463541.1.

[12491] SEQ ID:98489 detected in mouse EST Accession BF661464.1.

[12492] GAM794 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM794 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12493] An enzyme complex designated DICER COMPLEX, dices the GAM794 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM794 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM794 RNA is designated SEQ ID:2443, and is provided hereinbelow with reference to the sequence listing part.

[12494] GAM794 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM794 target RNA, herein designated GAM TARGET RNA. GAM794 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12495] GAM794 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM794 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM794 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM794 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM794 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12496] The complementary binding of GAM794 RNA, herein designated GAM RNA, to target binding sites on GAM794 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM794 target RNA, herein designated GAM TARGET RNA, into GAM794 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12497] It is appreciated that GAM794 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM794 target genes. The mRNA of each one of this plurality of GAM794 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM794 RNA, herein designated GAM RNA, and which when bound by GAM794 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM794 target proteins.

[12498] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM794 gene, herein designated GAM GENE, on one or more GAM794 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12499] It is yet further appreciated that specific functions, and accordingly utilities, of GAM794 correlate with, and may be deduced from, the identity of the target genes which GAM794 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12500] Nucleotide sequences of the GAM794 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM794 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM794 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM794 are further described hereinbelow with reference to Table Table1.

[12501] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM794 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12502] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 795 (GAM795) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12503] GAM795 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM795 was detected is described hereinabove with reference to Figs. 2-8.

[12504] GAM795 gene, herein designated GAM GENE, and GAM795 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12505] GAM795 gene, herein designated GAM GENE, encodes a GAM795 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM795 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM795 precursor RNA is designated SEQ ID:768, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:768 is located at position 881700 relative to contig NT_024812.8, on chromosome 16.

[12506] GAM795 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM795 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[12507] An enzyme complex designated DICER COMPLEX, dices the GAM795 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM795 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM795 RNA is designated SEQ ID:2444, and is provided hereinbelow with reference to the sequence listing part.

[12508] GAM795 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM795 target RNA, herein designated GAM TARGET RNA.
GAM795 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12509] GAM795 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM795 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM795 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM795 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM795 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12510] The complementary binding of GAM795 RNA, herein designated GAM RNA, to target binding sites on GAM795 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM795 target RNA, herein designated GAM TARGET RNA, into GAM795 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12511] It is appreciated that GAM795 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM795 target genes. The mRNA of each one of this plurality of GAM795 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM795 RNA, herein designated GAM RNA, and which when bound by GAM795 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM795 target proteins.

[12512] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM795 gene, herein designated GAM GENE, on one or more GAM795 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12513] It is yet further appreciated that specific functions, and accordingly utilities, of GAM795 correlate with, and may be deduced from, the identity of the target genes which GAM795 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12514] Nucleotide sequences of the GAM795 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM795 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM795 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM795 are further described hereinbelow with reference to Table Table1.

[12515] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM795 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12516] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 796 (GAM796) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12517] GAM796 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM796 was detected is described hereinabove with reference to Figs. 2-8.

[12518] GAM796 gene, herein designated GAM GENE, and GAM796 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12519] GAM796 gene, herein designated GAM GENE, encodes a GAM796 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM796 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM796 precursor RNA is designated SEQ ID:769, and is provided hereinbelow with reference to the sequence listing part.

[12520] GAM796 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM796 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12521] An enzyme complex designated DICER COMPLEX, dices the GAM796 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM796 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM796 RNA is designated SEQ ID:2445, and is provided hereinbelow with reference to the sequence listing part.

[12522] GAM796 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM796 target RNA, herein designated GAM TARGET RNA.

GAM796 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12523] GAM796 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM796 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM796 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM796 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM796 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12524] The complementary binding of GAM796 RNA, herein designated GAM RNA, to target binding sites on GAM796 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM796 target RNA, herein designated GAM TARGET RNA, into GAM796 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12525] It is appreciated that GAM796 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM796 target genes. The mRNA of each one of this plurality of GAM796 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM796 RNA, herein designated GAM RNA, and which when bound by GAM796 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM796 target proteins.

[12526] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM796 gene, herein designated GAM GENE, on one or more GAM796 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12527] It is yet further appreciated that specific functions, and accordingly utilities, of GAM796 correlate with, and may be deduced from, the identity of the target genes which GAM796 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12528] Nucleotide sequences of the GAM796 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM796 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM796 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM796 are further described hereinbelow with reference to Table Table1.

[12529] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM796 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12530] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 797 (GAM797) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12531] GAM797 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM797 was detected is described hereinabove with reference to Figs. 2-8.

[12532] GAM797 gene, herein designated GAM GENE, and GAM797 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12533] GAM797 gene, herein designated GAM GENE, encodes a GAM797 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM797 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM797 precursor RNA is designated SEQ ID:770, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:770 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[12534] GAM797 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM797 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12535] An enzyme complex designated DICER COMPLEX, dices the GAM797 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM797 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM797 RNA is designated SEQ ID:2446, and is provided hereinbelow with reference to the sequence listing part.

[12536] GAM797 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM797 target RNA, herein designated GAM TARGET RNA. GAM797 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12537] GAM797 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM797 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM797 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM797 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM797 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12538] The complementary binding of GAM797 RNA, herein designated GAM RNA, to target binding sites on GAM797 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM797 target RNA, herein designated GAM TARGET RNA, into GAM797 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12539] It is appreciated that GAM797 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM797 target genes. The mRNA of each one of this plu-

rality of GAM797 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM797 RNA, herein designated GAM RNA, and which when bound by GAM797 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM797 target proteins.

[12540] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM797 gene, herein designated GAM GENE, on one or more GAM797 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12541] It is yet further appreciated that specific functions, and accordingly utilities, of GAM797 correlate with, and may be deduced from, the identity of the target genes which GAM797 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12542] Nucleotide sequences of the GAM797 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM797 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM797 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM797 are further described hereinbelow with reference to Table Table1.

[12543] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM797 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12544] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 798 (GAM798) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[12545] GAM798 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM798 was detected is described hereinabove with reference to Figs. 2-8.

[12546] GAM798 gene, herein designated GAM GENE, and GAM798 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12547] GAM798 gene, herein designated GAM GENE, encodes a GAM798 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM798 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM798 precursor RNA is designated SEQ ID:771, and is provided hereinbelow with reference to the sequence listing part.

[12548] GAM798 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12549] An enzyme complex designated DICER COMPLEX, dices the GAM798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM798 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM798 RNA is designated SEQ ID:2447, and is provided hereinbelow with reference to the sequence listing part.

[12550] GAM798 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM798 target RNA, herein designated GAM TARGET RNA. GAM798 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12551] GAM798 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM798 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM798 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM798 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM798 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12552] The complementary binding of GAM798 RNA, herein designated GAM RNA, to target binding sites on GAM798 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM798 target RNA, herein designated GAM TARGET RNA, into GAM798 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12553] It is appreciated that GAM798 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM798 target genes. The mRNA of each one of this plurality of GAM798 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM798 RNA, herein designated GAM RNA, and which when bound by GAM798 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM798 target proteins.

[12554] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM798 gene, herein designated GAM GENE, on one or more GAM798 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12555] It is yet further appreciated that specific functions, and accordingly utilities, of GAM798 correlate with, and may be deduced from, the identity of the target genes which GAM798 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12556] Nucleotide sequences of the GAM798 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM798 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM798 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM798 are further described hereinbelow with reference to Table Table1.

[12557] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM798 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12558] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 799 (GAM799) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12559] GAM799 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM799 was detected is described hereinabove with reference to Figs. 2-8.

[12560] GAM799 gene, herein designated GAM GENE, and GAM799 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12561] GAM799 gene, herein designated GAM GENE, encodes a GAM799 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM799 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM799 precursor RNA is desig-

nated SEQ ID:772, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:772 is located at position 9792242 relative to contig NT_023974.13, on chromosome 9.

[12562] GAM799 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12563] An enzyme complex designated DICER COMPLEX, dices the GAM799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM799 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM799 RNA is designated SEQ ID:2448, and is provided hereinbelow with reference to the sequence listing part.

[12564] GAM799 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM799 target RNA, herein designated GAM TARGET RNA.

GAM799 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12565] GAM799 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM799 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM799 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM799 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM799 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12566] The complementary binding of GAM799 RNA, herein designated GAM RNA, to target binding sites on GAM799 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM799 target RNA, herein designated GAM TARGET RNA, into GAM799 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12567] It is appreciated that GAM799 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM799 target genes. The mRNA of each one of this plurality of GAM799 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM799 RNA, herein designated GAM RNA, and which when bound by GAM799 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM799 target proteins.

[12568] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM799 gene, herein designated GAM GENE, on one or more GAM799 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12569] It is yet further appreciated that specific functions, and accordingly utilities, of GAM799 correlate with, and may be deduced from, the identity of the target genes which GAM799 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12570] Nucleotide sequences of the GAM799 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM799 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM799 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM799 are further described hereinbelow with reference to Table Table1.

[12571] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM799 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12572] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 800 (GAM800) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12573] GAM800 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM800 was detected is described hereinabove with reference to Figs. 2-8.

[12574] GAM800 gene, herein designated GAM GENE, and GAM800 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12575] GAM800 gene, herein designated GAM GENE, encodes a GAM800 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM800 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM800 precursor RNA is designated SEQ ID:773, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:773 is located at position 2383129 relative to contig NT_009714.13, on chromosome 12.

[12576] GAM800 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[12577] An enzyme complex designated DICER COMPLEX, dices the GAM800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM800 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM800 RNA is designated SEQ ID:2449, and is provided hereinbelow with reference to the sequence listing part.

[12578] GAM800 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM800 target RNA, herein designated GAM TARGET RNA. GAM800 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12579] GAM800 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM800 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM800 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM800 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM800 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12580] The complementary binding of GAM800 RNA, herein designated GAM RNA, to target binding sites on GAM800 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM800 target RNA, herein designated GAM TARGET RNA, into GAM800 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12581] It is appreciated that GAM800 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM800 target genes. The mRNA of each one of this plurality of GAM800 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM800 RNA, herein designated GAM RNA, and which when bound by GAM800 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM800 target proteins.

[12582] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM800 gene, herein designated GAM GENE, on one or more GAM800 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12583] It is yet further appreciated that specific functions, and accordingly utilities, of GAM800 correlate with, and may be deduced from, the identity of the target genes which GAM800 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12584] Nucleotide sequences of the GAM800 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM800 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM800 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM800 are further described hereinbelow with reference to Table Table1.

[12585] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM800 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12586] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 801 (GAM801) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12587] GAM801 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM801 was detected is described hereinabove with reference to Figs. 2-8.

[12588] GAM801 gene, herein designated GAM GENE, and GAM801 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12589] GAM801 gene, herein designated GAM GENE, encodes a GAM801 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM801 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM801 precursor RNA is designated SEQ ID:774, and is provided hereinbelow with reference to the sequence listing part.

[12590] GAM801 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM801 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12591] An enzyme complex designated DICER COMPLEX, dices the GAM801 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM801 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM801 RNA is designated SEQ ID:2450, and is provided hereinbelow with reference to the sequence listing part.

[12592] GAM801 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM801 target RNA, herein designated GAM TARGET RNA.

GAM801 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12593] GAM801 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM801 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM801 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM801 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM801 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12594] The complementary binding of GAM801 RNA, herein designated GAM RNA, to target binding sites on GAM801 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM801 target RNA, herein designated GAM TARGET RNA, into GAM801 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12595] It is appreciated that GAM801 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM801 target genes. The mRNA of each one of this plurality of GAM801 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM801 RNA, herein designated GAM RNA, and which when bound by GAM801 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM801 target proteins.

[12596] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM801 gene, herein designated GAM GENE, on one or more GAM801 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12597] It is yet further appreciated that specific functions, and accordingly utilities, of GAM801 correlate with, and may be deduced from, the identity of the target genes which GAM801 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12598] Nucleotide sequences of the GAM801 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM801 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM801 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM801 are further described hereinbelow with reference to Table Table1.

[12599] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM801 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12600] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 802 (GAM802) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12601] GAM802 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM802 was detected is described hereinabove with reference to Figs. 2-8.

[12602] GAM802 gene, herein designated GAM GENE, and GAM802 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12603] GAM802 gene, herein designated GAM GENE, encodes a GAM802 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM802 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM802 precursor RNA is designated SEQ ID:775, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:775 is located at position 8354528 relative to contig NT_010265.13, on chromosome 15.

[12604] GAM802 has 64 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[12605] SEQ ID:99673 detected in mouse EST Accession BF452017.1.

[12606] SEQ ID:99674 detected in mouse EST Accession BF015849.1.

[12607] SEQ ID:99675 detected in mouse EST Accession AL362409.1.

[12608] SEQ ID:99676 detected in mouse EST Accession BG801787.1.

[12609] SEQ ID:99677 detected in mouse EST Accession

BE914459.1.

[12610] SEQ ID:99678 detected in mouse EST Accession BE376995.1.

[12611] SEQ ID:99679 detected in mouse EST Accession BG800940.1.

[12612] SEQ ID:99680 detected in mouse EST Accession BE292306.1.

[12613] SEQ ID:99681 detected in mouse EST Accession BE303075.1.

[12614] SEQ ID:99682 detected in mouse EST Accession BE373137.1.

[12615] SEQ ID:99683 detected in mouse EST Accession BI083603.1.

[12616] SEQ ID:99684 detected in mouse EST Accession BI854337.1.

[12617] SEQ ID:99685 detected in mouse EST Accession BF163926.1.

[12618] SEQ ID:99686 detected in mouse EST Accession BG924008.1.

[12619] SEQ ID:99687 detected in mouse EST Accession BI650104.1.

[12620] SEQ ID:99688 detected in mouse EST Accession BI853976.1.

[12621] SEQ ID:99689 detected in mouse EST Accession AI265126.1.

[12622] SEQ ID:99690 detected in mouse EST Accession BG921974.1.

[12623] SEQ ID:99691 detected in mouse EST Accession BF012105.1.

[12624] SEQ ID:99692 detected in mouse EST Accession BI556436.1.

[12625] SEQ ID:99693 detected in mouse EST Accession BI555745.1.

[12626] SEQ ID:99694 detected in mouse EST Accession BI083588.1.

[12627] SEQ ID:99695 detected in mouse EST Accession AW701577.1.

[12628] SEQ ID:99696 detected in mouse EST Accession BF101754.1.

[12629] SEQ ID:99697 detected in mouse EST Accession BI852358.1.

[12630] SEQ ID:99698 detected in mouse EST Accession BI694455.1.

[12631] SEQ ID:99699 detected in mouse EST Accession BG175980.1.

[12632] SEQ ID:99700 detected in mouse EST Accession

AI663898.1.

[12633] SEQ ID:99701 detected in mouse EST Accession BI738823.1.

[12634] SEQ ID:99702 detected in mouse EST Accession BI409574.1.

[12635] SEQ ID:99703 detected in mouse EST Accession BI456615.1.

[12636] SEQ ID:99704 detected in mouse EST Accession BI693927.1.

[12637] SEQ ID:99705 detected in mouse EST Accession BI655653.1.

[12638] SEQ ID:99706 detected in mouse EST Accession BI657639.1.

[12639] SEQ ID:99707 detected in mouse EST Accession BI734747.1.

[12640] SEQ ID:99708 detected in mouse EST Accession BG294046.1.

[12641] SEQ ID:99709 detected in mouse EST Accession BF577749.1.

[12642] SEQ ID:99710 detected in mouse EST Accession BF140771.1.

[12643] SEQ ID:99711 detected in mouse EST Accession BI411947.1.

[12644] SEQ ID:99712 detected in mouse EST Accession BF152379.1.

[12645] SEQ ID:99713 detected in mouse EST Accession AW647174.1.

[12646] SEQ ID:99714 detected in mouse EST Accession BE303776.1.

[12647] SEQ ID:99715 detected in mouse EST Accession BG975521.1.

[12648] SEQ ID:99716 detected in mouse EST Accession BI852502.1.

[12649] SEQ ID:99717 detected in mouse EST Accession BF163477.1.

[12650] SEQ ID:99718 detected in mouse EST Accession BI408319.1.

[12651] SEQ ID:99719 detected in mouse EST Accession BI852269.1.

[12652] SEQ ID:99720 detected in mouse EST Accession BI736057.1.

[12653] SEQ ID:99721 detected in mouse EST Accession BI408871.1.

[12654] SEQ ID:99722 detected in mouse EST Accession BI648592.1.

[12655] SEQ ID:99723 detected in mouse EST Accession

BI988340.1.

[12656] SEQ ID:99724 detected in mouse EST Accession BI656566.1.

[12657] SEQ ID:99725 detected in mouse EST Accession BG298294.1.

[12658] SEQ ID:99726 detected in mouse EST Accession BI733929.1.

[12659] SEQ ID:99727 detected in mouse EST Accession BE570088.1.

[12660] SEQ ID:99728 detected in mouse EST Accession BI738891.1.

[12661] SEQ ID:99729 detected in mouse EST Accession BI158228.1.

[12662] SEQ ID:99730 detected in mouse EST Accession BI693477.1.

[12663] SEQ ID:99731 detected in mouse EST Accession BI555521.1.

[12664] SEQ ID:99732 detected in mouse EST Accession BI697435.1.

[12665] SEQ ID:99733 detected in mouse EST Accession BI657771.1.

[12666] SEQ ID:99734 detected in mouse EST Accession BI411902.1.

[12667] SEQ ID:99735 detected in mouse EST Accession BI408453.1.

[12668] SEQ ID:100241 detected in mouse EST Accession BI412697.1.

[12669] GAM802 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM802 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12670] An enzyme complex designated DICER COMPLEX, dices the GAM802 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM802 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM802 RNA is designated SEQ ID:2451, and is provided hereinbelow with reference to the sequence listing part.

[12671] GAM802 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM802 target RNA, herein designated GAM TARGET RNA. GAM802 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12672] GAM802 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM802 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM802 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM802 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM802 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12673] The complementary binding of GAM802 RNA, herein designated GAM RNA, to target binding sites on GAM802 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM802 target RNA, herein designated GAM TARGET RNA, into GAM802 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12674] It is appreciated that GAM802 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM802 target genes. The mRNA of each one of this plurality of GAM802 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM802 RNA, herein designated GAM RNA, and which when bound by GAM802 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM802 target proteins.

[12675] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM802 gene, herein designated GAM GENE, on one or more GAM802 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12676] It is yet further appreciated that specific functions, and accordingly utilities, of GAM802 correlate with, and may be deduced from, the identity of the target genes which GAM802 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12677] Nucleotide sequences of the GAM802 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM802 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM802 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM802 are further described hereinbelow with reference to Table Table1.

[12678] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM802 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12679] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 803 (GAM803) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12680] GAM803 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM803 was detected is described hereinabove with reference to Figs. 2-8.

[12681] GAM803 gene, herein designated GAM GENE, and GAM803 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12682] GAM803 gene, herein designated GAM GENE, encodes a GAM803 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM803 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM803 precursor RNA is designated SEQ ID:776, and is provided hereinbelow with reference to the sequence listing part.

[12683] GAM803 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM803 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12684] An enzyme complex designated DICER COMPLEX, dices

the GAM803 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM803 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM803 RNA is designated SEQ ID:2452, and is provided hereinbelow with reference to the sequence listing part.

[12685] GAM803 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM803 target RNA, herein designated GAM TARGET RNA.

GAM803 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12686] GAM803 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM803 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM803

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM803 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM803 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12687] The complementary binding of GAM803 RNA, herein designated GAM RNA, to target binding sites on GAM803 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM803 target RNA, herein designated GAM TARGET RNA, into GAM803 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12688] It is appreciated that GAM803 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM803 target genes. The mRNA of each one of this plurality of GAM803 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM803 RNA, herein designated GAM RNA, and which when bound by GAM803 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM803 target proteins.

[12689] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM803 gene, herein designated GAM GENE, on one or more GAM803 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12690] It is yet further appreciated that specific functions, and accordingly utilities, of GAM803 correlate with, and may be deduced from, the identity of the target genes which GAM803 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12691] Nucleotide sequences of the GAM803 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM803 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM803 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM803 are further described hereinbelow with reference to Table Table1.

[12692] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM803 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12693] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 804 (GAM804) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12694] GAM804 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM804 was detected is described hereinabove with reference to Figs. 2-8.

[12695] GAM804 gene, herein designated GAM GENE, and GAM804 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12696] GAM804 gene, herein designated GAM GENE, encodes a GAM804 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM804 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM804 precursor RNA is designated SEQ ID:777, and is provided hereinbelow with reference to the sequence listing part.

[12697] GAM804 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM804 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12698] An enzyme complex designated DICER COMPLEX, dices the GAM804 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM804 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM804 RNA is designated SEQ ID:2453, and is provided hereinbelow with reference to the sequence listing part.

[12699] GAM804 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM804 target RNA, herein designated GAM TARGET RNA. GAM804 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12700] GAM804 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM804 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM804 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM804 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM804 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12701] The complementary binding of GAM804 RNA, herein designated GAM RNA, to target binding sites on GAM804 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM804 target RNA, herein designated GAM TARGET RNA, into GAM804 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12702] It is appreciated that GAM804 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM804 target genes. The mRNA of each one of this plurality of GAM804 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM804 RNA, herein designated GAM RNA, and which when bound by GAM804 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM804 target proteins.

[12703] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM804 gene, herein designated GAM GENE, on one or more GAM804 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12704] It is yet further appreciated that specific functions, and accordingly utilities, of GAM804 correlate with, and may be deduced from, the identity of the target genes which GAM804 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12705] Nucleotide sequences of the GAM804 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM804 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM804 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM804 are further described hereinbelow with reference to Table Table1.

[12706] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM804 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12707] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 805 (GAM805) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12708] GAM805 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM805 was detected is described hereinabove with reference to Figs. 2-8.

[12709] GAM805 gene, herein designated GAM GENE, and GAM805 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12710] GAM805 gene, herein designated GAM GENE, encodes a GAM805 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM805 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM805 precursor RNA is designated SEQ ID:778, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:778 is located at position 617375 relative to contig NT_030584.7, on chromosome 1.

[12711] GAM805 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM805 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12712] An enzyme complex designated DICER COMPLEX, dices the GAM805 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM805 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM805 RNA is designated SEQ ID:2454, and is provided hereinbelow with reference to the sequence listing part.

[12713] GAM805 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM805 target RNA, herein designated GAM TARGET RNA. GAM805 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12714] GAM805 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM805 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM805 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM805 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM805 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12715] The complementary binding of GAM805 RNA, herein designated GAM RNA, to target binding sites on GAM805 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM805 target RNA, herein designated GAM TARGET RNA, into GAM805 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12716] It is appreciated that GAM805 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM805 target genes. The mRNA of each one of this plurality of GAM805 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM805 RNA, herein designated GAM RNA, and which when bound by GAM805 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM805 target proteins.

[12717] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM805 gene, herein designated GAM GENE, on one or more GAM805 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12718] It is yet further appreciated that specific functions, and accordingly utilities, of GAM805 correlate with, and may

be deduced from, the identity of the target genes which GAM805 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12719] Nucleotide sequences of the GAM805 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM805 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM805 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM805 are further described hereinbelow with reference to Table Table1.

[12720] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM805 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12721] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 806 (GAM806) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12722] GAM806 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM806 was detected is described hereinabove with reference to Figs. 2-8.

[12723] GAM806 gene, herein designated GAM GENE, and GAM806 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12724] GAM806 gene, herein designated GAM GENE, encodes a GAM806 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM806 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM806 precursor RNA is designated SEQ ID:779, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:779 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[12725] GAM806 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12726] An enzyme complex designated DICER COMPLEX, dices the GAM806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM806 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM806 RNA is designated SEQ ID:2455, and is provided hereinbelow with reference to the sequence listing part.

[12727] GAM806 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM806 target RNA, herein designated GAM TARGET RNA.
GAM806 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12728] GAM806 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM806 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM806 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM806 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM806 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12729] The complementary binding of GAM806 RNA, herein designated GAM RNA, to target binding sites on GAM806 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM806 target RNA, herein designated GAM TARGET RNA, into GAM806 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12730] It is appreciated that GAM806 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM806 target genes. The mRNA of each one of this plurality of GAM806 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM806 RNA, herein designated GAM RNA, and which when bound by GAM806 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM806 target proteins.

[12731] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM806 gene, herein designated GAM GENE, on one or more GAM806 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12732] It is yet further appreciated that specific functions, and accordingly utilities, of GAM806 correlate with, and may be deduced from, the identity of the target genes which GAM806 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12733] Nucleotide sequences of the GAM806 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM806 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM806 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM806 are further described hereinbelow with reference to Table Table1.

[12734] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM806 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12735] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 807 (GAM807) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12736] GAM807 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM807 was detected is described hereinabove with reference to Figs. 2-8.

[12737] GAM807 gene, herein designated GAM GENE, and GAM807 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12738] GAM807 gene, herein designated GAM GENE, encodes a GAM807 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM807 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM807 precursor RNA is desig-

nated SEQ ID:780, and is provided hereinbelow with reference to the sequence listing part.

[12739] GAM807 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12740] An enzyme complex designated DICER COMPLEX, dices the GAM807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM807 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM807 RNA is designated SEQ ID:2456, and is provided hereinbelow with reference to the sequence listing part.

[12741] GAM807 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM807 target RNA, herein designated GAM TARGET RNA. GAM807 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12742] GAM807 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM807 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM807 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM807 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM807

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12743] The complementary binding of GAM807 RNA, herein designated GAM RNA, to target binding sites on GAM807 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM807 target RNA, herein designated GAM TARGET RNA, into GAM807 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12744] It is appreciated that GAM807 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM807 target genes. The mRNA of each one of this plurality of GAM807 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM807 RNA, herein designated GAM RNA, and which when bound by GAM807 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM807 target proteins.

[12745] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM807 gene, herein designated GAM GENE, on one or more GAM807 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12746] It is yet further appreciated that specific functions, and accordingly utilities, of GAM807 correlate with, and may be deduced from, the identity of the target genes which GAM807 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12747] Nucleotide sequences of the GAM807 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM807 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM807 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM807 are further described hereinbelow with reference to Table Table1.

[12748] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM807 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12749] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 808 (GAM808) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12750] GAM808 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM808 was detected is described hereinabove with reference to Figs. 2-8.

[12751] GAM808 gene, herein designated GAM GENE, and GAM808 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[12752] GAM808 gene, herein designated GAM GENE, encodes a GAM808 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM808 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM808 precursor RNA is designated SEQ ID:781, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:781 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[12753] GAM808 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM808 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12754] An enzyme complex designated DICER COMPLEX, dices

the GAM808 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM808 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM808 RNA is designated SEQ ID:2457, and is provided hereinbelow with reference to the sequence listing part.

[12755] GAM808 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM808 target RNA, herein designated GAM TARGET RNA.

GAM808 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12756] GAM808 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM808 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM808

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM808 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM808 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12757] The complementary binding of GAM808 RNA, herein designated GAM RNA, to target binding sites on GAM808 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM808 target RNA, herein designated GAM TARGET RNA, into GAM808 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12758] It is appreciated that GAM808 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM808 target genes. The mRNA of each one of this plurality of GAM808 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM808 RNA, herein designated GAM RNA, and which when bound by GAM808 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM808 target proteins.

[12759] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM808 gene, herein designated GAM GENE, on one or more GAM808 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12760] It is yet further appreciated that specific functions, and accordingly utilities, of GAM808 correlate with, and may be deduced from, the identity of the target genes which GAM808 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12761] Nucleotide sequences of the GAM808 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM808 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM808 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM808 are further described hereinbelow with reference to Table Table1.

[12762] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM808 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12763] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 809 (GAM809) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12764] GAM809 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM809 was detected is described hereinabove with reference to Figs. 2-8.

[12765] GAM809 gene, herein designated GAM GENE, and GAM809 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12766] GAM809 gene, herein designated GAM GENE, encodes a GAM809 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM809 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM809 precursor RNA is designated SEQ ID:782, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:782 is located at position 3434864 relative to contig NT_009714.13, on chromosome 12.

[12767] GAM809 has a highly conserved, expressed mouse ho-

molog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98949, which mouse homolog is detected in mouse EST accession BG288438.1.

[12768] GAM809 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12769] An enzyme complex designated DICER COMPLEX, dices the GAM809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM809 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM809 RNA is designated SEQ ID:2458, and is provided hereinbelow with reference to the sequence listing part.

[12770] GAM809 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM809 target RNA, herein designated GAM TARGET RNA. GAM809 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12771] GAM809 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM809 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM809 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM809 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM809 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12772] The complementary binding of GAM809 RNA, herein designated GAM RNA, to target binding sites on GAM809 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM809 target RNA, herein designated GAM TARGET RNA, into GAM809 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12773] It is appreciated that GAM809 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM809 target genes. The mRNA of each one of this plurality of GAM809 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM809 RNA, herein designated GAM RNA, and which when bound by GAM809 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM809 target proteins.

[12774] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM809 gene, herein designated GAM GENE, on one or more GAM809 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12775] It is yet further appreciated that specific functions, and accordingly utilities, of GAM809 correlate with, and may be deduced from, the identity of the target genes which GAM809 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12776] Nucleotide sequences of the GAM809 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM809 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM809 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM809 are further described hereinbelow with reference to Table Table1.

[12777] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM809 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12778] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 810 (GAM810) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12779] GAM810 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM810 was detected is described hereinabove with reference to Figs. 2-8.

[12780] GAM810 gene, herein designated GAM GENE, and GAM810 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12781] GAM810 gene, herein designated GAM GENE, encodes a GAM810 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM810 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM810 precursor RNA is designated SEQ ID:783, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:783 is located at position 11960372 relative to contig NT_009799.11, on chromosome 13.

[12782] GAM810 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[12783] An enzyme complex designated DICER COMPLEX, dices the GAM810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM810 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM810 RNA is designated SEQ ID:2459, and is provided hereinbelow with reference to the sequence listing part.

[12784] GAM810 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM810 target RNA, herein designated GAM TARGET RNA. GAM810 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12785] GAM810 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM810 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM810 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM810 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM810 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12786] The complementary binding of GAM810 RNA, herein designated GAM RNA, to target binding sites on GAM810 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM810 target RNA, herein designated GAM TARGET RNA, into GAM810 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12787] It is appreciated that GAM810 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM810 target genes. The mRNA of each one of this plurality of GAM810 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM810 RNA, herein designated GAM RNA, and which when bound by GAM810 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM810 target proteins.

[12788] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM810 gene, herein designated GAM GENE, on one or more GAM810 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12789] It is yet further appreciated that specific functions, and accordingly utilities, of GAM810 correlate with, and may be deduced from, the identity of the target genes which GAM810 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12790] Nucleotide sequences of the GAM810 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM810 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM810 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM810 are further described hereinbelow with reference to Table Table1.

[12791] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM810 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12792] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 811 (GAM811) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12793] GAM811 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM811 was detected is described hereinabove with reference to Figs. 2-8.

[12794] GAM811 gene, herein designated GAM GENE, and GAM811 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12795] GAM811 gene, herein designated GAM GENE, encodes a GAM811 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM811 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM811 precursor RNA is designated SEQ ID:784, and is provided hereinbelow with reference to the sequence listing part.

[12796] GAM811 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM811 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12797] An enzyme complex designated DICER COMPLEX, dices the GAM811 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM811 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM811 RNA is designated SEQ ID:2460, and is provided hereinbelow with reference to the sequence listing part.

[12798] GAM811 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM811 target RNA, herein designated GAM TARGET RNA.

GAM811 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12799] GAM811 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM811 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM811 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM811 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM811 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12800] The complementary binding of GAM811 RNA, herein designated GAM RNA, to target binding sites on GAM811 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM811 target RNA, herein designated GAM TARGET RNA, into GAM811 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12801] It is appreciated that GAM811 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM811 target genes. The mRNA of each one of this plurality of GAM811 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM811 RNA, herein designated GAM RNA, and which when bound by GAM811 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM811 target proteins.

[12802] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM811 gene, herein designated GAM GENE, on one or more GAM811 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12803] It is yet further appreciated that specific functions, and accordingly utilities, of GAM811 correlate with, and may be deduced from, the identity of the target genes which GAM811 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12804] Nucleotide sequences of the GAM811 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM811 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM811 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM811 are further described hereinbelow with reference to Table Table1.

[12805] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM811 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12806] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 812 (GAM812) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12807] GAM812 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM812 was detected is described hereinabove with reference to Figs. 2-8.

[12808] GAM812 gene, herein designated GAM GENE, and GAM812 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12809] GAM812 gene, herein designated GAM GENE, encodes a GAM812 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM812 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM812 precursor RNA is designated SEQ ID:785, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:785 is located at position 4851355 relative to contig NT_022517.13, on chromosome 3.

[12810] GAM812 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM812 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12811] An enzyme complex designated DICER COMPLEX, dices the GAM812 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM812 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM812 RNA is designated SEQ ID:2461, and is provided hereinbelow with reference to the sequence listing part.

[12812] GAM812 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM812 target RNA, herein designated GAM TARGET RNA. GAM812 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12813] GAM812 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM812 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM812 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM812 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM812 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12814] The complementary binding of GAM812 RNA, herein designated GAM RNA, to target binding sites on GAM812 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM812 target RNA, herein designated GAM TARGET RNA, into GAM812 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12815] It is appreciated that GAM812 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM812 target genes. The mRNA of each one of this plu-

rality of GAM812 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM812 RNA, herein designated GAM RNA, and which when bound by GAM812 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM812 target proteins.

[12816] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM812 gene, herein designated GAM GENE, on one or more GAM812 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12817] It is yet further appreciated that specific functions, and accordingly utilities, of GAM812 correlate with, and may be deduced from, the identity of the target genes which GAM812 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12818] Nucleotide sequences of the GAM812 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM812 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM812 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM812 are further described hereinbelow with reference to Table Table1.

[12819] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM812 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12820] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 813 (GAM813) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[12821] GAM813 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM813 was detected is described hereinabove with reference to Figs. 2-8.

[12822] GAM813 gene, herein designated GAM GENE, and GAM813 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12823] GAM813 gene, herein designated GAM GENE, encodes a GAM813 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM813 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM813 precursor RNA is designated SEQ ID:786, and is provided hereinbelow with reference to the sequence listing part.

[12824] GAM813 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM813 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12825] An enzyme complex designated DICER COMPLEX, dices the GAM813 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM813 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM813 RNA is designated SEQ ID:2462, and is provided hereinbelow with reference to the sequence listing part.

[12826] GAM813 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM813 target RNA, herein designated GAM TARGET RNA. GAM813 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12827] GAM813 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM813 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM813 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM813 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM813 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12828] The complementary binding of GAM813 RNA, herein designated GAM RNA, to target binding sites on GAM813 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM813 target RNA, herein designated GAM TARGET RNA, into GAM813 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12829] It is appreciated that GAM813 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM813 target genes. The mRNA of each one of this plurality of GAM813 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM813 RNA, herein designated GAM RNA, and which when bound by GAM813 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM813 target proteins.

[12830] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM813 gene, herein designated GAM GENE, on one or more GAM813 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12831] It is yet further appreciated that specific functions, and accordingly utilities, of GAM813 correlate with, and may be deduced from, the identity of the target genes which GAM813 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12832] Nucleotide sequences of the GAM813 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM813 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM813 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM813 are further described hereinbelow with reference to Table Table1.

[12833] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM813 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12834] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 814 (GAM814) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12835] GAM814 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM814 was detected is described hereinabove with reference to Figs. 2-8.

[12836] GAM814 gene, herein designated GAM GENE, and GAM814 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12837] GAM814 gene, herein designated GAM GENE, encodes a GAM814 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM814 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM814 precursor RNA is desig-

nated SEQ ID:787, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:787 is located at position 6427837 relative to contig NT_011362.7, on chromosome 20.

[12838] GAM814 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12839] An enzyme complex designated DICER COMPLEX, dices the GAM814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM814 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM814 RNA is designated SEQ ID:2463, and is provided hereinbelow with reference to the sequence listing part.

[12840] GAM814 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM814 target RNA, herein designated GAM TARGET RNA. GAM814 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12841] GAM814 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM814 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM814 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM814 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM814 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12842] The complementary binding of GAM814 RNA, herein designated GAM RNA, to target binding sites on GAM814 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM814 target RNA, herein designated GAM TARGET RNA, into GAM814 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12843] It is appreciated that GAM814 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM814 target genes. The mRNA of each one of this plurality of GAM814 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM814 RNA, herein designated GAM RNA, and which when bound by GAM814 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM814 target proteins.

[12844] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM814 gene, herein designated GAM GENE, on one or more GAM814 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12845] It is yet further appreciated that specific functions, and accordingly utilities, of GAM814 correlate with, and may be deduced from, the identity of the target genes which GAM814 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12846] Nucleotide sequences of the GAM814 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM814 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM814 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM814 are further described hereinbelow with reference to Table Table1.

[12847] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM814 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12848] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 815 (GAM815) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12849] GAM815 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM815 was detected is described hereinabove with reference to Figs. 2-8.

[12850] GAM815 gene, herein designated GAM GENE, and GAM815 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12851] GAM815 gene, herein designated GAM GENE, encodes a GAM815 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM815 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM815 precursor RNA is designated SEQ ID:788, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:788 is located at position 4851356 relative to contig NT_022517.13, on chromosome 3.

[12852] GAM815 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM815 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[12853] An enzyme complex designated DICER COMPLEX, dices the GAM815 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM815 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM815 RNA is designated SEQ ID:2464, and is provided hereinbelow with reference to the sequence listing part.

[12854] GAM815 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM815 target RNA, herein designated GAM TARGET RNA. GAM815 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12855] GAM815 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM815 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM815 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM815 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM815 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12856] The complementary binding of GAM815 RNA, herein designated GAM RNA, to target binding sites on GAM815 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM815 target RNA, herein designated GAM TARGET RNA, into GAM815 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12857] It is appreciated that GAM815 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM815 target genes. The mRNA of each one of this plurality of GAM815 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM815 RNA, herein designated GAM RNA, and which when bound by GAM815 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM815 target proteins.

[12858] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM815 gene, herein designated GAM GENE, on one or more GAM815 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12859] It is yet further appreciated that specific functions, and accordingly utilities, of GAM815 correlate with, and may be deduced from, the identity of the target genes which GAM815 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12860] Nucleotide sequences of the GAM815 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM815 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM815 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM815 are further described hereinbelow with reference to Table Table1.

[12861] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM815 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12862] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 816 (GAM816) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12863] GAM816 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM816 was detected is described hereinabove with reference to Figs. 2-8.

[12864] GAM816 gene, herein designated GAM GENE, and GAM816 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12865] GAM816 gene, herein designated GAM GENE, encodes a GAM816 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM816 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM816 precursor RNA is designated SEQ ID:789, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:789 is located at position 436795 relative to contig

NT_008413.13, on chromosome 9.

[12866] GAM816 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM816 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12867] An enzyme complex designated DICER COMPLEX, dices the GAM816 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM816 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM816 RNA is designated SEQ ID:2465, and is provided hereinbelow with reference to the sequence listing part.

[12868] GAM816 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM816 target RNA, herein designated GAM TARGET RNA.

GAM816 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12869] GAM816 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM816 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM816 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM816 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM816 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12870] The complementary binding of GAM816 RNA, herein designated GAM RNA, to target binding sites on GAM816 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM816 target RNA, herein designated GAM TARGET RNA, into GAM816 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12871] It is appreciated that GAM816 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM816 target genes. The mRNA of each one of this plurality of GAM816 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM816 RNA, herein designated GAM RNA, and which when bound by GAM816 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM816 target proteins.

[12872] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM816 gene, herein designated GAM GENE, on one or more GAM816 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12873] It is yet further appreciated that specific functions, and accordingly utilities, of GAM816 correlate with, and may be deduced from, the identity of the target genes which GAM816 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12874] Nucleotide sequences of the GAM816 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM816 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM816 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM816 are further described hereinbelow with reference to Table Table1.

[12875] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM816 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12876] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 817 (GAM817) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12877] GAM817 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM817 was detected is described hereinabove with reference to Figs. 2-8.

[12878] GAM817 gene, herein designated GAM GENE, and GAM817 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12879] GAM817 gene, herein designated GAM GENE, encodes a GAM817 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM817 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM817 precursor RNA is designated SEQ ID:790, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:790 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[12880] GAM817 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12881] An enzyme complex designated DICER COMPLEX, dices the GAM817 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM817 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM817 RNA is designated SEQ ID:2466, and is provided hereinbelow with reference to the sequence listing part.

[12882] GAM817 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM817 target RNA, herein designated GAM TARGET RNA. GAM817 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12883] GAM817 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM817 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM817 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM817 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM817 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12884] The complementary binding of GAM817 RNA, herein designated GAM RNA, to target binding sites on GAM817 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM817 target RNA, herein designated GAM TARGET RNA, into GAM817 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12885] It is appreciated that GAM817 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM817 target genes. The mRNA of each one of this plurality of GAM817 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM817 RNA, herein designated GAM RNA, and which when bound by GAM817 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM817 target proteins.

[12886] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM817 gene, herein designated GAM GENE, on one or more GAM817 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12887] It is yet further appreciated that specific functions, and accordingly utilities, of GAM817 correlate with, and may be deduced from, the identity of the target genes which GAM817 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12888] Nucleotide sequences of the GAM817 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM817 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM817 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM817 are further described hereinbelow with reference to Table Table1.

[12889] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM817 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12890] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

818 (GAM818) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12891] GAM818 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM818 was detected is described hereinabove with reference to Figs. 2-8.

[12892] GAM818 gene, herein designated GAM GENE, and GAM818 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12893] GAM818 gene, herein designated GAM GENE, encodes a GAM818 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM818 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM818 precursor RNA is designated SEQ ID:791, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:791 is located at position 55744460 relative to contig NT_026437.9, on chromosome 14.

[12894] GAM818 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM818 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12895] An enzyme complex designated DICER COMPLEX, dices the GAM818 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM818 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM818 RNA is designated SEQ ID:2467, and is provided hereinbelow with reference to the sequence listing part.

[12896] GAM818 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM818 target RNA, herein designated GAM TARGET RNA. GAM818 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12897] GAM818 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM818 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM818 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM818 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM818 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[12898] The complementary binding of GAM818 RNA, herein designated GAM RNA, to target binding sites on GAM818 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM818 target RNA, herein designated GAM TARGET RNA, into GAM818 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12899] It is appreciated that GAM818 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM818 target genes. The mRNA of each one of this plurality of GAM818 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM818 RNA, herein designated GAM RNA, and which when bound by GAM818 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM818 target proteins.

[12900] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM818 gene, herein designated GAM GENE, on one or

more GAM818 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12901] It is yet further appreciated that specific functions, and accordingly utilities, of GAM818 correlate with, and may be deduced from, the identity of the target genes which GAM818 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12902] Nucleotide sequences of the GAM818 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM818 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM818 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM818 are further de-

scribed hereinbelow with reference to Table Table1.

[12903] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM818 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12904] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 819 (GAM819) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12905] GAM819 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM819 was detected is described hereinabove with reference to Figs. 2-8.

[12906] GAM819 gene, herein designated GAM GENE, and GAM819 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12907] GAM819 gene, herein designated GAM GENE, encodes a GAM819 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM819 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM819 precursor RNA is designated SEQ ID:792, and is provided hereinbelow with reference to the sequence listing part.

[12908] GAM819 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM819 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12909] An enzyme complex designated DICER COMPLEX, dices the GAM819 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM819 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM819 RNA is designated SEQ ID:2468, and is provided hereinbelow with reference to the sequence listing part.

[12910] GAM819 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM819 target RNA, herein designated GAM TARGET RNA. GAM819 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12911] GAM819 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM819 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM819 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM819 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM819 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12912] The complementary binding of GAM819 RNA, herein designated GAM RNA, to target binding sites on GAM819 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM819 target RNA, herein designated GAM TARGET RNA, into GAM819 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12913] It is appreciated that GAM819 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM819 target genes. The mRNA of each one of this plurality of GAM819 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM819 RNA,

herein designated GAM RNA, and which when bound by GAM819 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM819 target proteins.

[12914] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM819 gene, herein designated GAM GENE, on one or more GAM819 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12915] It is yet further appreciated that specific functions, and accordingly utilities, of GAM819 correlate with, and may be deduced from, the identity of the target genes which

GAM819 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12916] Nucleotide sequences of the GAM819 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM819 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM819 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM819 are further described hereinbelow with reference to Table Table1.

[12917] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM819 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12918] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 820 (GAM820) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12919] GAM820 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM820 was detected is described hereinabove with reference to Figs. 2-8.

[12920] GAM820 gene, herein designated GAM GENE, and GAM820 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12921] GAM820 gene, herein designated GAM GENE, encodes a GAM820 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM820 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM820 precursor RNA is designated SEQ ID:793, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:793 is located at position 3263793 relative to contig NT_028392.4, on chromosome 20.

[12922] GAM820 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12923] An enzyme complex designated DICER COMPLEX, dices the GAM820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM820 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM820 RNA is designated SEQ ID:2469, and is provided hereinbelow with reference to the sequence listing part.

[12924] GAM820 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM820 target RNA, herein designated GAM TARGET RNA. GAM820 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12925] GAM820 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM820 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM820 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM820 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM820 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12926] The complementary binding of GAM820 RNA, herein designated GAM RNA, to target binding sites on GAM820 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM820 target RNA, herein designated GAM TARGET RNA, into GAM820 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12927] It is appreciated that GAM820 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM820 target genes. The mRNA of each one of this plurality of GAM820 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM820 RNA, herein designated GAM RNA, and which when bound by GAM820 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM820 target proteins.

[12928] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM820 gene, herein designated GAM GENE, on one or more GAM820 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12929] It is yet further appreciated that specific functions, and accordingly utilities, of GAM820 correlate with, and may be deduced from, the identity of the target genes which GAM820 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12930] Nucleotide sequences of the GAM820 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM820 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM820 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM820 are further described hereinbelow with reference to Table Table1.

[12931] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM820 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12932] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 821 (GAM821) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12933] GAM821 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM821 was detected is described hereinabove with reference to Figs. 2-8.

[12934] GAM821 gene, herein designated GAM GENE, and GAM821 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12935] GAM821 gene, herein designated GAM GENE, encodes a GAM821 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM821 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM821 precursor RNA is designated SEQ ID:794, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:794 is located at position 25819165 relative to contig NT_007933.10, on chromosome 7.

[12936] GAM821 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12937] An enzyme complex designated DICER COMPLEX, dices the GAM821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM821 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM821 RNA is designated SEQ ID:2470, and is provided

hereinbelow with reference to the sequence listing part.

[12938] GAM821 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM821 target RNA, herein designated GAM TARGET RNA.

GAM821 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12939] GAM821 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM821 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM821 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM821 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM821 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12940] The complementary binding of GAM821 RNA, herein designated GAM RNA, to target binding sites on GAM821 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM821 target RNA, herein designated GAM TARGET RNA, into GAM821 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12941] It is appreciated that GAM821 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM821 target genes. The mRNA of each one of this plurality of GAM821 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM821 RNA, herein designated GAM RNA, and which when bound by GAM821 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM821 tar-

get proteins.

[12942] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM821 gene, herein designated GAM GENE, on one or more GAM821 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12943] It is yet further appreciated that specific functions, and accordingly utilities, of GAM821 correlate with, and may be deduced from, the identity of the target genes which GAM821 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12944] Nucleotide sequences of the GAM821 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM821 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM821 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM821 are further described hereinbelow with reference to Table Table1.

[12945] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM821 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12946] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 822 (GAM822) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12947] GAM822 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM822 was detected is described hereinabove with reference to Figs. 2-8.

[12948] GAM822 gene, herein designated GAM GENE, and

GAM822 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12949] GAM822 gene, herein designated GAM GENE, encodes a GAM822 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM822 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM822 precursor RNA is designated SEQ ID:795, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:795 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[12950] GAM822 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM822 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12951] An enzyme complex designated DICER COMPLEX, dices the GAM822 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM822 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM822 RNA is designated SEQ ID:2471, and is provided hereinbelow with reference to the sequence listing part.

[12952] GAM822 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM822 target RNA, herein designated GAM TARGET RNA. GAM822 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12953] GAM822 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM822 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM822 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM822 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM822 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12954] The complementary binding of GAM822 RNA, herein designated GAM RNA, to target binding sites on GAM822 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM822 target RNA, herein designated GAM TARGET RNA, into GAM822 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[12955] It is appreciated that GAM822 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM822 target genes. The mRNA of each one of this plurality of GAM822 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM822 RNA, herein designated GAM RNA, and which when bound by GAM822 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM822 target proteins.

[12956] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM822 gene, herein designated GAM GENE, on one or more GAM822 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12957] It is yet further appreciated that specific functions, and accordingly utilities, of GAM822 correlate with, and may be deduced from, the identity of the target genes which GAM822 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12958] Nucleotide sequences of the GAM822 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM822 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM822 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM822 are further described hereinbelow with reference to Table Table1.

[12959] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM822 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12960] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 823 (GAM823) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12961] GAM823 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM823 was detected is described hereinabove with reference to Figs. 2-8.

[12962] GAM823 gene, herein designated GAM GENE, and GAM823 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12963] GAM823 gene, herein designated GAM GENE, encodes a GAM823 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM823 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM823 precursor RNA is designated SEQ ID:796, and is provided hereinbelow with reference to the sequence listing part.

[12964] GAM823 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM823 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12965] An enzyme complex designated DICER COMPLEX, dices the GAM823 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM823 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM823 RNA is designated SEQ ID:2472, and is provided hereinbelow with reference to the sequence listing part.

[12966] GAM823 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM823 target RNA, herein designated GAM TARGET RNA. GAM823 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12967] GAM823 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM823 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM823 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM823 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM823 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[12968] The complementary binding of GAM823 RNA, herein designated GAM RNA, to target binding sites on GAM823 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM823 target RNA, herein designated GAM TARGET RNA, into GAM823 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12969] It is appreciated that GAM823 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM823 target genes. The mRNA of each one of this plurality of GAM823 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM823 RNA, herein designated GAM RNA, and which when bound by GAM823 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM823 target proteins.

[12970] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM823 gene, herein designated GAM GENE, on one or

more GAM823 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12971] It is yet further appreciated that specific functions, and accordingly utilities, of GAM823 correlate with, and may be deduced from, the identity of the target genes which GAM823 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12972] Nucleotide sequences of the GAM823 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM823 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM823 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM823 are further de-

scribed hereinbelow with reference to Table Table1.

[12973] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM823 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12974] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 824 (GAM824) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12975] GAM824 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM824 was detected is described hereinabove with reference to Figs. 2-8.

[12976] GAM824 gene, herein designated GAM GENE, and GAM824 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12977] GAM824 gene, herein designated GAM GENE, encodes a GAM824 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM824 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM824 precursor RNA is designated SEQ ID:797, and is provided hereinbelow with reference to the sequence listing part.

[12978] GAM824 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM824 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[12979] An enzyme complex designated DICER COMPLEX, dices the GAM824 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM824 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM824 RNA is designated SEQ ID:2473, and is provided hereinbelow with reference to the sequence listing part.

[12980] GAM824 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM824 target RNA, herein designated GAM TARGET RNA. GAM824 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[12981] GAM824 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM824 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM824 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM824 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM824 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[12982] The complementary binding of GAM824 RNA, herein designated GAM RNA, to target binding sites on GAM824 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM824 target RNA, herein designated GAM TARGET RNA, into GAM824 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[12983] It is appreciated that GAM824 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM824 target genes. The mRNA of each one of this plurality of GAM824 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM824 RNA,

herein designated GAM RNA, and which when bound by GAM824 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM824 target proteins.

[12984] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM824 gene, herein designated GAM GENE, on one or more GAM824 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[12985] It is yet further appreciated that specific functions, and accordingly utilities, of GAM824 correlate with, and may be deduced from, the identity of the target genes which

GAM824 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[12986] Nucleotide sequences of the GAM824 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM824 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM824 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM824 are further described hereinbelow with reference to Table Table1.

[12987] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM824 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[12988] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 825 (GAM825) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[12989] GAM825 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM825 was detected is described hereinabove with reference to Figs. 2-8.

[12990] GAM825 gene, herein designated GAM GENE, and GAM825 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[12991] GAM825 gene, herein designated GAM GENE, encodes a GAM825 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM825 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM825 precursor RNA is designated SEQ ID:798, and is provided hereinbelow with reference to the sequence listing part.

[12992] GAM825 has 48 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[12993] SEQ ID:99397 detected in mouse EST Accession AA517267.1.

[12994] SEQ ID:99398 detected in mouse EST Accession BF730308.1.

[12995] SEQ ID:99399 detected in mouse EST Accession AW488637.1.

[12996] SEQ ID:99400 detected in mouse EST Accession AA681088.1.

[12997] SEQ ID:99401 detected in mouse EST Accession BE689804.1.

[12998] SEQ ID:99402 detected in mouse EST Accession AA397244.1.

[12999] SEQ ID:99403 detected in mouse EST Accession AA142786.1.

[13000] SEQ ID:99404 detected in mouse EST Accession AA770810.1.

[13001] SEQ ID:99405 detected in mouse EST Accession AI788525.1.

[13002] SEQ ID:99406 detected in mouse EST Accession AA590571.1.

[13003] SEQ ID:99407 detected in mouse EST Accession AA870305.1.

[13004] SEQ ID:99408 detected in mouse EST Accession BF788679.1.

[13005] SEQ ID:99409 detected in mouse EST Accession AA086955.1.

[13006] SEQ ID:99410 detected in mouse EST Accession

AA771187.1.

[13007] SEQ ID:99411 detected in mouse EST Accession BG145851.1.

[13008] SEQ ID:99412 detected in mouse EST Accession AA691443.1.

[13009] SEQ ID:99413 detected in mouse EST Accession BG090143.1.

[13010] SEQ ID:99414 detected in mouse EST Accession AA221182.1.

[13011] SEQ ID:99418 detected in mouse EST Accession AA895720.1.

[13012] SEQ ID:99419 detected in mouse EST Accession BE626527.1.

[13013] SEQ ID:99420 detected in mouse EST Accession BI714485.1.

[13014] SEQ ID:99421 detected in mouse EST Accession AI390190.1.

[13015] SEQ ID:99422 detected in mouse EST Accession AA272020.1.

[13016] SEQ ID:99423 detected in mouse EST Accession AA123201.1.

[13017] SEQ ID:99424 detected in mouse EST Accession AW551233.1.

[13018] SEQ ID:99425 detected in mouse EST Accession BE134018.1.

[13019] SEQ ID:99426 detected in mouse EST Accession AA396997.1.

[13020] SEQ ID:99427 detected in mouse EST Accession AA547023.1.

[13021] SEQ ID:99428 detected in mouse EST Accession AA238167.1.

[13022] SEQ ID:99429 detected in mouse EST Accession BG073645.1.

[13023] SEQ ID:99430 detected in mouse EST Accession BE198361.1.

[13024] SEQ ID:99431 detected in mouse EST Accession BF467940.1.

[13025] SEQ ID:99432 detected in mouse EST Accession BE134116.1.

[13026] SEQ ID:99433 detected in mouse EST Accession BG695432.1.

[13027] SEQ ID:99434 detected in mouse EST Accession BG870423.1.

[13028] SEQ ID:99435 detected in mouse EST Accession AA869587.1.

[13029] SEQ ID:99436 detected in mouse EST Accession

BE623908.1.

[13030] SEQ ID:99437 detected in mouse EST Accession AA672838.1.

[13031] SEQ ID:99438 detected in mouse EST Accession AA624895.1.

[13032] SEQ ID:99439 detected in mouse EST Accession BB624139.1.

[13033] SEQ ID:99440 detected in mouse EST Accession BE951532.1.

[13034] SEQ ID:99441 detected in mouse EST Accession BI650479.1.

[13035] SEQ ID:99442 detected in mouse EST Accession BE367851.1.

[13036] SEQ ID:99443 detected in mouse EST Accession AA691295.1.

[13037] SEQ ID:99444 detected in mouse EST Accession AW491159.1.

[13038] SEQ ID:99447 detected in mouse EST Accession BG276809.1.

[13039] SEQ ID:99448 detected in mouse EST Accession BF135327.1.

[13040] SEQ ID:99449 detected in mouse EST Accession AA118820.1.

[13041] GAM825 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM825 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13042] An enzyme complex designated DICER COMPLEX, dices the GAM825 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM825 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM825 RNA is designated SEQ ID:2474, and is provided hereinbelow with reference to the sequence listing part.

[13043] GAM825 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM825

target RNA, herein designated GAM TARGET RNA.

GAM825 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13044] GAM825 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM825 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM825 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM825 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM825 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13045] The complementary binding of GAM825 RNA, herein designated GAM RNA, to target binding sites on GAM825 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM825 target RNA, herein designated GAM TARGET RNA, into GAM825 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13046] It is appreciated that GAM825 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM825 target genes. The mRNA of each one of this plurality of GAM825 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM825 RNA, herein designated GAM RNA, and which when bound by GAM825 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM825 target proteins.

[13047] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM825 gene, herein designated GAM GENE, on one or more GAM825 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13048] It is yet further appreciated that specific functions, and accordingly utilities, of GAM825 correlate with, and may be deduced from, the identity of the target genes which GAM825 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13049] Nucleotide sequences of the GAM825 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM825 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM825 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM825 are further described hereinbelow with reference to Table Table1.

[13050] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM825 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13051] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 826 (GAM826) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13052] GAM826 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM826 was detected is described hereinabove with reference to Figs. 2-8.

[13053] GAM826 gene, herein designated GAM GENE, and GAM826 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13054] GAM826 gene, herein designated GAM GENE, encodes a

GAM826 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM826 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM826 precursor RNA is designated SEQ ID:799, and is provided hereinbelow with reference to the sequence listing part.

[13055] GAM826 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM826 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13056] An enzyme complex designated DICER COMPLEX, dices the GAM826 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM826 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM826 RNA is designated SEQ ID:2475, and is provided hereinbelow with reference to the sequence listing part.

[13057] GAM826 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM826 target RNA, herein designated GAM TARGET RNA. GAM826 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13058] GAM826 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM826 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM826 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM826 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM826 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13059] The complementary binding of GAM826 RNA, herein designated GAM RNA, to target binding sites on GAM826 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM826 target RNA, herein designated GAM TARGET RNA, into GAM826 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13060] It is appreciated that GAM826 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM826 target genes. The mRNA of each one of this plurality of GAM826 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM826 RNA, herein designated GAM RNA, and which when bound by GAM826 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM826 target proteins.

[13061] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM826 gene, herein designated GAM GENE, on one or more GAM826 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13062] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM826 correlate with, and may be deduced from, the identity of the target genes which GAM826 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13063] Nucleotide sequences of the GAM826 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM826 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM826 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM826 are further described hereinbelow with reference to Table Table1.

[13064] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM826 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13065] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 827 (GAM827) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13066] GAM827 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM827 was detected is described hereinabove with reference to Figs. 2-8.

[13067] GAM827 gene, herein designated GAM GENE, and GAM827 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13068] GAM827 gene, herein designated GAM GENE, encodes a GAM827 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM827 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM827 precursor RNA is designated SEQ ID:800, and is provided hereinbelow with reference to the sequence listing part.

[13069] GAM827 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98325, which mouse homolog is detected in mouse EST accession BG916606.1.

[13070] GAM827 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM827 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13071] An enzyme complex designated DICER COMPLEX, dices the GAM827 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM827 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM827 RNA is designated SEQ ID:2476, and is provided hereinbelow with reference to the sequence listing part.

[13072] GAM827 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM827 target RNA, herein designated GAM TARGET RNA. GAM827 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13073] GAM827 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM827 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM827 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM827 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM827 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[13074] The complementary binding of GAM827 RNA, herein designated GAM RNA, to target binding sites on GAM827 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM827 target RNA, herein designated GAM TARGET RNA, into GAM827 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13075] It is appreciated that GAM827 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM827 target genes. The mRNA of each one of this plurality of GAM827 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM827 RNA, herein designated GAM RNA, and which when bound by GAM827 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM827 target proteins.

[13076] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM827 gene, herein designated GAM GENE, on one or

more GAM827 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13077] It is yet further appreciated that specific functions, and accordingly utilities, of GAM827 correlate with, and may be deduced from, the identity of the target genes which GAM827 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13078] Nucleotide sequences of the GAM827 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM827 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM827 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM827 are further de-

scribed hereinbelow with reference to Table Table1.

[13079] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM827 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13080] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 828 (GAM828) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13081] GAM828 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM828 was detected is described hereinabove with reference to Figs. 2-8.

[13082] GAM828 gene, herein designated GAM GENE, and GAM828 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13083] GAM828 gene, herein designated GAM GENE, encodes a GAM828 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM828 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM828 precursor RNA is designated SEQ ID:801, and is provided hereinbelow with reference to the sequence listing part.

[13084] GAM828 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13085] An enzyme complex designated DICER COMPLEX, dices the GAM828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM828 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM828 RNA is designated SEQ ID:2477, and is provided hereinbelow with reference to the sequence listing part.

[13086] GAM828 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM828 target RNA, herein designated GAM TARGET RNA. GAM828 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13087] GAM828 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM828 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM828 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM828 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM828 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13088] The complementary binding of GAM828 RNA, herein designated GAM RNA, to target binding sites on GAM828 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM828 target RNA, herein designated GAM TARGET RNA, into GAM828 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13089] It is appreciated that GAM828 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM828 target genes. The mRNA of each one of this plurality of GAM828 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM828 RNA,

herein designated GAM RNA, and which when bound by GAM828 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM828 target proteins.

[13090] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM828 gene, herein designated GAM GENE, on one or more GAM828 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13091] It is yet further appreciated that specific functions, and accordingly utilities, of GAM828 correlate with, and may be deduced from, the identity of the target genes which

GAM828 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13092] Nucleotide sequences of the GAM828 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM828 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM828 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM828 are further described hereinbelow with reference to Table Table1.

[13093] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM828 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13094] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 829 (GAM829) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13095] GAM829 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM829 was detected is described hereinabove with reference to Figs. 2-8.

[13096] GAM829 gene, herein designated GAM GENE, and GAM829 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13097] GAM829 gene, herein designated GAM GENE, encodes a GAM829 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM829 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM829 precursor RNA is designated SEQ ID:802, and is provided hereinbelow with reference to the sequence listing part.

[13098] GAM829 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM829 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[13099] An enzyme complex designated DICER COMPLEX, dices the GAM829 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM829 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM829 RNA is designated SEQ ID:2478, and is provided hereinbelow with reference to the sequence listing part.

[13100] GAM829 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM829 target RNA, herein designated GAM TARGET RNA. GAM829 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13101] GAM829 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM829 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM829 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM829 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM829 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13102] The complementary binding of GAM829 RNA, herein designated GAM RNA, to target binding sites on GAM829 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM829 target RNA, herein designated GAM TARGET RNA, into GAM829 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13103] It is appreciated that GAM829 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM829 target genes. The mRNA of each one of this plurality of GAM829 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM829 RNA, herein designated GAM RNA, and which when bound by GAM829 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM829 target proteins.

[13104] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM829 gene, herein designated GAM GENE, on one or more GAM829 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13105] It is yet further appreciated that specific functions, and accordingly utilities, of GAM829 correlate with, and may be deduced from, the identity of the target genes which GAM829 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13106] Nucleotide sequences of the GAM829 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM829 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM829 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM829 are further described hereinbelow with reference to Table Table1.

[13107] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM829 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13108] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 830 (GAM830) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13109] GAM830 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM830 was detected is described hereinabove with reference to Figs. 2-8.

[13110] GAM830 gene, herein designated GAM GENE, and GAM830 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13111] GAM830 gene, herein designated GAM GENE, encodes a GAM830 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM830 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM830 precursor RNA is designated SEQ ID:803, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:803 is located at position 7678827 relative to con-

tig NT_004852.13, on chromosome 1.

[13112] GAM830 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM830 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13113] An enzyme complex designated DICER COMPLEX, dices the GAM830 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM830 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM830 RNA is designated SEQ ID:2479, and is provided hereinbelow with reference to the sequence listing part.

[13114] GAM830 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM830 target RNA, herein designated GAM TARGET RNA.

GAM830 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13115] GAM830 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM830 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM830 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM830 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM830 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13116] The complementary binding of GAM830 RNA, herein designated GAM RNA, to target binding sites on GAM830 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM830 target RNA, herein designated GAM TARGET RNA, into GAM830 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13117] It is appreciated that GAM830 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM830 target genes. The mRNA of each one of this plurality of GAM830 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM830 RNA, herein designated GAM RNA, and which when bound by GAM830 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM830 target proteins.

[13118] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM830 gene, herein designated GAM GENE, on one or more GAM830 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13119] It is yet further appreciated that specific functions, and accordingly utilities, of GAM830 correlate with, and may be deduced from, the identity of the target genes which GAM830 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13120] Nucleotide sequences of the GAM830 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM830 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM830 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM830 are further described hereinbelow with reference to Table Table1.

[13121] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM830 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13122] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 831 (GAM831) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13123] GAM831 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM831 was detected is described hereinabove with reference to Figs. 2-8.

[13124] GAM831 gene, herein designated GAM GENE, and GAM831 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13125] GAM831 gene, herein designated GAM GENE, encodes a GAM831 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM831 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM831 precursor RNA is designated SEQ ID:804, and is provided hereinbelow with reference to the sequence listing part.

[13126] GAM831 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM831 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13127] An enzyme complex designated DICER COMPLEX, dices the GAM831 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM831 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM831 RNA is designated SEQ ID:2480, and is provided hereinbelow with reference to the sequence listing part.

[13128] GAM831 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM831 target RNA, herein designated GAM TARGET RNA. GAM831 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13129] GAM831 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM831 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM831 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM831 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM831 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13130] The complementary binding of GAM831 RNA, herein designated GAM RNA, to target binding sites on GAM831 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM831 target RNA, herein designated GAM TARGET RNA, into GAM831 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13131] It is appreciated that GAM831 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM831 target genes. The mRNA of each one of this plu-

rality of GAM831 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM831 RNA, herein designated GAM RNA, and which when bound by GAM831 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM831 target proteins.

[13132] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM831 gene, herein designated GAM GENE, on one or more GAM831 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13133] It is yet further appreciated that specific functions, and accordingly utilities, of GAM831 correlate with, and may be deduced from, the identity of the target genes which GAM831 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13134] Nucleotide sequences of the GAM831 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM831 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM831 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM831 are further described hereinbelow with reference to Table Table1.

[13135] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM831 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13136] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 832 (GAM832) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[13137] GAM832 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM832 was detected is described hereinabove with reference to Figs. 2-8.

[13138] GAM832 gene, herein designated GAM GENE, and GAM832 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13139] GAM832 gene, herein designated GAM GENE, encodes a GAM832 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM832 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM832 precursor RNA is designated SEQ ID:805, and is provided hereinbelow with reference to the sequence listing part.

[13140] GAM832 has 46 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[13141] SEQ ID:98326 detected in mouse EST Accession

AA517267.1.

[13142] SEQ ID:98327 detected in mouse EST Accession BF730308.1.

[13143] SEQ ID:98328 detected in mouse EST Accession AW488637.1.

[13144] SEQ ID:98329 detected in mouse EST Accession AA681088.1.

[13145] SEQ ID:98330 detected in mouse EST Accession BE689804.1.

[13146] SEQ ID:98331 detected in mouse EST Accession AA397244.1.

[13147] SEQ ID:98332 detected in mouse EST Accession AA770810.1.

[13148] SEQ ID:98333 detected in mouse EST Accession AA142786.1.

[13149] SEQ ID:98334 detected in mouse EST Accession AA895720.1.

[13150] SEQ ID:98335 detected in mouse EST Accession AA086955.1.

[13151] SEQ ID:98336 detected in mouse EST Accession AA771187.1.

[13152] SEQ ID:98337 detected in mouse EST Accession BG145851.1.

[13153] SEQ ID:98338 detected in mouse EST Accession BG090143.1.

[13154] SEQ ID:98339 detected in mouse EST Accession AA221182.1.

[13155] SEQ ID:98340 detected in mouse EST Accession BE623908.1.

[13156] SEQ ID:98341 detected in mouse EST Accession AA672838.1.

[13157] SEQ ID:98342 detected in mouse EST Accession AA624895.1.

[13158] SEQ ID:98343 detected in mouse EST Accession AI390190.1.

[13159] SEQ ID:98344 detected in mouse EST Accession AA272020.1.

[13160] SEQ ID:98345 detected in mouse EST Accession AI788525.1.

[13161] SEQ ID:98346 detected in mouse EST Accession AA590571.1.

[13162] SEQ ID:98347 detected in mouse EST Accession AA870305.1.

[13163] SEQ ID:98348 detected in mouse EST Accession BF788679.1.

[13164] SEQ ID:98349 detected in mouse EST Accession

AA691443.1.

[13165] SEQ ID:98350 detected in mouse EST Accession BE626527.1.

[13166] SEQ ID:98351 detected in mouse EST Accession BI714485.1.

[13167] SEQ ID:98352 detected in mouse EST Accession AA123201.1.

[13168] SEQ ID:98353 detected in mouse EST Accession AA396997.1.

[13169] SEQ ID:98354 detected in mouse EST Accession AW551233.1.

[13170] SEQ ID:98355 detected in mouse EST Accession BE134018.1.

[13171] SEQ ID:98356 detected in mouse EST Accession BE198361.1.

[13172] SEQ ID:98357 detected in mouse EST Accession BE134116.1.

[13173] SEQ ID:98358 detected in mouse EST Accession BG695432.1.

[13174] SEQ ID:98359 detected in mouse EST Accession BE951532.1.

[13175] SEQ ID:98360 detected in mouse EST Accession BI650479.1.

[13176] SEQ ID:98361 detected in mouse EST Accession AA691295.1.

[13177] SEQ ID:98362 detected in mouse EST Accession AA547023.1.

[13178] SEQ ID:98363 detected in mouse EST Accession AA238167.1.

[13179] SEQ ID:98364 detected in mouse EST Accession BG073645.1.

[13180] SEQ ID:98365 detected in mouse EST Accession BB624139.1.

[13181] SEQ ID:98366 detected in mouse EST Accession AA118820.1.

[13182] SEQ ID:98367 detected in mouse EST Accession BG276809.1.

[13183] SEQ ID:98368 detected in mouse EST Accession BF467940.1.

[13184] SEQ ID:98369 detected in mouse EST Accession BG870423.1.

[13185] SEQ ID:98370 detected in mouse EST Accession AA869587.1.

[13186] SEQ ID:98371 detected in mouse EST Accession AW491159.1.

[13187] GAM832 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM832 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13188] An enzyme complex designated DICER COMPLEX, dices the GAM832 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM832 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM832 RNA is designated SEQ ID:2481, and is provided hereinbelow with reference to the sequence listing part.

[13189] GAM832 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM832 target RNA, herein designated GAM TARGET RNA.

GAM832 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13190] GAM832 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM832 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM832 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM832 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM832 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13191] The complementary binding of GAM832 RNA, herein designated GAM RNA, to target binding sites on GAM832 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM832 target RNA, herein designated GAM TARGET RNA, into GAM832 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13192] It is appreciated that GAM832 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM832 target genes. The mRNA of each one of this plurality of GAM832 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM832 RNA, herein designated GAM RNA, and which when bound by GAM832 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM832 target proteins.

[13193] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM832 gene, herein designated GAM GENE, on one or more GAM832 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13194] It is yet further appreciated that specific functions, and accordingly utilities, of GAM832 correlate with, and may be deduced from, the identity of the target genes which GAM832 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13195] Nucleotide sequences of the GAM832 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM832 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM832 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM832 are further described hereinbelow with reference to Table Table1.

[13196] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM832 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13197] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 833 (GAM833) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13198] GAM833 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM833 was detected is described hereinabove with reference to Figs. 2-8.

[13199] GAM833 gene, herein designated GAM GENE, and GAM833 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13200] GAM833 gene, herein designated GAM GENE, encodes a GAM833 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM833 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM833 precursor RNA is designated SEQ ID:806, and is provided hereinbelow with reference to the sequence listing part.

[13201] GAM833 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM833 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13202] An enzyme complex designated DICER COMPLEX, dices the GAM833 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM833 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM833 RNA is designated SEQ ID:2482, and is provided hereinbelow with reference to the sequence listing part.

[13203] GAM833 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM833 target RNA, herein designated GAM TARGET RNA. GAM833 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13204] GAM833 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM833 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM833 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM833 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM833 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13205] The complementary binding of GAM833 RNA, herein designated GAM RNA, to target binding sites on GAM833 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM833 target RNA, herein designated GAM TARGET RNA, into GAM833 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13206] It is appreciated that GAM833 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM833 target genes. The mRNA of each one of this plurality of GAM833 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM833 RNA, herein designated GAM RNA, and which when bound by GAM833 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM833 target proteins.

[13207] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM833 gene, herein designated GAM GENE, on one or more GAM833 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13208] It is yet further appreciated that specific functions, and accordingly utilities, of GAM833 correlate with, and may

be deduced from, the identity of the target genes which GAM833 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13209] Nucleotide sequences of the GAM833 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM833 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM833 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM833 are further described hereinbelow with reference to Table Table1.

[13210] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM833 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13211] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 834 (GAM834) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13212] GAM834 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM834 was detected is described hereinabove with reference to Figs. 2-8.

[13213] GAM834 gene, herein designated GAM GENE, and GAM834 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13214] GAM834 gene, herein designated GAM GENE, encodes a GAM834 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM834 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM834 precursor RNA is designated SEQ ID:807, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:807 is located at position 48498830 relative to contig NT_007933.10, on chromosome 7.

[13215] GAM834 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13216] An enzyme complex designated DICER COMPLEX, dices the GAM834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM834 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM834 RNA is designated SEQ ID:2483, and is provided hereinbelow with reference to the sequence listing part.

[13217] GAM834 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM834 target RNA, herein designated GAM TARGET RNA. GAM834 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13218] GAM834 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM834 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM834 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM834 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM834 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13219] The complementary binding of GAM834 RNA, herein designated GAM RNA, to target binding sites on GAM834 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM834 target RNA, herein designated GAM TARGET RNA, into GAM834 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13220] It is appreciated that GAM834 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM834 target genes. The mRNA of each one of this plurality of GAM834 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM834 RNA, herein designated GAM RNA, and which when bound by GAM834 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM834 target proteins.

[13221] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM834 gene, herein designated GAM GENE, on one or more GAM834 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13222] It is yet further appreciated that specific functions, and accordingly utilities, of GAM834 correlate with, and may be deduced from, the identity of the target genes which GAM834 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13223] Nucleotide sequences of the GAM834 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM834 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM834 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM834 are further described hereinbelow with reference to Table Table1.

[13224] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM834 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13225] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 835 (GAM835) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13226] GAM835 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM835 was detected is described hereinabove with reference to Figs. 2-8.

[13227] GAM835 gene, herein designated GAM GENE, and GAM835 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13228] GAM835 gene, herein designated GAM GENE, encodes a GAM835 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM835 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM835 precursor RNA is desig-

nated SEQ ID:808, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:808 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[13229] GAM835 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13230] An enzyme complex designated DICER COMPLEX, dices the GAM835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM835 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM835 RNA is designated SEQ ID:2484, and is provided hereinbelow with reference to the sequence listing part.

[13231] GAM835 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM835 target RNA, herein designated GAM TARGET RNA.

GAM835 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13232] GAM835 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM835 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM835 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM835 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM835 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13233] The complementary binding of GAM835 RNA, herein designated GAM RNA, to target binding sites on GAM835 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM835 target RNA, herein designated GAM TARGET RNA, into GAM835 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13234] It is appreciated that GAM835 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM835 target genes. The mRNA of each one of this plurality of GAM835 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM835 RNA, herein designated GAM RNA, and which when bound by GAM835 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM835 target proteins.

[13235] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM835 gene, herein designated GAM GENE, on one or more GAM835 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13236] It is yet further appreciated that specific functions, and accordingly utilities, of GAM835 correlate with, and may be deduced from, the identity of the target genes which GAM835 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13237] Nucleotide sequences of the GAM835 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM835 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM835 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM835 are further described hereinbelow with reference to Table Table1.

[13238] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM835 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13239] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 836 (GAM836) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13240] GAM836 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM836 was detected is described hereinabove with reference to Figs. 2-8.

[13241] GAM836 gene, herein designated GAM GENE, and GAM836 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13242] GAM836 gene, herein designated GAM GENE, encodes a GAM836 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM836 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM836 precursor RNA is designated SEQ ID:809, and is provided hereinbelow with reference to the sequence listing part.

[13243] GAM836 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13244] An enzyme complex designated DICER COMPLEX, dices

the GAM836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM836 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM836 RNA is designated SEQ ID:2485, and is provided hereinbelow with reference to the sequence listing part.

[13245] GAM836 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM836 target RNA, herein designated GAM TARGET RNA. GAM836 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13246] GAM836 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM836 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM836

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM836 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM836 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13247] The complementary binding of GAM836 RNA, herein designated GAM RNA, to target binding sites on GAM836 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM836 target RNA, herein designated GAM TARGET RNA, into GAM836 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13248] It is appreciated that GAM836 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM836 target genes. The mRNA of each one of this plurality of GAM836 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM836 RNA, herein designated GAM RNA, and which when bound by GAM836 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM836 target proteins.

[13249] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM836 gene, herein designated GAM GENE, on one or more GAM836 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13250] It is yet further appreciated that specific functions, and accordingly utilities, of GAM836 correlate with, and may be deduced from, the identity of the target genes which GAM836 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13251] Nucleotide sequences of the GAM836 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM836 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM836 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM836 are further described hereinbelow with reference to Table Table1.

[13252] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM836 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13253] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 837 (GAM837) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13254] GAM837 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM837 was detected is described hereinabove with reference to Figs. 2-8.

[13255] GAM837 gene, herein designated GAM GENE, and GAM837 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13256] GAM837 gene, herein designated GAM GENE, encodes a GAM837 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM837 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM837 precursor RNA is designated SEQ ID:810, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:810 is located at position 2349702 relative to contig NT_021907.13, on chromosome 1.

[13257] GAM837 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM837 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13258] An enzyme complex designated DICER COMPLEX, dices the GAM837 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM837 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM837 RNA is designated SEQ ID:2486, and is provided hereinbelow with reference to the sequence listing part.

[13259] GAM837 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM837 target RNA, herein designated GAM TARGET RNA.

GAM837 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13260] GAM837 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM837 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM837 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM837 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM837 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13261] The complementary binding of GAM837 RNA, herein designated GAM RNA, to target binding sites on GAM837 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM837 target RNA, herein designated GAM TARGET RNA, into GAM837 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13262] It is appreciated that GAM837 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM837 target genes. The mRNA of each one of this plurality of GAM837 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM837 RNA, herein designated GAM RNA, and which when bound by GAM837 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM837 target proteins.

[13263] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM837 gene, herein designated GAM GENE, on one or more GAM837 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13264] It is yet further appreciated that specific functions, and accordingly utilities, of GAM837 correlate with, and may be deduced from, the identity of the target genes which GAM837 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13265] Nucleotide sequences of the GAM837 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM837 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM837 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM837 are further described hereinbelow with reference to Table Table1.

[13266] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM837 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13267] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 838 (GAM838) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13268] GAM838 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM838 was detected is described hereinabove with reference to Figs. 2-8.

[13269] GAM838 gene, herein designated GAM GENE, and GAM838 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13270] GAM838 gene, herein designated GAM GENE, encodes a GAM838 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM838 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM838 precursor RNA is designated SEQ ID:811, and is provided hereinbelow with reference to the sequence listing part.

[13271] GAM838 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM838 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13272] An enzyme complex designated DICER COMPLEX, dices the GAM838 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM838 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM838 RNA is designated SEQ ID:2487, and is provided hereinbelow with reference to the sequence listing part.

[13273] GAM838 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM838 target RNA, herein designated GAM TARGET RNA. GAM838 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13274] GAM838 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM838 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM838 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM838 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM838 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13275] The complementary binding of GAM838 RNA, herein designated GAM RNA, to target binding sites on GAM838 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM838 target RNA, herein designated GAM TARGET RNA, into GAM838 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13276] It is appreciated that GAM838 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM838 target genes. The mRNA of each one of this plurality of GAM838 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM838 RNA, herein designated GAM RNA, and which when bound by GAM838 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM838 target proteins.

[13277] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM838 gene, herein designated GAM GENE, on one or more GAM838 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13278] It is yet further appreciated that specific functions, and accordingly utilities, of GAM838 correlate with, and may be deduced from, the identity of the target genes which GAM838 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13279] Nucleotide sequences of the GAM838 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM838 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM838 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM838 are further described hereinbelow with reference to Table Table1.

[13280] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM838 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13281] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 839 (GAM839) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13282] GAM839 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM839 was detected is described hereinabove with reference to Figs. 2-8.

[13283] GAM839 gene, herein designated GAM GENE, and GAM839 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13284] GAM839 gene, herein designated GAM GENE, encodes a GAM839 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM839 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM839 precursor RNA is desig-

nated SEQ ID:812, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:812 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[13285] GAM839 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM839 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13286] An enzyme complex designated DICER COMPLEX, dices the GAM839 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM839 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM839 RNA is designated SEQ ID:2488, and is provided hereinbelow with reference to the sequence listing part.

[13287] GAM839 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM839 target RNA, herein designated GAM TARGET RNA. GAM839 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13288] GAM839 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM839 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM839 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM839 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM839 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13289] The complementary binding of GAM839 RNA, herein designated GAM RNA, to target binding sites on GAM839 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM839 target RNA, herein designated GAM TARGET RNA, into GAM839 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13290] It is appreciated that GAM839 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM839 target genes. The mRNA of each one of this plurality of GAM839 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM839 RNA, herein designated GAM RNA, and which when bound by GAM839 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM839 target proteins.

[13291] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM839 gene, herein designated GAM GENE, on one or more GAM839 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13292] It is yet further appreciated that specific functions, and accordingly utilities, of GAM839 correlate with, and may be deduced from, the identity of the target genes which GAM839 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13293] Nucleotide sequences of the GAM839 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM839 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM839 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM839 are further described hereinbelow with reference to Table Table1.

[13294] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM839 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13295] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 840 (GAM840) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13296] GAM840 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM840 was detected is described hereinabove with reference to Figs. 2-8.

[13297] GAM840 gene, herein designated GAM GENE, and GAM840 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13298] GAM840 gene, herein designated GAM GENE, encodes a GAM840 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM840 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM840 precursor RNA is designated SEQ ID:813, and is provided hereinbelow with reference to the sequence listing part.

[13299] GAM840 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13300] An enzyme complex designated DICER COMPLEX, dices

the GAM840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM840 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM840 RNA is designated SEQ ID:2489, and is provided hereinbelow with reference to the sequence listing part.

[13301] GAM840 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM840 target RNA, herein designated GAM TARGET RNA. GAM840 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13302] GAM840 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM840 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM840

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM840 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM840 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13303] The complementary binding of GAM840 RNA, herein designated GAM RNA, to target binding sites on GAM840 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM840 target RNA, herein designated GAM TARGET RNA, into GAM840 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13304] It is appreciated that GAM840 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM840 target genes. The mRNA of each one of this plurality of GAM840 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM840 RNA, herein designated GAM RNA, and which when bound by GAM840 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM840 target proteins.

[13305] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM840 gene, herein designated GAM GENE, on one or more GAM840 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13306] It is yet further appreciated that specific functions, and accordingly utilities, of GAM840 correlate with, and may be deduced from, the identity of the target genes which GAM840 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13307] Nucleotide sequences of the GAM840 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM840 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM840 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM840 are further described hereinbelow with reference to Table Table1.

[13308] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM840 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13309] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 841 (GAM841) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13310] GAM841 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM841 was detected is described hereinabove with reference to Figs. 2-8.

[13311] GAM841 gene, herein designated GAM GENE, and GAM841 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13312] GAM841 gene, herein designated GAM GENE, encodes a GAM841 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM841 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM841 precursor RNA is designated SEQ ID:814, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:814 is located at position 393991 relative to contig NT_010704.11, on chromosome 17.

[13313] GAM841 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM841 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13314] An enzyme complex designated DICER COMPLEX, dices the GAM841 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM841 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM841 RNA is designated SEQ ID:2490, and is provided hereinbelow with reference to the sequence listing part.

[13315] GAM841 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM841 target RNA, herein designated GAM TARGET RNA.

GAM841 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13316] GAM841 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM841 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM841 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM841 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM841 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13317] The complementary binding of GAM841 RNA, herein designated GAM RNA, to target binding sites on GAM841 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM841 target RNA, herein designated GAM TARGET RNA, into GAM841 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13318] It is appreciated that GAM841 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM841 target genes. The mRNA of each one of this plurality of GAM841 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM841 RNA, herein designated GAM RNA, and which when bound by GAM841 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM841 target proteins.

[13319] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM841 gene, herein designated GAM GENE, on one or more GAM841 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13320] It is yet further appreciated that specific functions, and accordingly utilities, of GAM841 correlate with, and may be deduced from, the identity of the target genes which GAM841 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13321] Nucleotide sequences of the GAM841 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM841 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM841 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM841 are further described hereinbelow with reference to Table Table1.

[13322] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM841 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13323] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 842 (GAM842) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13324] GAM842 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM842 was detected is described hereinabove with reference to Figs. 2-8.

[13325] GAM842 gene, herein designated GAM GENE, and GAM842 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13326] GAM842 gene, herein designated GAM GENE, encodes a GAM842 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM842 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM842 precursor RNA is designated SEQ ID:815, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:815 is located at position 4665824 relative to contig NT_004852.13, on chromosome 1.

[13327] GAM842 has 17 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[13328] SEQ ID:98008 detected in mouse EST Accession AL364580.1.

[13329] SEQ ID:98009 detected in mouse EST Accession AA968124.1.

[13330] SEQ ID:98010 detected in mouse EST Accession AA670995.1.

[13331] SEQ ID:98011 detected in mouse EST Accession AI892667.1.

[13332] SEQ ID:98012 detected in mouse EST Accession

BE310323.1.

[13333] SEQ ID:98013 detected in mouse EST Accession W81953.1.

[13334] SEQ ID:98014 detected in mouse EST Accession AA168282.1.

[13335] SEQ ID:98015 detected in mouse EST Accession BI697701.1.

[13336] SEQ ID:98016 detected in mouse EST Accession BG863165.1.

[13337] SEQ ID:98017 detected in mouse EST Accession BG975985.1.

[13338] SEQ ID:98018 detected in mouse EST Accession BI650187.1.

[13339] SEQ ID:98019 detected in mouse EST Accession BI686558.1.

[13340] SEQ ID:98020 detected in mouse EST Accession BI646213.1.

[13341] SEQ ID:98021 detected in mouse EST Accession BI414768.1.

[13342] SEQ ID:98022 detected in mouse EST Accession BI408030.1.

[13343] SEQ ID:98023 detected in mouse EST Accession BF785049.1.

[13344] SEQ ID:98024 detected in mouse EST Accession BE913515.1.

[13345] GAM842 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13346] An enzyme complex designated DICER COMPLEX, dices the GAM842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM842 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM842 RNA is designated SEQ ID:2491, and is provided hereinbelow with reference to the sequence listing part.

[13347] GAM842 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM842 target RNA, herein designated GAM TARGET RNA. GAM842 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13348] GAM842 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM842 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM842 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM842 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM842

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13349] The complementary binding of GAM842 RNA, herein designated GAM RNA, to target binding sites on GAM842 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM842 target RNA, herein designated GAM TARGET RNA, into GAM842 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13350] It is appreciated that GAM842 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM842 target genes. The mRNA of each one of this plurality of GAM842 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM842 RNA, herein designated GAM RNA, and which when bound by GAM842 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM842 target proteins.

[13351] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM842 gene, herein designated GAM GENE, on one or more GAM842 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13352] It is yet further appreciated that specific functions, and accordingly utilities, of GAM842 correlate with, and may be deduced from, the identity of the target genes which GAM842 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13353] Nucleotide sequences of the GAM842 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM842 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM842 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM842 are further described hereinbelow with reference to Table Table1.

[13354] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM842 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13355] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 843 (GAM843) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13356] GAM843 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM843 was detected is described hereinabove with reference to Figs. 2-8.

[13357] GAM843 gene, herein designated GAM GENE, and GAM843 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[13358] GAM843 gene, herein designated GAM GENE, encodes a GAM843 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM843 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM843 precursor RNA is designated SEQ ID:816, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:816 is located at position 507121 relative to contig NT_011225.10, on chromosome 19.

[13359] GAM843 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM843 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13360] An enzyme complex designated DICER COMPLEX, dices

the GAM843 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM843 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM843 RNA is designated SEQ ID:2492, and is provided hereinbelow with reference to the sequence listing part.

[13361] GAM843 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM843 target RNA, herein designated GAM TARGET RNA.

GAM843 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13362] GAM843 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM843 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM843

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM843 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM843 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13363] The complementary binding of GAM843 RNA, herein designated GAM RNA, to target binding sites on GAM843 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM843 target RNA, herein designated GAM TARGET RNA, into GAM843 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13364] It is appreciated that GAM843 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM843 target genes. The mRNA of each one of this plurality of GAM843 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM843 RNA, herein designated GAM RNA, and which when bound by GAM843 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM843 target proteins.

[13365] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM843 gene, herein designated GAM GENE, on one or more GAM843 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13366] It is yet further appreciated that specific functions, and accordingly utilities, of GAM843 correlate with, and may be deduced from, the identity of the target genes which GAM843 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13367] Nucleotide sequences of the GAM843 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM843 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM843 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM843 are further described hereinbelow with reference to Table Table1.

[13368] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM843 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13369] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 844 (GAM844) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13370] GAM844 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM844 was detected is described hereinabove with reference to Figs. 2-8.

[13371] GAM844 gene, herein designated GAM GENE, and GAM844 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13372] GAM844 gene, herein designated GAM GENE, encodes a GAM844 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM844 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM844 precursor RNA is designated SEQ ID:817, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:817 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[13373] GAM844 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM844 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13374] An enzyme complex designated DICER COMPLEX, dices the GAM844 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM844 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM844 RNA is designated SEQ ID:2493, and is provided hereinbelow with reference to the sequence listing part.

[13375] GAM844 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM844 target RNA, herein designated GAM TARGET RNA.

GAM844 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13376] GAM844 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM844 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM844 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM844 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM844 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13377] The complementary binding of GAM844 RNA, herein designated GAM RNA, to target binding sites on GAM844 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM844 target RNA, herein designated GAM TARGET RNA, into GAM844 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13378] It is appreciated that GAM844 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM844 target genes. The mRNA of each one of this plurality of GAM844 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM844 RNA, herein designated GAM RNA, and which when bound by GAM844 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM844 target proteins.

[13379] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM844 gene, herein designated GAM GENE, on one or more GAM844 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13380] It is yet further appreciated that specific functions, and accordingly utilities, of GAM844 correlate with, and may be deduced from, the identity of the target genes which GAM844 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13381] Nucleotide sequences of the GAM844 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM844 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM844 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM844 are further described hereinbelow with reference to Table Table1.

[13382] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM844 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13383] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 845 (GAM845) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13384] GAM845 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM845 was detected is described hereinabove with reference to Figs. 2-8.

[13385] GAM845 gene, herein designated GAM GENE, and GAM845 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13386] GAM845 gene, herein designated GAM GENE, encodes a GAM845 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM845 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM845 precursor RNA is designated SEQ ID:818, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:818 is located at position 4421892 relative to contig NT_022155.11, on chromosome 2.

[13387] GAM845 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13388] An enzyme complex designated DICER COMPLEX, dices the GAM845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM845 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM845 RNA is designated SEQ ID:2494, and is provided hereinbelow with reference to the sequence listing part.

[13389] GAM845 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM845 target RNA, herein designated GAM TARGET RNA. GAM845 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13390] GAM845 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM845 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM845 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM845 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM845 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13391] The complementary binding of GAM845 RNA, herein designated GAM RNA, to target binding sites on GAM845 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM845 target RNA, herein designated GAM TARGET RNA, into GAM845 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13392] It is appreciated that GAM845 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM845 target genes. The mRNA of each one of this plu-

rality of GAM845 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM845 RNA, herein designated GAM RNA, and which when bound by GAM845 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM845 target proteins.

[13393] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM845 gene, herein designated GAM GENE, on one or more GAM845 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13394] It is yet further appreciated that specific functions, and accordingly utilities, of GAM845 correlate with, and may be deduced from, the identity of the target genes which GAM845 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13395] Nucleotide sequences of the GAM845 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM845 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM845 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM845 are further described hereinbelow with reference to Table Table1.

[13396] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM845 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13397] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 846 (GAM846) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[13398] GAM846 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM846 was detected is described hereinabove with reference to Figs. 2-8.

[13399] GAM846 gene, herein designated GAM GENE, and GAM846 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13400] GAM846 gene, herein designated GAM GENE, encodes a GAM846 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM846 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM846 precursor RNA is designated SEQ ID:819, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:819 is located at position 350283 relative to contig NT_030118.8, on chromosome 12.

[13401] GAM846 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99450, which mouse homolog is detected in

mouse EST accession AI326203.1.

[13402] GAM846 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13403] An enzyme complex designated DICER COMPLEX, dices the GAM846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM846 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM846 RNA is designated SEQ ID:2495, and is provided hereinbelow with reference to the sequence listing part.

[13404] GAM846 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM846 target RNA, herein designated GAM TARGET RNA.

GAM846 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13405] GAM846 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM846 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM846 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM846 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM846 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13406] The complementary binding of GAM846 RNA, herein designated GAM RNA, to target binding sites on GAM846 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM846 target RNA, herein designated GAM TARGET RNA, into GAM846 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13407] It is appreciated that GAM846 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM846 target genes. The mRNA of each one of this plurality of GAM846 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM846 RNA, herein designated GAM RNA, and which when bound by GAM846 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM846 target proteins.

[13408] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM846 gene, herein designated GAM GENE, on one or more GAM846 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13409] It is yet further appreciated that specific functions, and accordingly utilities, of GAM846 correlate with, and may be deduced from, the identity of the target genes which GAM846 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13410] Nucleotide sequences of the GAM846 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM846 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM846 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM846 are further described hereinbelow with reference to Table Table1.

[13411] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM846 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13412] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 847 (GAM847) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13413] GAM847 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM847 was detected is described hereinabove with reference to Figs. 2-8.

[13414] GAM847 gene, herein designated GAM GENE, and GAM847 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13415] GAM847 gene, herein designated GAM GENE, encodes a GAM847 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM847 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM847 precursor RNA is designated SEQ ID:820, and is provided hereinbelow with reference to the sequence listing part.

[13416] GAM847 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM847 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13417] An enzyme complex designated DICER COMPLEX, dices the GAM847 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM847 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM847 RNA is designated SEQ ID:2496, and is provided hereinbelow with reference to the sequence listing part.

[13418] GAM847 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM847 target RNA, herein designated GAM TARGET RNA. GAM847 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13419] GAM847 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM847 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM847 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM847 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM847 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13420] The complementary binding of GAM847 RNA, herein designated GAM RNA, to target binding sites on GAM847 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM847 target RNA, herein designated GAM TARGET RNA, into GAM847 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13421] It is appreciated that GAM847 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM847 target genes. The mRNA of each one of this plu-

rality of GAM847 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM847 RNA, herein designated GAM RNA, and which when bound by GAM847 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM847 target proteins.

[13422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM847 gene, herein designated GAM GENE, on one or more GAM847 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13423] It is yet further appreciated that specific functions, and accordingly utilities, of GAM847 correlate with, and may be deduced from, the identity of the target genes which GAM847 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13424] Nucleotide sequences of the GAM847 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM847 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM847 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM847 are further described hereinbelow with reference to Table Table1.

[13425] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM847 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13426] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 848 (GAM848) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[13427] GAM848 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM848 was detected is described hereinabove with reference to Figs. 2-8.

[13428] GAM848 gene, herein designated GAM GENE, and GAM848 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13429] GAM848 gene, herein designated GAM GENE, encodes a GAM848 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM848 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM848 precursor RNA is designated SEQ ID:821, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:821 is located at position 582596 relative to contig NT_009775.11, on chromosome 12.

[13430] GAM848 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98025, which mouse homolog is detected in

mouse EST accession AW125630.1.

[13431] GAM848 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM848 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13432] An enzyme complex designated DICER COMPLEX, dices the GAM848 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM848 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM848 RNA is designated SEQ ID:2497, and is provided hereinbelow with reference to the sequence listing part.

[13433] GAM848 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM848 target RNA, herein designated GAM TARGET RNA.

GAM848 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13434] GAM848 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM848 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM848 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM848 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM848 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13435] The complementary binding of GAM848 RNA, herein designated GAM RNA, to target binding sites on GAM848 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM848 target RNA, herein designated GAM TARGET RNA, into GAM848 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13436] It is appreciated that GAM848 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM848 target genes. The mRNA of each one of this plurality of GAM848 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM848 RNA, herein designated GAM RNA, and which when bound by GAM848 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM848 target proteins.

[13437] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM848 gene, herein designated GAM GENE, on one or more GAM848 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13438] It is yet further appreciated that specific functions, and accordingly utilities, of GAM848 correlate with, and may be deduced from, the identity of the target genes which GAM848 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13439] Nucleotide sequences of the GAM848 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM848 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM848 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM848 are further described hereinbelow with reference to Table Table1.

[13440] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM848 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13441] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 849 (GAM849) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13442] GAM849 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM849 was detected is described hereinabove with reference to Figs. 2-8.

[13443] GAM849 gene, herein designated GAM GENE, and GAM849 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13444] GAM849 gene, herein designated GAM GENE, encodes a GAM849 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM849 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM849 precursor RNA is designated SEQ ID:822, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:822 is located at position 31829830 relative to contig NT_007592.11, on chromosome 6.

[13445] GAM849 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM849 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13446] An enzyme complex designated DICER COMPLEX, dices the GAM849 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM849 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM849 RNA is designated SEQ ID:2498, and is provided hereinbelow with reference to the sequence listing part.

[13447] GAM849 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM849 target RNA, herein designated GAM TARGET RNA. GAM849 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13448] GAM849 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM849 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM849 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM849 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM849 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13449] The complementary binding of GAM849 RNA, herein designated GAM RNA, to target binding sites on GAM849 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM849 target RNA, herein designated GAM TARGET RNA, into GAM849 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13450] It is appreciated that GAM849 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM849 target genes. The mRNA of each one of this plurality of GAM849 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM849 RNA, herein designated GAM RNA, and which when bound by GAM849 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM849 target proteins.

[13451] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM849 gene, herein designated GAM GENE, on one or more GAM849 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13452] It is yet further appreciated that specific functions, and accordingly utilities, of GAM849 correlate with, and may be deduced from, the identity of the target genes which GAM849 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13453] Nucleotide sequences of the GAM849 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM849 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM849 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM849 are further described hereinbelow with reference to Table Table1.

[13454] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM849 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13455] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

850 (GAM850) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13456] GAM850 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM850 was detected is described hereinabove with reference to Figs. 2-8.

[13457] GAM850 gene, herein designated GAM GENE, and GAM850 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13458] GAM850 gene, herein designated GAM GENE, encodes a GAM850 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM850 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM850 precursor RNA is designated SEQ ID:823, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:823 is located at position 4816360 relative to contig NT_022184.10, on chromosome 2.

[13459] GAM850 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM850 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13460] An enzyme complex designated DICER COMPLEX, dices the GAM850 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM850 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM850 RNA is designated SEQ ID:2499, and is provided hereinbelow with reference to the sequence listing part.

[13461] GAM850 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM850 target RNA, herein designated GAM TARGET RNA. GAM850 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13462] GAM850 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM850 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM850 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM850 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM850 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[13463] The complementary binding of GAM850 RNA, herein designated GAM RNA, to target binding sites on GAM850 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM850 target RNA, herein designated GAM TARGET RNA, into GAM850 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13464] It is appreciated that GAM850 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM850 target genes. The mRNA of each one of this plurality of GAM850 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM850 RNA, herein designated GAM RNA, and which when bound by GAM850 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM850 target proteins.

[13465] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM850 gene, herein designated GAM GENE, on one or

more GAM850 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13466] It is yet further appreciated that specific functions, and accordingly utilities, of GAM850 correlate with, and may be deduced from, the identity of the target genes which GAM850 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13467] Nucleotide sequences of the GAM850 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM850 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM850 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM850 are further de-

scribed hereinbelow with reference to Table Table1.

[13468] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM850 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13469] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 851 (GAM851) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13470] GAM851 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM851 was detected is described hereinabove with reference to Figs. 2-8.

[13471] GAM851 gene, herein designated GAM GENE, and GAM851 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13472] GAM851 gene, herein designated GAM GENE, encodes a GAM851 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM851 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM851 precursor RNA is designated SEQ ID:824, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:824 is located at position 1274572 relative to contig NT_010552.11, on chromosome 16.

[13473] GAM851 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM851 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13474] An enzyme complex designated DICER COMPLEX, dices the GAM851 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM851 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM851 RNA is designated SEQ ID:2500, and is provided hereinbelow with reference to the sequence listing part.

[13475] GAM851 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM851 target RNA, herein designated GAM TARGET RNA. GAM851 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13476] GAM851 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM851 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM851 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM851 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM851 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13477] The complementary binding of GAM851 RNA, herein designated GAM RNA, to target binding sites on GAM851 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM851 target RNA, herein designated GAM TARGET RNA, into GAM851 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13478] It is appreciated that GAM851 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM851 target genes. The mRNA of each one of this plurality of GAM851 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM851 RNA, herein designated GAM RNA, and which when bound by GAM851 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM851 target proteins.

[13479] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM851 gene, herein designated GAM GENE, on one or more GAM851 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13480] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM851 correlate with, and may be deduced from, the identity of the target genes which GAM851 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13481] Nucleotide sequences of the GAM851 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM851 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM851 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM851 are further described hereinbelow with reference to Table Table1.

[13482] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM851 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13483] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 852 (GAM852) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13484] GAM852 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM852 was detected is described hereinabove with reference to Figs. 2-8.

[13485] GAM852 gene, herein designated GAM GENE, and GAM852 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13486] GAM852 gene, herein designated GAM GENE, encodes a GAM852 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM852 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM852 precursor RNA is designated SEQ ID:825, and is provided hereinbelow with reference to the sequence listing part.

[13487] GAM852 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM852 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13488] An enzyme complex designated DICER COMPLEX, dices the GAM852 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM852 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM852 RNA is designated SEQ ID:2501, and is provided hereinbelow with reference to the sequence listing part.

[13489] GAM852 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM852 target RNA, herein designated GAM TARGET RNA. GAM852 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13490] GAM852 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM852 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM852 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM852 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM852 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13491] The complementary binding of GAM852 RNA, herein designated GAM RNA, to target binding sites on GAM852 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM852 target RNA, herein designated GAM TARGET RNA, into GAM852 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13492] It is appreciated that GAM852 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM852 target genes. The mRNA of each one of this plurality of GAM852 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM852 RNA, herein designated GAM RNA, and which when bound by GAM852 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM852 target proteins.

[13493] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM852 gene, herein designated GAM GENE, on one or more GAM852 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13494] It is yet further appreciated that specific functions, and accordingly utilities, of GAM852 correlate with, and may be deduced from, the identity of the target genes which GAM852 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13495] Nucleotide sequences of the GAM852 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM852 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM852 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM852 are further described hereinbelow with reference to Table Table1.

[13496] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM852 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13497] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 853 (GAM853) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13498] GAM853 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM853 was detected is described hereinabove with reference to Figs. 2-8.

[13499] GAM853 gene, herein designated GAM GENE, and GAM853 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13500] GAM853 gene, herein designated GAM GENE, encodes a GAM853 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM853 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM853 precursor RNA is designated SEQ ID:826, and is provided hereinbelow with refer-

ence to the sequence listing part.

[13501] GAM853 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM853 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13502] An enzyme complex designated DICER COMPLEX, dices the GAM853 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM853 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM853 RNA is designated SEQ ID:2502, and is provided hereinbelow with reference to the sequence listing part.

[13503] GAM853 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM853 target RNA, herein designated GAM TARGET RNA.

GAM853 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13504] GAM853 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM853 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM853 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM853 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM853 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13505] The complementary binding of GAM853 RNA, herein designated GAM RNA, to target binding sites on GAM853 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM853 target RNA, herein designated GAM TARGET RNA, into GAM853 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13506] It is appreciated that GAM853 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM853 target genes. The mRNA of each one of this plurality of GAM853 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM853 RNA, herein designated GAM RNA, and which when bound by GAM853 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM853 target proteins.

[13507] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM853 gene, herein designated GAM GENE, on one or more GAM853 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13508] It is yet further appreciated that specific functions, and accordingly utilities, of GAM853 correlate with, and may be deduced from, the identity of the target genes which GAM853 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13509] Nucleotide sequences of the GAM853 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM853 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM853 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM853 are further described hereinbelow with reference to Table Table1.

[13510] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM853 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13511] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 854 (GAM854) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13512] GAM854 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM854 was detected is described hereinabove with reference to Figs. 2-8.

[13513] GAM854 gene, herein designated GAM GENE, and GAM854 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13514] GAM854 gene, herein designated GAM GENE, encodes a GAM854 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM854 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM854 precursor RNA is designated SEQ ID:827, and is provided hereinbelow with reference to the sequence listing part.

[13515] GAM854 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13516] An enzyme complex designated DICER COMPLEX, dices the GAM854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM854 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM854 RNA is designated SEQ ID:2503, and is provided hereinbelow with reference to the sequence listing part.

[13517] GAM854 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM854 target RNA, herein designated GAM TARGET RNA. GAM854 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13518] GAM854 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM854 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM854 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM854 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM854 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13519] The complementary binding of GAM854 RNA, herein designated GAM RNA, to target binding sites on GAM854 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM854 target RNA, herein designated GAM TARGET RNA, into GAM854 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13520] It is appreciated that GAM854 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM854 target genes. The mRNA of each one of this plu-

rality of GAM854 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM854 RNA, herein designated GAM RNA, and which when bound by GAM854 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM854 target proteins.

[13521] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM854 gene, herein designated GAM GENE, on one or more GAM854 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13522] It is yet further appreciated that specific functions, and accordingly utilities, of GAM854 correlate with, and may be deduced from, the identity of the target genes which GAM854 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13523] Nucleotide sequences of the GAM854 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM854 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM854 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM854 are further described hereinbelow with reference to Table Table1.

[13524] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM854 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13525] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 855 (GAM855) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[13526] GAM855 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM855 was detected is described hereinabove with reference to Figs. 2-8.

[13527] GAM855 gene, herein designated GAM GENE, and GAM855 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13528] GAM855 gene, herein designated GAM GENE, encodes a GAM855 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM855 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM855 precursor RNA is designated SEQ ID:828, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:828 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[13529] GAM855 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse

EST's in which these homologs were detected are:

[13530] SEQ ID:98040 detected in mouse EST Accession BE943987.1.

[13531] SEQ ID:98041 detected in mouse EST Accession BG808025.1.

[13532] SEQ ID:98042 detected in mouse EST Accession BG808010.1.

[13533] SEQ ID:98043 detected in mouse EST Accession BG807850.1.

[13534] SEQ ID:98044 detected in mouse EST Accession BG805970.1.

[13535] SEQ ID:98192 detected in mouse EST Accession AA144533.1.

[13536] SEQ ID:98193 detected in mouse EST Accession AA671455.1.

[13537] SEQ ID:98194 detected in mouse EST Accession BE691413.1.

[13538] SEQ ID:98195 detected in mouse EST Accession BE691447.1.

[13539] SEQ ID:98196 detected in mouse EST Accession BG145596.1.

[13540] SEQ ID:98197 detected in mouse EST Accession BE692802.1.

[13541] SEQ ID:98198 detected in mouse EST Accession AW208601.1.

[13542] SEQ ID:98199 detected in mouse EST Accession BB610842.1.

[13543] SEQ ID:98200 detected in mouse EST Accession AW824753.1.

[13544] SEQ ID:98207 detected in mouse EST Accession BB609859.1.

[13545] GAM855 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM855 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13546] An enzyme complex designated DICER COMPLEX, dices the GAM855 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM855 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM855 RNA is designated SEQ ID:2504, and is provided hereinbelow with reference to the sequence listing part.

[13547] GAM855 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM855 target RNA, herein designated GAM TARGET RNA. GAM855 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13548] GAM855 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM855 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM855 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM855 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM855 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13549] The complementary binding of GAM855 RNA, herein designated GAM RNA, to target binding sites on GAM855 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM855 target RNA, herein designated GAM TARGET RNA, into GAM855 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13550] It is appreciated that GAM855 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM855 target genes. The mRNA of each one of this plurality of GAM855 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM855 RNA, herein designated GAM RNA, and which when bound by GAM855 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM855 target proteins.

[13551] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM855 gene, herein designated GAM GENE, on one or more GAM855 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13552] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM855 correlate with, and may be deduced from, the identity of the target genes which GAM855 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13553] Nucleotide sequences of the GAM855 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM855 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM855 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM855 are further described hereinbelow with reference to Table Table1.

[13554] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM855 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13555] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 856 (GAM856) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13556] GAM856 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM856 was detected is described hereinabove with reference to Figs. 2-8.

[13557] GAM856 gene, herein designated GAM GENE, and GAM856 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13558] GAM856 gene, herein designated GAM GENE, encodes a GAM856 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM856 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM856 precursor RNA is designated SEQ ID:829, and is provided hereinbelow with reference to the sequence listing part.

[13559] GAM856 has 11 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[13560] SEQ ID:99188 detected in mouse EST Accession AA432947.1.

[13561] SEQ ID:99189 detected in mouse EST Accession AW227840.1.

[13562] SEQ ID:99190 detected in mouse EST Accession BE690423.1.

[13563] SEQ ID:99191 detected in mouse EST Accession AA265848.1.

[13564] SEQ ID:99192 detected in mouse EST Accession AW210282.1.

[13565] SEQ ID:99193 detected in mouse EST Accession AW412057.1.

[13566] SEQ ID:99194 detected in mouse EST Accession BI499093.1.

[13567] SEQ ID:99195 detected in mouse EST Accession BF147979.1.

[13568] SEQ ID:99196 detected in mouse EST Accession BF143309.1.

[13569] SEQ ID:99197 detected in mouse EST Accession BI663103.1.

[13570] SEQ ID:99198 detected in mouse EST Accession AW412051.1.

[13571] GAM856 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM856 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13572] An enzyme complex designated DICER COMPLEX, dices the GAM856 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM856 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM856 RNA is designated SEQ ID:2505, and is provided hereinbelow with reference to the sequence listing part.

[13573] GAM856 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM856 target RNA, herein designated GAM TARGET RNA. GAM856 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13574] GAM856 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM856 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM856 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM856 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM856 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13575] The complementary binding of GAM856 RNA, herein designated GAM RNA, to target binding sites on GAM856 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM856 target RNA, herein designated GAM TARGET RNA, into GAM856 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13576] It is appreciated that GAM856 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM856 target genes. The mRNA of each one of this plurality of GAM856 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM856 RNA, herein designated GAM RNA, and which when bound by GAM856 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM856 target proteins.

[13577] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM856 gene, herein designated GAM GENE, on one or more GAM856 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13578] It is yet further appreciated that specific functions, and accordingly utilities, of GAM856 correlate with, and may be deduced from, the identity of the target genes which GAM856 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13579] Nucleotide sequences of the GAM856 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM856 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM856 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM856 are further described hereinbelow with reference to Table Table1.

[13580] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM856 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13581] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 857 (GAM857) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13582] GAM857 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM857 was detected is described hereinabove with reference to Figs. 2-8.

[13583] GAM857 gene, herein designated GAM GENE, and GAM857 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13584] GAM857 gene, herein designated GAM GENE, encodes a GAM857 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM857 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM857 precursor RNA is designated SEQ ID:830, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:830 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[13585] GAM857 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM857 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13586] An enzyme complex designated DICER COMPLEX, dices the GAM857 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM857 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM857 RNA is designated SEQ ID:2506, and is provided hereinbelow with reference to the sequence listing part.

[13587] GAM857 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM857 target RNA, herein designated GAM TARGET RNA. GAM857 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13588] GAM857 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM857 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM857 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM857 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM857 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13589] The complementary binding of GAM857 RNA, herein designated GAM RNA, to target binding sites on GAM857 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM857 target RNA, herein designated GAM TARGET RNA, into GAM857 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13590] It is appreciated that GAM857 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM857 target genes. The mRNA of each one of this plurality of GAM857 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM857 RNA, herein designated GAM RNA, and which when bound by GAM857 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM857 target proteins.

[13591] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM857 gene, herein designated GAM GENE, on one or more GAM857 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13592] It is yet further appreciated that specific functions, and accordingly utilities, of GAM857 correlate with, and may

be deduced from, the identity of the target genes which GAM857 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13593] Nucleotide sequences of the GAM857 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM857 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM857 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM857 are further described hereinbelow with reference to Table Table1.

[13594] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM857 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13595] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 858 (GAM858) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13596] GAM858 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM858 was detected is described hereinabove with reference to Figs. 2-8.

[13597] GAM858 gene, herein designated GAM GENE, and GAM858 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13598] GAM858 gene, herein designated GAM GENE, encodes a GAM858 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM858 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM858 precursor RNA is designated SEQ ID:831, and is provided hereinbelow with reference to the sequence listing part.

[13599] GAM858 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM858 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[13600] An enzyme complex designated DICER COMPLEX, dices the GAM858 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM858 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM858 RNA is designated SEQ ID:2507, and is provided hereinbelow with reference to the sequence listing part.

[13601] GAM858 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM858 target RNA, herein designated GAM TARGET RNA.
GAM858 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13602] GAM858 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM858 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM858 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM858 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM858 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13603] The complementary binding of GAM858 RNA, herein designated GAM RNA, to target binding sites on GAM858 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM858 target RNA, herein desig-

nated GAM TARGET RNA, into GAM858 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13604] It is appreciated that GAM858 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM858 target genes. The mRNA of each one of this plurality of GAM858 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM858 RNA, herein designated GAM RNA, and which when bound by GAM858 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM858 target proteins.

[13605] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM858 gene, herein designated GAM GENE, on one or more GAM858 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13606] It is yet further appreciated that specific functions, and accordingly utilities, of GAM858 correlate with, and may be deduced from, the identity of the target genes which GAM858 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13607] Nucleotide sequences of the GAM858 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM858 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM858 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM858 are further described hereinbelow with reference to Table Table1.

[13608] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM858 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[13609] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 859 (GAM859) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13610] GAM859 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM859 was detected is described hereinabove with reference to Figs. 2-8.

[13611] GAM859 gene, herein designated GAM GENE, and GAM859 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13612] GAM859 gene, herein designated GAM GENE, encodes a GAM859 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM859 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM859 precursor RNA is designated SEQ ID:832, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:832 is located at position 7652379 relative to contig NT_010393.11, on chromosome 16.

[13613] GAM859 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM859 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13614] An enzyme complex designated DICER COMPLEX, dices the GAM859 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM859 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM859 RNA is designated SEQ ID:2508, and is provided hereinbelow with reference to the sequence listing part.

[13615] GAM859 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM859 target RNA, herein designated GAM TARGET RNA. GAM859 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13616] GAM859 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM859 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM859 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM859 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM859

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13617] The complementary binding of GAM859 RNA, herein designated GAM RNA, to target binding sites on GAM859 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM859 target RNA, herein designated GAM TARGET RNA, into GAM859 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13618] It is appreciated that GAM859 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM859 target genes. The mRNA of each one of this plurality of GAM859 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM859 RNA, herein designated GAM RNA, and which when bound by GAM859 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM859 target proteins.

[13619] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM859 gene, herein designated GAM GENE, on one or more GAM859 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13620] It is yet further appreciated that specific functions, and accordingly utilities, of GAM859 correlate with, and may be deduced from, the identity of the target genes which GAM859 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13621] Nucleotide sequences of the GAM859 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM859 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM859 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM859 are further described hereinbelow with reference to Table Table1.

[13622] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM859 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13623] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 860 (GAM860) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13624] GAM860 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM860 was detected is described hereinabove with reference to Figs. 2-8.

[13625] GAM860 gene, herein designated GAM GENE, and GAM860 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[13626] GAM860 gene, herein designated GAM GENE, encodes a GAM860 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM860 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM860 precursor RNA is designated SEQ ID:833, and is provided hereinbelow with reference to the sequence listing part.

[13627] GAM860 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13628] An enzyme complex designated DICER COMPLEX, dices the GAM860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM860 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM860 RNA is designated SEQ ID:2509, and is provided hereinbelow with reference to the sequence listing part.

[13629] GAM860 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM860 target RNA, herein designated GAM TARGET RNA. GAM860 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13630] GAM860 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM860 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM860 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM860 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM860 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13631] The complementary binding of GAM860 RNA, herein designated GAM RNA, to target binding sites on GAM860 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM860 target RNA, herein designated GAM TARGET RNA, into GAM860 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13632] It is appreciated that GAM860 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM860 target genes. The mRNA of each one of this plurality of GAM860 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM860 RNA, herein designated GAM RNA, and which when bound by GAM860 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM860 target proteins.

[13633] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM860 gene, herein designated GAM GENE, on one or more GAM860 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[13634] It is yet further appreciated that specific functions, and accordingly utilities, of GAM860 correlate with, and may be deduced from, the identity of the target genes which GAM860 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13635] Nucleotide sequences of the GAM860 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM860 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM860 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM860 are further described hereinbelow with reference to Table Table1.

[13636] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM860 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13637] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 861 (GAM861) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[13638] GAM861 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM861 was detected is described hereinabove with reference to Figs. 2-8.

[13639] GAM861 gene, herein designated GAM GENE, and GAM861 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13640] GAM861 gene, herein designated GAM GENE, encodes a GAM861 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM861 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM861 precursor RNA is designated SEQ ID:834, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:834 is located at position 1274560 relative to contig NT_010552.11, on chromosome 16.

[13641] GAM861 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM861 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13642] An enzyme complex designated DICER COMPLEX, dices the GAM861 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM861 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM861 RNA is designated SEQ ID:2510, and is provided hereinbelow with reference to the sequence listing part.

[13643] GAM861 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM861 target RNA, herein designated GAM TARGET RNA. GAM861 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13644] GAM861 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM861 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM861 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM861 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM861 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13645] The complementary binding of GAM861 RNA, herein designated GAM RNA, to target binding sites on GAM861 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM861 target RNA, herein designated GAM TARGET RNA, into GAM861 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13646] It is appreciated that GAM861 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM861 target genes. The mRNA of each one of this plurality of GAM861 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM861 RNA, herein designated GAM RNA, and which when bound by GAM861 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM861 target proteins.

[13647] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM861 gene, herein designated GAM GENE, on one or more GAM861 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13648] It is yet further appreciated that specific functions, and accordingly utilities, of GAM861 correlate with, and may be deduced from, the identity of the target genes which GAM861 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13649] Nucleotide sequences of the GAM861 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM861 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM861 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM861 are further described hereinbelow with reference to Table Table1.

[13650] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM861 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13651] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 862 (GAM862) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13652] GAM862 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM862 was detected is described hereinabove with reference to Figs. 2-8.

[13653] GAM862 gene, herein designated GAM GENE, and GAM862 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13654] GAM862 gene, herein designated GAM GENE, encodes a GAM862 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM862 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM862 precursor RNA is designated SEQ ID:835, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:835 is located at position 36924270 relative to contig NT_007592.11, on chromosome 6.

[13655] GAM862 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM862 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13656] An enzyme complex designated DICER COMPLEX, dices the GAM862 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM862 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM862 RNA is designated SEQ ID:2511, and is provided hereinbelow with reference to the sequence listing part.

[13657] GAM862 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM862 target RNA, herein designated GAM TARGET RNA. GAM862 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13658] GAM862 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM862 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM862 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM862 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM862 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13659] The complementary binding of GAM862 RNA, herein designated GAM RNA, to target binding sites on GAM862 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM862 target RNA, herein designated GAM TARGET RNA, into GAM862 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13660] It is appreciated that GAM862 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM862 target genes. The mRNA of each one of this plurality of GAM862 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM862 RNA, herein designated GAM RNA, and which when bound by GAM862 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM862 target proteins.

[13661] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM862 gene, herein designated GAM GENE, on one or more GAM862 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13662] It is yet further appreciated that specific functions, and accordingly utilities, of GAM862 correlate with, and may

be deduced from, the identity of the target genes which GAM862 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13663] Nucleotide sequences of the GAM862 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM862 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM862 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM862 are further described hereinbelow with reference to Table Table1.

[13664] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM862 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13665] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 863 (GAM863) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13666] GAM863 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM863 was detected is described hereinabove with reference to Figs. 2-8.

[13667] GAM863 gene, herein designated GAM GENE, and GAM863 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13668] GAM863 gene, herein designated GAM GENE, encodes a GAM863 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM863 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM863 precursor RNA is designated SEQ ID:836, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:836 is located at position 236386 relative to contig NT_004836.13, on chromosome 1.

[13669] GAM863 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13670] An enzyme complex designated DICER COMPLEX, dices the GAM863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM863 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM863 RNA is designated SEQ ID:2512, and is provided hereinbelow with reference to the sequence listing part.

[13671] GAM863 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM863 target RNA, herein designated GAM TARGET RNA.
GAM863 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13672] GAM863 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM863 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM863 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM863 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM863 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13673] The complementary binding of GAM863 RNA, herein designated GAM RNA, to target binding sites on GAM863 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM863 target RNA, herein designated GAM TARGET RNA, into GAM863 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13674] It is appreciated that GAM863 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM863 target genes. The mRNA of each one of this plurality of GAM863 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM863 RNA, herein designated GAM RNA, and which when bound by GAM863 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM863 target proteins.

[13675] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM863 gene, herein designated GAM GENE, on one or more GAM863 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13676] It is yet further appreciated that specific functions, and accordingly utilities, of GAM863 correlate with, and may be deduced from, the identity of the target genes which GAM863 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13677] Nucleotide sequences of the GAM863 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM863 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM863 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM863 are further described hereinbelow with reference to Table Table1.

[13678] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM863 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13679] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 864 (GAM864) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13680] GAM864 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM864 was detected is described hereinabove with reference to Figs. 2-8.

[13681] GAM864 gene, herein designated GAM GENE, and GAM864 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13682] GAM864 gene, herein designated GAM GENE, encodes a GAM864 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM864 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM864 precursor RNA is desig-

nated SEQ ID:837, and is provided hereinbelow with reference to the sequence listing part.

[13683] GAM864 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13684] An enzyme complex designated DICER COMPLEX, dices the GAM864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM864 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM864 RNA is designated SEQ ID:2513, and is provided hereinbelow with reference to the sequence listing part.

[13685] GAM864 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM864 target RNA, herein designated GAM TARGET RNA. GAM864 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13686] GAM864 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM864 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM864 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM864 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM864

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13687] The complementary binding of GAM864 RNA, herein designated GAM RNA, to target binding sites on GAM864 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM864 target RNA, herein designated GAM TARGET RNA, into GAM864 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13688] It is appreciated that GAM864 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM864 target genes. The mRNA of each one of this plurality of GAM864 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM864 RNA, herein designated GAM RNA, and which when bound by GAM864 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM864 target proteins.

[13689] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM864 gene, herein designated GAM GENE, on one or more GAM864 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13690] It is yet further appreciated that specific functions, and accordingly utilities, of GAM864 correlate with, and may be deduced from, the identity of the target genes which GAM864 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13691] Nucleotide sequences of the GAM864 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM864 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM864 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM864 are further described hereinbelow with reference to Table Table1.

[13692] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM864 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13693] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 865 (GAM865) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13694] GAM865 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM865 was detected is described hereinabove with reference to Figs. 2-8.

[13695] GAM865 gene, herein designated GAM GENE, and GAM865 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[13696] GAM865 gene, herein designated GAM GENE, encodes a GAM865 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM865 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM865 precursor RNA is designated SEQ ID:838, and is provided hereinbelow with reference to the sequence listing part.

[13697] GAM865 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM865 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13698] An enzyme complex designated DICER COMPLEX, dices the GAM865 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM865 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM865 RNA is designated SEQ ID:2514, and is provided hereinbelow with reference to the sequence listing part.

[13699] GAM865 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM865 target RNA, herein designated GAM TARGET RNA. GAM865 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13700] GAM865 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM865 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM865 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM865 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM865 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13701] The complementary binding of GAM865 RNA, herein designated GAM RNA, to target binding sites on GAM865 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM865 target RNA, herein designated GAM TARGET RNA, into GAM865 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13702] It is appreciated that GAM865 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM865 target genes. The mRNA of each one of this plurality of GAM865 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM865 RNA, herein designated GAM RNA, and which when bound by GAM865 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM865 target proteins.

[13703] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM865 gene, herein designated GAM GENE, on one or more GAM865 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[13704] It is yet further appreciated that specific functions, and accordingly utilities, of GAM865 correlate with, and may be deduced from, the identity of the target genes which GAM865 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13705] Nucleotide sequences of the GAM865 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM865 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM865 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM865 are further described hereinbelow with reference to Table Table1.

[13706] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM865 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13707] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 866 (GAM866) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[13708] GAM866 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM866 was detected is described hereinabove with reference to Figs. 2-8.

[13709] GAM866 gene, herein designated GAM GENE, and GAM866 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13710] GAM866 gene, herein designated GAM GENE, encodes a GAM866 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM866 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM866 precursor RNA is designated SEQ ID:839, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:839 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[13711] GAM866 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM866 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13712] An enzyme complex designated DICER COMPLEX, dices the GAM866 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM866 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM866 RNA is designated SEQ ID:2515, and is provided hereinbelow with reference to the sequence listing part.

[13713] GAM866 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM866 target RNA, herein designated GAM TARGET RNA. GAM866 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13714] GAM866 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM866 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM866 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM866 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM866 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13715] The complementary binding of GAM866 RNA, herein designated GAM RNA, to target binding sites on GAM866 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM866 target RNA, herein designated GAM TARGET RNA, into GAM866 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13716] It is appreciated that GAM866 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM866 target genes. The mRNA of each one of this plurality of GAM866 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM866 RNA, herein designated GAM RNA, and which when bound by GAM866 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM866 target proteins.

[13717] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM866 gene, herein designated GAM GENE, on one or more GAM866 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13718] It is yet further appreciated that specific functions, and accordingly utilities, of GAM866 correlate with, and may be deduced from, the identity of the target genes which GAM866 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13719] Nucleotide sequences of the GAM866 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM866 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM866 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM866 are further described hereinbelow with reference to Table Table1.

[13720] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM866 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13721] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 867 (GAM867) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13722] GAM867 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM867 was detected is described hereinabove with reference to Figs. 2-8.

[13723] GAM867 gene, herein designated GAM GENE, and GAM867 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13724] GAM867 gene, herein designated GAM GENE, encodes a GAM867 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM867 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM867 precursor RNA is designated SEQ ID:840, and is provided hereinbelow with reference to the sequence listing part.

[13725] GAM867 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM867 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13726] An enzyme complex designated DICER COMPLEX, dices the GAM867 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM867 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM867 RNA is designated SEQ ID:2516, and is provided hereinbelow with reference to the sequence listing part.

[13727] GAM867 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM867 target RNA, herein designated GAM TARGET RNA. GAM867 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13728] GAM867 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM867 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM867 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM867 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM867 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13729] The complementary binding of GAM867 RNA, herein designated GAM RNA, to target binding sites on GAM867 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM867 target RNA, herein designated GAM TARGET RNA, into GAM867 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13730] It is appreciated that GAM867 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM867 target genes. The mRNA of each one of this plurality of GAM867 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM867 RNA, herein designated GAM RNA, and which when bound by

GAM867 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM867 target proteins.

[13731] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM867 gene, herein designated GAM GENE, on one or more GAM867 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13732] It is yet further appreciated that specific functions, and accordingly utilities, of GAM867 correlate with, and may be deduced from, the identity of the target genes which GAM867 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[13733] Nucleotide sequences of the GAM867 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM867 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM867 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM867 are further described hereinbelow with reference to Table Table1.

[13734] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM867 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13735] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 868 (GAM868) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13736] GAM868 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM868 was detected is described hereinabove

with reference to Figs. 2-8.

[13737] GAM868 gene, herein designated GAM GENE, and GAM868 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13738] GAM868 gene, herein designated GAM GENE, encodes a GAM868 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM868 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM868 precursor RNA is designated SEQ ID:841, and is provided hereinbelow with reference to the sequence listing part.

[13739] GAM868 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13740] An enzyme complex designated DICER COMPLEX, dices the GAM868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM868 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM868 RNA is designated SEQ ID:2517, and is provided hereinbelow with reference to the sequence listing part.

[13741] GAM868 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM868 target RNA, herein designated GAM TARGET RNA. GAM868 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13742] GAM868 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM868 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM868 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM868 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM868 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13743] The complementary binding of GAM868 RNA, herein designated GAM RNA, to target binding sites on GAM868 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM868 target RNA, herein designated GAM TARGET RNA, into GAM868 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[13744] It is appreciated that GAM868 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM868 target genes. The mRNA of each one of this plurality of GAM868 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM868 RNA, herein designated GAM RNA, and which when bound by GAM868 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM868 target proteins.

[13745] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM868 gene, herein designated GAM GENE, on one or more GAM868 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13746] It is yet further appreciated that specific functions, and accordingly utilities, of GAM868 correlate with, and may be deduced from, the identity of the target genes which GAM868 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13747] Nucleotide sequences of the GAM868 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM868 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM868 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM868 are further described hereinbelow with reference to Table Table1.

[13748] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM868 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13749] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 869 (GAM869) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13750] GAM869 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM869 was detected is described hereinabove with reference to Figs. 2-8.

[13751] GAM869 gene, herein designated GAM GENE, and GAM869 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13752] GAM869 gene, herein designated GAM GENE, encodes a GAM869 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM869 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM869 precursor RNA is designated SEQ ID:842, and is provided hereinbelow with reference to the sequence listing part.

[13753] GAM869 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's.

Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[13754] SEQ ID:99806 detected in mouse EST Accession AA500296.1.

[13755] SEQ ID:99807 detected in mouse EST Accession BE554084.1.

[13756] SEQ ID:99811 detected in mouse EST Accession BG922170.1.

[13757] SEQ ID:99813 detected in mouse EST Accession AA106737.1.

[13758] GAM869 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM869 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13759] An enzyme complex designated DICER COMPLEX, dices the GAM869 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM869 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM869 RNA is designated SEQ ID:2518, and is provided hereinbelow with reference to the sequence listing part.

[13760] GAM869 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM869 target RNA, herein designated GAM TARGET RNA. GAM869 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13761] GAM869 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM869 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM869 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM869 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM869 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13762] The complementary binding of GAM869 RNA, herein designated GAM RNA, to target binding sites on GAM869 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM869 target RNA, herein designated GAM TARGET RNA, into GAM869 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13763] It is appreciated that GAM869 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM869 target genes. The mRNA of each one of this plurality of GAM869 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM869 RNA, herein designated GAM RNA, and which when bound by GAM869 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM869 target proteins.

[13764] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM869 gene, herein designated GAM GENE, on one or more GAM869 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13765] It is yet further appreciated that specific functions, and accordingly utilities, of GAM869 correlate with, and may be deduced from, the identity of the target genes which GAM869 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13766] Nucleotide sequences of the GAM869 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM869 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM869 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM869 are further described hereinbelow with reference to Table Table1.

[13767] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM869 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13768] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

870 (GAM870) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13769] GAM870 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM870 was detected is described hereinabove with reference to Figs. 2-8.

[13770] GAM870 gene, herein designated GAM GENE, and GAM870 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13771] GAM870 gene, herein designated GAM GENE, encodes a GAM870 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM870 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM870 precursor RNA is designated SEQ ID:843, and is provided hereinbelow with reference to the sequence listing part.

[13772] GAM870 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM870 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13773] An enzyme complex designated DICER COMPLEX, dices the GAM870 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM870 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM870 RNA is designated SEQ ID:2519, and is provided hereinbelow with reference to the sequence listing part.

[13774] GAM870 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM870 target RNA, herein designated GAM TARGET RNA. GAM870 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13775] GAM870 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM870 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM870 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM870 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM870 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13776] The complementary binding of GAM870 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM870 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM870 target RNA, herein designated GAM TARGET RNA, into GAM870 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13777] It is appreciated that GAM870 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM870 target genes. The mRNA of each one of this plurality of GAM870 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM870 RNA, herein designated GAM RNA, and which when bound by GAM870 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM870 target proteins.

[13778] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM870 gene, herein designated GAM GENE, on one or more GAM870 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13779] It is yet further appreciated that specific functions, and accordingly utilities, of GAM870 correlate with, and may be deduced from, the identity of the target genes which GAM870 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13780] Nucleotide sequences of the GAM870 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM870 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM870 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM870 are further described hereinbelow with reference to Table Table1.

[13781] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM870 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13782] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 871 (GAM871) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13783] GAM871 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM871 was detected is described hereinabove with reference to Figs. 2-8.

[13784] GAM871 gene, herein designated GAM GENE, and GAM871 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13785] GAM871 gene, herein designated GAM GENE, encodes a GAM871 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM871 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM871 precursor RNA is designated SEQ ID:844, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:844 is located at position 2907490 relative to contig NT_015805.11, on chromosome 2.

[13786] GAM871 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM871 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13787] An enzyme complex designated DICER COMPLEX, dices the GAM871 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM871 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM871 RNA is designated SEQ ID:2520, and is provided hereinbelow with reference to the sequence listing part.

[13788] GAM871 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM871 target RNA, herein designated GAM TARGET RNA. GAM871 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13789] GAM871 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM871 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM871 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM871 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM871 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13790] The complementary binding of GAM871 RNA, herein designated GAM RNA, to target binding sites on GAM871 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM871 target RNA, herein designated GAM TARGET RNA, into GAM871 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13791] It is appreciated that GAM871 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM871 target genes. The mRNA of each one of this plurality of GAM871 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM871 RNA,

herein designated GAM RNA, and which when bound by GAM871 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM871 target proteins.

[13792] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM871 gene, herein designated GAM GENE, on one or more GAM871 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13793] It is yet further appreciated that specific functions, and accordingly utilities, of GAM871 correlate with, and may be deduced from, the identity of the target genes which

GAM871 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13794] Nucleotide sequences of the GAM871 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM871 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM871 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM871 are further described hereinbelow with reference to Table Table1.

[13795] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM871 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13796] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 872 (GAM872) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13797] GAM872 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM872 was detected is described hereinabove with reference to Figs. 2-8.

[13798] GAM872 gene, herein designated GAM GENE, and GAM872 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13799] GAM872 gene, herein designated GAM GENE, encodes a GAM872 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM872 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM872 precursor RNA is designated SEQ ID:845, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:845 is located at position 10508750 relative to contig NT_004668.13, on chromosome 1.

[13800] GAM872 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM872 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13801] An enzyme complex designated DICER COMPLEX, dices the GAM872 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM872 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM872 RNA is designated SEQ ID:2521, and is provided hereinbelow with reference to the sequence listing part.

[13802] GAM872 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM872 target RNA, herein designated GAM TARGET RNA. GAM872 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13803] GAM872 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM872 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM872 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM872 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM872 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13804] The complementary binding of GAM872 RNA, herein designated GAM RNA, to target binding sites on GAM872 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM872 target RNA, herein designated GAM TARGET RNA, into GAM872 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13805] It is appreciated that GAM872 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM872 target genes. The mRNA of each one of this plurality of GAM872 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM872 RNA, herein designated GAM RNA, and which when bound by GAM872 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM872 target proteins.

[13806] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM872 gene, herein designated GAM GENE, on one or more GAM872 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13807] It is yet further appreciated that specific functions, and accordingly utilities, of GAM872 correlate with, and may be deduced from, the identity of the target genes which GAM872 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13808] Nucleotide sequences of the GAM872 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM872 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM872 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM872 are further described hereinbelow with reference to Table Table1.

[13809] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM872 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13810] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 873 (GAM873) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13811] GAM873 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM873 was detected is described hereinabove with reference to Figs. 2-8.

[13812] GAM873 gene, herein designated GAM GENE, and GAM873 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13813] GAM873 gene, herein designated GAM GENE, encodes a GAM873 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM873 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM873 precursor RNA is designated SEQ ID:846, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:846 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[13814] GAM873 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM873 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13815] An enzyme complex designated DICER COMPLEX, dices the GAM873 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM873 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM873 RNA is designated SEQ ID:2522, and is provided

hereinbelow with reference to the sequence listing part.

[13816] GAM873 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM873 target RNA, herein designated GAM TARGET RNA.

GAM873 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13817] GAM873 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM873 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM873 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM873 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM873 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13818] The complementary binding of GAM873 RNA, herein designated GAM RNA, to target binding sites on GAM873 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM873 target RNA, herein designated GAM TARGET RNA, into GAM873 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13819] It is appreciated that GAM873 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM873 target genes. The mRNA of each one of this plurality of GAM873 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM873 RNA, herein designated GAM RNA, and which when bound by GAM873 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM873 tar-

get proteins.

[13820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM873 gene, herein designated GAM GENE, on one or more GAM873 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13821] It is yet further appreciated that specific functions, and accordingly utilities, of GAM873 correlate with, and may be deduced from, the identity of the target genes which GAM873 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13822] Nucleotide sequences of the GAM873 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM873 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM873 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM873 are further described hereinbelow with reference to Table Table1.

[13823] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM873 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13824] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 874 (GAM874) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13825] GAM874 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM874 was detected is described hereinabove with reference to Figs. 2-8.

[13826] GAM874 gene, herein designated GAM GENE, and

GAM874 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13827] GAM874 gene, herein designated GAM GENE, encodes a GAM874 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM874 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM874 precursor RNA is designated SEQ ID:847, and is provided hereinbelow with reference to the sequence listing part.

[13828] GAM874 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM874 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13829] An enzyme complex designated DICER COMPLEX, dices the GAM874 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM874 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM874 RNA is designated SEQ ID:2523, and is provided hereinbelow with reference to the sequence listing part.

[13830] GAM874 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM874 target RNA, herein designated GAM TARGET RNA. GAM874 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13831] GAM874 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM874 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM874 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM874 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM874 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13832] The complementary binding of GAM874 RNA, herein designated GAM RNA, to target binding sites on GAM874 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM874 target RNA, herein designated GAM TARGET RNA, into GAM874 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13833] It is appreciated that GAM874 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM874 target genes. The mRNA of each one of this plurality of GAM874 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM874 RNA, herein designated GAM RNA, and which when bound by GAM874 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM874 target proteins.

[13834] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM874 gene, herein designated GAM GENE, on one or more GAM874 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13835] It is yet further appreciated that specific functions, and accordingly utilities, of GAM874 correlate with, and may be deduced from, the identity of the target genes which GAM874 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13836] Nucleotide sequences of the GAM874 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM874 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM874 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM874 are further described hereinbelow with reference to Table Table1.

[13837] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM874 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13838] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

875 (GAM875) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13839] GAM875 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM875 was detected is described hereinabove with reference to Figs. 2-8.

[13840] GAM875 gene, herein designated GAM GENE, and GAM875 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13841] GAM875 gene, herein designated GAM GENE, encodes a GAM875 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM875 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM875 precursor RNA is designated SEQ ID:848, and is provided hereinbelow with reference to the sequence listing part.

[13842] GAM875 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM875 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13843] An enzyme complex designated DICER COMPLEX, dices the GAM875 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM875 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM875 RNA is designated SEQ ID:2524, and is provided hereinbelow with reference to the sequence listing part.

[13844] GAM875 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM875 target RNA, herein designated GAM TARGET RNA. GAM875 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13845] GAM875 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM875 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM875 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM875 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM875 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13846] The complementary binding of GAM875 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM875 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM875 target RNA, herein designated GAM TARGET RNA, into GAM875 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13847] It is appreciated that GAM875 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM875 target genes. The mRNA of each one of this plurality of GAM875 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM875 RNA, herein designated GAM RNA, and which when bound by GAM875 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM875 target proteins.

[13848] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM875 gene, herein designated GAM GENE, on one or more GAM875 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13849] It is yet further appreciated that specific functions, and accordingly utilities, of GAM875 correlate with, and may be deduced from, the identity of the target genes which GAM875 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13850] Nucleotide sequences of the GAM875 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM875 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM875 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM875 are further described hereinbelow with reference to Table Table1.

[13851] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM875 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13852] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 876 (GAM876) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13853] GAM876 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM876 was detected is described hereinabove with reference to Figs. 2-8.

[13854] GAM876 gene, herein designated GAM GENE, and GAM876 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13855] GAM876 gene, herein designated GAM GENE, encodes a GAM876 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM876 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM876 precursor RNA is designated SEQ ID:849, and is provided hereinbelow with reference to the sequence listing part.

[13856] GAM876 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99047, which mouse homolog is detected in mouse EST accession AW476255.1.

[13857] GAM876 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM876 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13858] An enzyme complex designated DICER COMPLEX, dices the GAM876 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM876 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM876 RNA is designated SEQ ID:2525, and is provided hereinbelow with reference to the sequence listing part.

[13859] GAM876 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM876 target RNA, herein designated GAM TARGET RNA. GAM876 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13860] GAM876 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM876 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM876 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM876 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM876 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13861] The complementary binding of GAM876 RNA, herein designated GAM RNA, to target binding sites on GAM876 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM876 target RNA, herein designated GAM TARGET RNA, into GAM876 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13862] It is appreciated that GAM876 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM876 target genes. The mRNA of each one of this plu-

rality of GAM876 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM876 RNA, herein designated GAM RNA, and which when bound by GAM876 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM876 target proteins.

[13863] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM876 gene, herein designated GAM GENE, on one or more GAM876 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13864] It is yet further appreciated that specific functions, and accordingly utilities, of GAM876 correlate with, and may be deduced from, the identity of the target genes which GAM876 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13865] Nucleotide sequences of the GAM876 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM876 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM876 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM876 are further described hereinbelow with reference to Table Table1.

[13866] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM876 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13867] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 877 (GAM877) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[13868] GAM877 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM877 was detected is described hereinabove with reference to Figs. 2-8.

[13869] GAM877 gene, herein designated GAM GENE, and GAM877 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13870] GAM877 gene, herein designated GAM GENE, encodes a GAM877 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM877 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM877 precursor RNA is designated SEQ ID:850, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:850 is located at position 2349693 relative to contig NT_021907.13, on chromosome 1.

[13871] GAM877 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM877 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13872] An enzyme complex designated DICER COMPLEX, dices the GAM877 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM877 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM877 RNA is designated SEQ ID:2526, and is provided hereinbelow with reference to the sequence listing part.

[13873] GAM877 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM877 target RNA, herein designated GAM TARGET RNA. GAM877 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13874] GAM877 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM877 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM877 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM877 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM877 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13875] The complementary binding of GAM877 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM877 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM877 target RNA, herein designated GAM TARGET RNA, into GAM877 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13876] It is appreciated that GAM877 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM877 target genes. The mRNA of each one of this plurality of GAM877 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM877 RNA, herein designated GAM RNA, and which when bound by GAM877 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM877 target proteins.

[13877] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM877 gene, herein designated GAM GENE, on one or more GAM877 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13878] It is yet further appreciated that specific functions, and accordingly utilities, of GAM877 correlate with, and may be deduced from, the identity of the target genes which GAM877 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13879] Nucleotide sequences of the GAM877 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM877 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM877 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM877 are further described hereinbelow with reference to Table Table1.

[13880] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM877 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13881] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 878 (GAM878) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13882] GAM878 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM878 was detected is described hereinabove with reference to Figs. 2-8.

[13883] GAM878 gene, herein designated GAM GENE, and GAM878 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13884] GAM878 gene, herein designated GAM GENE, encodes a GAM878 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM878 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM878 precursor RNA is designated SEQ ID:851, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:851 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[13885] GAM878 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM878 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13886] An enzyme complex designated DICER COMPLEX, dices the GAM878 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM878 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM878 RNA is designated SEQ ID:2527, and is provided hereinbelow with reference to the sequence listing part.

[13887] GAM878 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM878 target RNA, herein designated GAM TARGET RNA. GAM878 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13888] GAM878 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM878 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM878 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM878 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM878 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13889] The complementary binding of GAM878 RNA, herein designated GAM RNA, to target binding sites on GAM878 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM878 target RNA, herein designated GAM TARGET RNA, into GAM878 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13890] It is appreciated that GAM878 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM878 target genes. The mRNA of each one of this plurality of GAM878 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM878 RNA,

herein designated GAM RNA, and which when bound by GAM878 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM878 target proteins.

[13891] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM878 gene, herein designated GAM GENE, on one or more GAM878 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13892] It is yet further appreciated that specific functions, and accordingly utilities, of GAM878 correlate with, and may be deduced from, the identity of the target genes which

GAM878 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13893] Nucleotide sequences of the GAM878 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM878 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM878 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM878 are further described hereinbelow with reference to Table Table1.

[13894] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM878 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13895] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 879 (GAM879) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13896] GAM879 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM879 was detected is described hereinabove with reference to Figs. 2-8.

[13897] GAM879 gene, herein designated GAM GENE, and GAM879 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13898] GAM879 gene, herein designated GAM GENE, encodes a GAM879 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM879 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM879 precursor RNA is designated SEQ ID:852, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:852 is located at position 6000551 relative to contig NT_005612.11, on chromosome 3.

[13899] GAM879 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM879 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13900] An enzyme complex designated DICER COMPLEX, dices the GAM879 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM879 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM879 RNA is designated SEQ ID:2528, and is provided hereinbelow with reference to the sequence listing part.

[13901] GAM879 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM879 target RNA, herein designated GAM TARGET RNA. GAM879 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13902] GAM879 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM879 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM879 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM879 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM879 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13903] The complementary binding of GAM879 RNA, herein designated GAM RNA, to target binding sites on GAM879 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM879 target RNA, herein designated GAM TARGET RNA, into GAM879 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13904] It is appreciated that GAM879 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM879 target genes. The mRNA of each one of this plurality of GAM879 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM879 RNA, herein designated GAM RNA, and which when bound by GAM879 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM879 target proteins.

[13905] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM879 gene, herein designated GAM GENE, on one or more GAM879 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13906] It is yet further appreciated that specific functions, and accordingly utilities, of GAM879 correlate with, and may be deduced from, the identity of the target genes which GAM879 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13907] Nucleotide sequences of the GAM879 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM879 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM879 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM879 are further described hereinbelow with reference to Table Table1.

[13908] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM879 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13909] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 880 (GAM880) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13910] GAM880 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM880 was detected is described hereinabove with reference to Figs. 2-8.

[13911] GAM880 gene, herein designated GAM GENE, and GAM880 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13912] GAM880 gene, herein designated GAM GENE, encodes a GAM880 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM880 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM880 precursor RNA is designated SEQ ID:853, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:853 is located at position 2556957 relative to contig NT_011196.11, on chromosome 19.

[13913] GAM880 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM880 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13914] An enzyme complex designated DICER COMPLEX, dices the GAM880 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM880 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM880 RNA is designated SEQ ID:2529, and is provided

hereinbelow with reference to the sequence listing part.

[13915] GAM880 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM880 target RNA, herein designated GAM TARGET RNA.

GAM880 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13916] GAM880 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM880 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM880 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM880 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM880 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13917] The complementary binding of GAM880 RNA, herein designated GAM RNA, to target binding sites on GAM880 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM880 target RNA, herein designated GAM TARGET RNA, into GAM880 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13918] It is appreciated that GAM880 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM880 target genes. The mRNA of each one of this plurality of GAM880 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM880 RNA, herein designated GAM RNA, and which when bound by GAM880 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM880 tar-

get proteins.

[13919] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM880 gene, herein designated GAM GENE, on one or more GAM880 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13920] It is yet further appreciated that specific functions, and accordingly utilities, of GAM880 correlate with, and may be deduced from, the identity of the target genes which GAM880 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13921] Nucleotide sequences of the GAM880 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM880 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM880 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM880 are further described hereinbelow with reference to Table Table1.

[13922] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM880 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13923] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 881 (GAM881) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13924] GAM881 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM881 was detected is described hereinabove with reference to Figs. 2-8.

[13925] GAM881 gene, herein designated GAM GENE, and

GAM881 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13926] GAM881 gene, herein designated GAM GENE, encodes a GAM881 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM881 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM881 precursor RNA is designated SEQ ID:854, and is provided hereinbelow with reference to the sequence listing part.

[13927] GAM881 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM881 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13928] An enzyme complex designated DICER COMPLEX, dices the GAM881 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM881 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM881 RNA is designated SEQ ID:2530, and is provided hereinbelow with reference to the sequence listing part.

[13929] GAM881 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM881 target RNA, herein designated GAM TARGET RNA. GAM881 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13930] GAM881 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM881 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM881 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM881 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM881 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13931] The complementary binding of GAM881 RNA, herein designated GAM RNA, to target binding sites on GAM881 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM881 target RNA, herein designated GAM TARGET RNA, into GAM881 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13932] It is appreciated that GAM881 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM881 target genes. The mRNA of each one of this plurality of GAM881 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM881 RNA, herein designated GAM RNA, and which when bound by GAM881 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM881 target proteins.

[13933] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM881 gene, herein designated GAM GENE, on one or more GAM881 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13934] It is yet further appreciated that specific functions, and accordingly utilities, of GAM881 correlate with, and may be deduced from, the identity of the target genes which GAM881 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13935] Nucleotide sequences of the GAM881 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM881 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM881 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM881 are further described hereinbelow with reference to Table Table1.

[13936] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM881 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13937] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

882 (GAM882) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13938] GAM882 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM882 was detected is described hereinabove with reference to Figs. 2-8.

[13939] GAM882 gene, herein designated GAM GENE, and GAM882 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13940] GAM882 gene, herein designated GAM GENE, encodes a GAM882 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM882 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM882 precursor RNA is designated SEQ ID:855, and is provided hereinbelow with reference to the sequence listing part.

[13941] GAM882 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse

EST's in which these homologs were detected are:

[13942] SEQ ID:99048 detected in mouse EST Accession BI965652.1.

[13943] SEQ ID:99352 detected in mouse EST Accession BI965972.1.

[13944] SEQ ID:99353 detected in mouse EST Accession AI326210.1.

[13945] GAM882 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM882 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13946] An enzyme complex designated DICER COMPLEX, dices the GAM882 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM882 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM882 RNA is designated SEQ ID:2531, and is provided hereinbelow with reference to the sequence listing part.

[13947] GAM882 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM882 target RNA, herein designated GAM TARGET RNA. GAM882 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13948] GAM882 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM882 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM882 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM882 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM882 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13949] The complementary binding of GAM882 RNA, herein designated GAM RNA, to target binding sites on GAM882 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM882 target RNA, herein designated GAM TARGET RNA, into GAM882 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13950] It is appreciated that GAM882 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM882 target genes. The mRNA of each one of this plurality of GAM882 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM882 RNA, herein designated GAM RNA, and which when bound by GAM882 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM882 target proteins.

[13951] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM882 gene, herein designated GAM GENE, on one or more GAM882 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13952] It is yet further appreciated that specific functions, and accordingly utilities, of GAM882 correlate with, and may

be deduced from, the identity of the target genes which GAM882 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13953] Nucleotide sequences of the GAM882 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM882 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM882 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM882 are further described hereinbelow with reference to Table Table1.

[13954] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM882 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13955] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 883 (GAM883) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13956] GAM883 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM883 was detected is described hereinabove with reference to Figs. 2-8.

[13957] GAM883 gene, herein designated GAM GENE, and GAM883 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13958] GAM883 gene, herein designated GAM GENE, encodes a GAM883 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM883 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM883 precursor RNA is designated SEQ ID:856, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:856 is located at position 23863967 relative to contig NT_026437.9, on chromosome 14.

[13959] GAM883 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM883 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13960] An enzyme complex designated DICER COMPLEX, dices the GAM883 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM883 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM883 RNA is designated SEQ ID:2532, and is provided hereinbelow with reference to the sequence listing part.

[13961] GAM883 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM883 target RNA, herein designated GAM TARGET RNA.
GAM883 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13962] GAM883 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM883 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM883 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM883 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM883 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13963] The complementary binding of GAM883 RNA, herein designated GAM RNA, to target binding sites on GAM883 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM883 target RNA, herein designated GAM TARGET RNA, into GAM883 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13964] It is appreciated that GAM883 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM883 target genes. The mRNA of each one of this plurality of GAM883 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM883 RNA, herein designated GAM RNA, and which when bound by GAM883 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM883 target proteins.

[13965] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM883 gene, herein designated GAM GENE, on one or more GAM883 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13966] It is yet further appreciated that specific functions, and accordingly utilities, of GAM883 correlate with, and may be deduced from, the identity of the target genes which GAM883 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13967] Nucleotide sequences of the GAM883 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM883 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM883 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM883 are further described hereinbelow with reference to Table Table1.

[13968] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM883 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13969] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 884 (GAM884) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13970] GAM884 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM884 was detected is described hereinabove with reference to Figs. 2-8.

[13971] GAM884 gene, herein designated GAM GENE, and GAM884 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13972] GAM884 gene, herein designated GAM GENE, encodes a GAM884 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM884 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM884 precursor RNA is desig-

nated SEQ ID:857, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:857 is located at position 37641993 relative to contig NT_007933.10, on chromosome 7.

[13973] GAM884 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13974] An enzyme complex designated DICER COMPLEX, dices the GAM884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM884 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM884 RNA is designated SEQ ID:2533, and is provided hereinbelow with reference to the sequence listing part.

[13975] GAM884 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM884 target RNA, herein designated GAM TARGET RNA. GAM884 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13976] GAM884 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM884 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM884 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM884 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM884 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13977] The complementary binding of GAM884 RNA, herein designated GAM RNA, to target binding sites on GAM884 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM884 target RNA, herein designated GAM TARGET RNA, into GAM884 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13978] It is appreciated that GAM884 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM884 target genes. The mRNA of each one of this plurality of GAM884 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM884 RNA, herein designated GAM RNA, and which when bound by GAM884 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM884 target proteins.

[13979] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM884 gene, herein designated GAM GENE, on one or more GAM884 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13980] It is yet further appreciated that specific functions, and accordingly utilities, of GAM884 correlate with, and may be deduced from, the identity of the target genes which GAM884 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13981] Nucleotide sequences of the GAM884 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM884 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM884 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM884 are further described hereinbelow with reference to Table Table1.

[13982] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM884 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13983] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 885 (GAM885) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13984] GAM885 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM885 was detected is described hereinabove with reference to Figs. 2-8.

[13985] GAM885 gene, herein designated GAM GENE, and GAM885 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[13986] GAM885 gene, herein designated GAM GENE, encodes a GAM885 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM885 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM885 precursor RNA is designated SEQ ID:858, and is provided hereinbelow with reference to the sequence listing part.

[13987] GAM885 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM885 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[13988] An enzyme complex designated DICER COMPLEX, dices

the GAM885 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM885 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM885 RNA is designated SEQ ID:2534, and is provided hereinbelow with reference to the sequence listing part.

[13989] GAM885 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM885 target RNA, herein designated GAM TARGET RNA. GAM885 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[13990] GAM885 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM885 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM885

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM885 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM885 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[13991] The complementary binding of GAM885 RNA, herein designated GAM RNA, to target binding sites on GAM885 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM885 target RNA, herein designated GAM TARGET RNA, into GAM885 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[13992] It is appreciated that GAM885 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM885 target genes. The mRNA of each one of this plurality of GAM885 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM885 RNA, herein designated GAM RNA, and which when bound by GAM885 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM885 target proteins.

[13993] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM885 gene, herein designated GAM GENE, on one or more GAM885 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[13994] It is yet further appreciated that specific functions, and accordingly utilities, of GAM885 correlate with, and may be deduced from, the identity of the target genes which GAM885 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[13995] Nucleotide sequences of the GAM885 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM885 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM885 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM885 are further described hereinbelow with reference to Table Table1.

[13996] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM885 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[13997] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 886 (GAM886) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[13998] GAM886 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM886 was detected is described hereinabove with reference to Figs. 2-8.

[13999] GAM886 gene, herein designated GAM GENE, and GAM886 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14000] GAM886 gene, herein designated GAM GENE, encodes a GAM886 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM886 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM886 precursor RNA is designated SEQ ID:859, and is provided hereinbelow with reference to the sequence listing part.

[14001] GAM886 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14002] An enzyme complex designated DICER COMPLEX, dices the GAM886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM886 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM886 RNA is designated SEQ ID:2535, and is provided hereinbelow with reference to the sequence listing part.

[14003] GAM886 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM886 target RNA, herein designated GAM TARGET RNA. GAM886 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14004] GAM886 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM886 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM886 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM886 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM886 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14005] The complementary binding of GAM886 RNA, herein designated GAM RNA, to target binding sites on GAM886 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM886 target RNA, herein designated GAM TARGET RNA, into GAM886 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14006] It is appreciated that GAM886 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM886 target genes. The mRNA of each one of this plurality of GAM886 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM886 RNA, herein designated GAM RNA, and which when bound by GAM886 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM886 target proteins.

[14007] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM886 gene, herein designated GAM GENE, on one or more GAM886 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14008] It is yet further appreciated that specific functions, and accordingly utilities, of GAM886 correlate with, and may be deduced from, the identity of the target genes which GAM886 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14009] Nucleotide sequences of the GAM886 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM886 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM886 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM886 are further described hereinbelow with reference to Table Table1.

[14010] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM886 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14011] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 887 (GAM887) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14012] GAM887 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM887 was detected is described hereinabove with reference to Figs. 2-8.

[14013] GAM887 gene, herein designated GAM GENE, and GAM887 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14014] GAM887 gene, herein designated GAM GENE, encodes a GAM887 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM887 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM887 precursor RNA is designated SEQ ID:860, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:860 is located at position 65228 relative to contig NT_024901.11, on chromosome 17.

[14015] GAM887 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14016] An enzyme complex designated DICER COMPLEX, dices the GAM887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM887 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM887 RNA is designated SEQ ID:2536, and is provided hereinbelow with reference to the sequence listing part.

[14017] GAM887 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM887 target RNA, herein designated GAM TARGET RNA. GAM887 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14018] GAM887 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM887 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM887 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM887 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM887 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14019] The complementary binding of GAM887 RNA, herein designated GAM RNA, to target binding sites on GAM887 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM887 target RNA, herein designated GAM TARGET RNA, into GAM887 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14020] It is appreciated that GAM887 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM887 target genes. The mRNA of each one of this plurality of GAM887 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM887 RNA, herein designated GAM RNA, and which when bound by GAM887 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM887 target proteins.

[14021] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM887 gene, herein designated GAM GENE, on one or more GAM887 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14022] It is yet further appreciated that specific functions, and accordingly utilities, of GAM887 correlate with, and may

be deduced from, the identity of the target genes which GAM887 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14023] Nucleotide sequences of the GAM887 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM887 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM887 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM887 are further described hereinbelow with reference to Table Table1.

[14024] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM887 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14025] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 888 (GAM888) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14026] GAM888 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM888 was detected is described hereinabove with reference to Figs. 2-8.

[14027] GAM888 gene, herein designated GAM GENE, and GAM888 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14028] GAM888 gene, herein designated GAM GENE, encodes a GAM888 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM888 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM888 precursor RNA is designated SEQ ID:861, and is provided hereinbelow with reference to the sequence listing part.

[14029] GAM888 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM888 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[14030] An enzyme complex designated DICER COMPLEX, dices the GAM888 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM888 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM888 RNA is designated SEQ ID:2537, and is provided hereinbelow with reference to the sequence listing part.

[14031] GAM888 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM888 target RNA, herein designated GAM TARGET RNA.
GAM888 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14032] GAM888 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM888 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM888 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM888 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM888 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14033] The complementary binding of GAM888 RNA, herein designated GAM RNA, to target binding sites on GAM888 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM888 target RNA, herein desig-

nated GAM TARGET RNA, into GAM888 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14034] It is appreciated that GAM888 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM888 target genes. The mRNA of each one of this plurality of GAM888 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM888 RNA, herein designated GAM RNA, and which when bound by GAM888 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM888 target proteins.

[14035] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM888 gene, herein designated GAM GENE, on one or more GAM888 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14036] It is yet further appreciated that specific functions, and accordingly utilities, of GAM888 correlate with, and may be deduced from, the identity of the target genes which GAM888 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14037] Nucleotide sequences of the GAM888 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM888 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM888 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM888 are further described hereinbelow with reference to Table Table1.

[14038] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM888 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[14039] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 889 (GAM889) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14040] GAM889 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM889 was detected is described hereinabove with reference to Figs. 2-8.

[14041] GAM889 gene, herein designated GAM GENE, and GAM889 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14042] GAM889 gene, herein designated GAM GENE, encodes a GAM889 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM889 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM889 precursor RNA is designated SEQ ID:862, and is provided hereinbelow with reference to the sequence listing part.

[14043] GAM889 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14044] An enzyme complex designated DICER COMPLEX, dices the GAM889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM889 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM889 RNA is designated SEQ ID:2538, and is provided hereinbelow with reference to the sequence listing part.

[14045] GAM889 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM889

target RNA, herein designated GAM TARGET RNA.

GAM889 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14046] GAM889 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM889 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM889 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM889 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM889 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14047] The complementary binding of GAM889 RNA, herein designated GAM RNA, to target binding sites on GAM889 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM889 target RNA, herein designated GAM TARGET RNA, into GAM889 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14048] It is appreciated that GAM889 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM889 target genes. The mRNA of each one of this plurality of GAM889 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM889 RNA, herein designated GAM RNA, and which when bound by GAM889 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM889 target proteins.

[14049] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM889 gene, herein designated GAM GENE, on one or more GAM889 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14050] It is yet further appreciated that specific functions, and accordingly utilities, of GAM889 correlate with, and may be deduced from, the identity of the target genes which GAM889 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14051] Nucleotide sequences of the GAM889 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM889 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM889 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM889 are further described hereinbelow with reference to Table Table1.

[14052] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM889 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14053] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 890 (GAM890) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14054] GAM890 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM890 was detected is described hereinabove with reference to Figs. 2-8.

[14055] GAM890 gene, herein designated GAM GENE, and GAM890 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14056] GAM890 gene, herein designated GAM GENE, encodes a

GAM890 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM890 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM890 precursor RNA is designated SEQ ID:863, and is provided hereinbelow with reference to the sequence listing part.

[14057] GAM890 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM890 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14058] An enzyme complex designated DICER COMPLEX, dices the GAM890 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM890 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM890 RNA is designated SEQ ID:2539, and is provided hereinbelow with reference to the sequence listing part.

[14059] GAM890 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM890 target RNA, herein designated GAM TARGET RNA. GAM890 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14060] GAM890 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM890 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM890 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM890 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM890 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14061] The complementary binding of GAM890 RNA, herein designated GAM RNA, to target binding sites on GAM890 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM890 target RNA, herein designated GAM TARGET RNA, into GAM890 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14062] It is appreciated that GAM890 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM890 target genes. The mRNA of each one of this plurality of GAM890 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM890 RNA, herein designated GAM RNA, and which when bound by GAM890 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM890 target proteins.

[14063] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM890 gene, herein designated GAM GENE, on one or more GAM890 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14064] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM890 correlate with, and may be deduced from, the identity of the target genes which GAM890 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14065] Nucleotide sequences of the GAM890 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM890 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM890 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM890 are further described hereinbelow with reference to Table Table1.

[14066] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM890 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14067] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 891 (GAM891) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14068] GAM891 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM891 was detected is described hereinabove with reference to Figs. 2-8.

[14069] GAM891 gene, herein designated GAM GENE, and GAM891 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14070] GAM891 gene, herein designated GAM GENE, encodes a GAM891 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM891 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM891 precursor RNA is designated SEQ ID:864, and is provided hereinbelow with reference to the sequence listing part.

[14071] GAM891 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM891 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14072] An enzyme complex designated DICER COMPLEX, dices the GAM891 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM891 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM891 RNA is designated SEQ ID:2540, and is provided hereinbelow with reference to the sequence listing part.

[14073] GAM891 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM891 target RNA, herein designated GAM TARGET RNA. GAM891 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14074] GAM891 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM891 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM891 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM891 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM891 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14075] The complementary binding of GAM891 RNA, herein designated GAM RNA, to target binding sites on GAM891 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM891 target RNA, herein designated GAM TARGET RNA, into GAM891 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14076] It is appreciated that GAM891 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM891 target genes. The mRNA of each one of this plurality of GAM891 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM891 RNA, herein designated GAM RNA, and which when bound by GAM891 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM891 target proteins.

[14077] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM891 gene, herein designated GAM GENE, on one or more GAM891 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14078] It is yet further appreciated that specific functions, and accordingly utilities, of GAM891 correlate with, and may be deduced from, the identity of the target genes which GAM891 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14079] Nucleotide sequences of the GAM891 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM891 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM891 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM891 are further described hereinbelow with reference to Table Table1.

[14080] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM891 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14081] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 892 (GAM892) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14082] GAM892 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM892 was detected is described hereinabove with reference to Figs. 2-8.

[14083] GAM892 gene, herein designated GAM GENE, and GAM892 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14084] GAM892 gene, herein designated GAM GENE, encodes a GAM892 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM892 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM892 precursor RNA is designated SEQ ID:865, and is provided hereinbelow with refer-

ence to the sequence listing part.

[14085] GAM892 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14086] An enzyme complex designated DICER COMPLEX, dices the GAM892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM892 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM892 RNA is designated SEQ ID:2541, and is provided hereinbelow with reference to the sequence listing part.

[14087] GAM892 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM892 target RNA, herein designated GAM TARGET RNA.

GAM892 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14088] GAM892 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM892 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM892 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM892 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM892 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14089] The complementary binding of GAM892 RNA, herein designated GAM RNA, to target binding sites on GAM892 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM892 target RNA, herein designated GAM TARGET RNA, into GAM892 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14090] It is appreciated that GAM892 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM892 target genes. The mRNA of each one of this plurality of GAM892 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM892 RNA, herein designated GAM RNA, and which when bound by GAM892 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM892 target proteins.

[14091] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM892 gene, herein designated GAM GENE, on one or more GAM892 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14092] It is yet further appreciated that specific functions, and accordingly utilities, of GAM892 correlate with, and may be deduced from, the identity of the target genes which GAM892 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14093] Nucleotide sequences of the GAM892 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM892 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM892 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM892 are further described hereinbelow with reference to Table Table1.

[14094] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM892 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14095] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 893 (GAM893) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14096] GAM893 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM893 was detected is described hereinabove with reference to Figs. 2-8.

[14097] GAM893 gene, herein designated GAM GENE, and GAM893 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14098] GAM893 gene, herein designated GAM GENE, encodes a GAM893 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM893 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM893 precursor RNA is designated SEQ ID:866, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:866 is located at position 2349689 relative to contig NT_021907.13, on chromosome 1.

[14099] GAM893 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM893 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14100] An enzyme complex designated DICER COMPLEX, dices the GAM893 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM893 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM893 RNA is designated SEQ ID:2542, and is provided hereinbelow with reference to the sequence listing part.

[14101] GAM893 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM893 target RNA, herein designated GAM TARGET RNA. GAM893 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14102] GAM893 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM893 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM893 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM893 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM893 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14103] The complementary binding of GAM893 RNA, herein designated GAM RNA, to target binding sites on GAM893 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM893 target RNA, herein designated GAM TARGET RNA, into GAM893 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14104] It is appreciated that GAM893 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM893 target genes. The mRNA of each one of this plurality of GAM893 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM893 RNA, herein designated GAM RNA, and which when bound by GAM893 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM893 target proteins.

[14105] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM893 gene, herein designated GAM GENE, on one or more GAM893 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14106] It is yet further appreciated that specific functions, and accordingly utilities, of GAM893 correlate with, and may be deduced from, the identity of the target genes which GAM893 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14107] Nucleotide sequences of the GAM893 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM893 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM893 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM893 are further described hereinbelow with reference to Table Table1.

[14108] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM893 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14109] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

894 (GAM894) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14110] GAM894 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM894 was detected is described hereinabove with reference to Figs. 2-8.

[14111] GAM894 gene, herein designated GAM GENE, and GAM894 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14112] GAM894 gene, herein designated GAM GENE, encodes a GAM894 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM894 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM894 precursor RNA is designated SEQ ID:867, and is provided hereinbelow with reference to the sequence listing part.

[14113] GAM894 has 9 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse

EST's in which these homologs were detected are:

[14114] SEQ ID:99303 detected in mouse EST Accession W98814.1.

[14115] SEQ ID:99304 detected in mouse EST Accession AA839842.1.

[14116] SEQ ID:99305 detected in mouse EST Accession BI554717.1.

[14117] SEQ ID:99306 detected in mouse EST Accession AA086501.1.

[14118] SEQ ID:99307 detected in mouse EST Accession BE448900.1.

[14119] SEQ ID:99308 detected in mouse EST Accession BF584264.1.

[14120] SEQ ID:99309 detected in mouse EST Accession AW761921.1.

[14121] SEQ ID:99310 detected in mouse EST Accession BG920670.1.

[14122] SEQ ID:99311 detected in mouse EST Accession AA637831.1.

[14123] GAM894 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM894 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14124] An enzyme complex designated DICER COMPLEX, dices the GAM894 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM894 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM894 RNA is designated SEQ ID:2543, and is provided hereinbelow with reference to the sequence listing part.

[14125] GAM894 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM894 target RNA, herein designated GAM TARGET RNA. GAM894 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14126] GAM894 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM894 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM894 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM894 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM894 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14127] The complementary binding of GAM894 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM894 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM894 target RNA, herein designated GAM TARGET RNA, into GAM894 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14128] It is appreciated that GAM894 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM894 target genes. The mRNA of each one of this plurality of GAM894 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM894 RNA, herein designated GAM RNA, and which when bound by GAM894 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM894 target proteins.

[14129] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM894 gene, herein designated GAM GENE, on one or more GAM894 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14130] It is yet further appreciated that specific functions, and accordingly utilities, of GAM894 correlate with, and may be deduced from, the identity of the target genes which GAM894 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14131] Nucleotide sequences of the GAM894 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM894 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM894 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM894 are further described hereinbelow with reference to Table Table1.

[14132] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM894 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14133] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 895 (GAM895) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14134] GAM895 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM895 was detected is described hereinabove with reference to Figs. 2-8.

[14135] GAM895 gene, herein designated GAM GENE, and GAM895 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14136] GAM895 gene, herein designated GAM GENE, encodes a GAM895 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM895 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM895 precursor RNA is designated SEQ ID:868, and is provided hereinbelow with reference to the sequence listing part.

[14137] GAM895 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14138] An enzyme complex designated DICER COMPLEX, dices the GAM895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM895 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM895 RNA is designated SEQ ID:2544, and is provided hereinbelow with reference to the sequence listing part.

[14139] GAM895 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM895 target RNA, herein designated GAM TARGET RNA.

GAM895 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14140] GAM895 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM895 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM895 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM895 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM895 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14141] The complementary binding of GAM895 RNA, herein designated GAM RNA, to target binding sites on GAM895 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM895 target RNA, herein designated GAM TARGET RNA, into GAM895 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14142] It is appreciated that GAM895 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM895 target genes. The mRNA of each one of this plurality of GAM895 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM895 RNA, herein designated GAM RNA, and which when bound by GAM895 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM895 target proteins.

[14143] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM895 gene, herein designated GAM GENE, on one or more GAM895 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14144] It is yet further appreciated that specific functions, and accordingly utilities, of GAM895 correlate with, and may be deduced from, the identity of the target genes which GAM895 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14145] Nucleotide sequences of the GAM895 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM895 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM895 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM895 are further described hereinbelow with reference to Table Table1.

[14146] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM895 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14147] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 896 (GAM896) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14148] GAM896 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM896 was detected is described hereinabove with reference to Figs. 2-8.

[14149] GAM896 gene, herein designated GAM GENE, and GAM896 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14150] GAM896 gene, herein designated GAM GENE, encodes a GAM896 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM896 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM896 precursor RNA is designated SEQ ID:869, and is provided hereinbelow with reference to the sequence listing part.

[14151] GAM896 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM896 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14152] An enzyme complex designated DICER COMPLEX, dices

the GAM896 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM896 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM896 RNA is designated SEQ ID:2545, and is provided hereinbelow with reference to the sequence listing part.

[14153] GAM896 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM896 target RNA, herein designated GAM TARGET RNA. GAM896 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14154] GAM896 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM896 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM896

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM896 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM896 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14155] The complementary binding of GAM896 RNA, herein designated GAM RNA, to target binding sites on GAM896 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM896 target RNA, herein designated GAM TARGET RNA, into GAM896 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14156] It is appreciated that GAM896 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM896 target genes. The mRNA of each one of this plurality of GAM896 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM896 RNA, herein designated GAM RNA, and which when bound by GAM896 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM896 target proteins.

[14157] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM896 gene, herein designated GAM GENE, on one or more GAM896 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14158] It is yet further appreciated that specific functions, and accordingly utilities, of GAM896 correlate with, and may be deduced from, the identity of the target genes which GAM896 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14159] Nucleotide sequences of the GAM896 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM896 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM896 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM896 are further described hereinbelow with reference to Table Table1.

[14160] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM896 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14161] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 897 (GAM897) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14162] GAM897 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM897 was detected is described hereinabove with reference to Figs. 2-8.

[14163] GAM897 gene, herein designated GAM GENE, and GAM897 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14164] GAM897 gene, herein designated GAM GENE, encodes a GAM897 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM897 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM897 precursor RNA is designated SEQ ID:870, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:870 is located at position 19308883 relative to contig NT_033899.3, on chromosome 11.

[14165] GAM897 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM897 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14166] An enzyme complex designated DICER COMPLEX, dices the GAM897 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM897 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM897 RNA is designated SEQ ID:2546, and is provided hereinbelow with reference to the sequence listing part.

[14167] GAM897 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM897 target RNA, herein designated GAM TARGET RNA.

GAM897 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14168] GAM897 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM897 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM897 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM897 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM897 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14169] The complementary binding of GAM897 RNA, herein designated GAM RNA, to target binding sites on GAM897 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM897 target RNA, herein designated GAM TARGET RNA, into GAM897 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14170] It is appreciated that GAM897 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM897 target genes. The mRNA of each one of this plurality of GAM897 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM897 RNA, herein designated GAM RNA, and which when bound by GAM897 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM897 target proteins.

[14171] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM897 gene, herein designated GAM GENE, on one or more GAM897 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14172] It is yet further appreciated that specific functions, and accordingly utilities, of GAM897 correlate with, and may be deduced from, the identity of the target genes which GAM897 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14173] Nucleotide sequences of the GAM897 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM897 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM897 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM897 are further described hereinbelow with reference to Table Table1.

[14174] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM897 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14175] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 898 (GAM898) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14176] GAM898 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM898 was detected is described hereinabove with reference to Figs. 2-8.

[14177] GAM898 gene, herein designated GAM GENE, and GAM898 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14178] GAM898 gene, herein designated GAM GENE, encodes a GAM898 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM898 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM898 precursor RNA is designated SEQ ID:871, and is provided hereinbelow with reference to the sequence listing part.

[14179] GAM898 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14180] An enzyme complex designated DICER COMPLEX, dices the GAM898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM898 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM898 RNA is designated SEQ ID:2547, and is provided hereinbelow with reference to the sequence listing part.

[14181] GAM898 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM898 target RNA, herein designated GAM TARGET RNA. GAM898 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14182] GAM898 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM898 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM898 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM898 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM898 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14183] The complementary binding of GAM898 RNA, herein designated GAM RNA, to target binding sites on GAM898 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM898 target RNA, herein designated GAM TARGET RNA, into GAM898 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14184] It is appreciated that GAM898 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM898 target genes. The mRNA of each one of this plurality of GAM898 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM898 RNA, herein designated GAM RNA, and which when bound by GAM898 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM898 target proteins.

[14185] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM898 gene, herein designated GAM GENE, on one or more GAM898 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14186] It is yet further appreciated that specific functions, and accordingly utilities, of GAM898 correlate with, and may

be deduced from, the identity of the target genes which GAM898 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14187] Nucleotide sequences of the GAM898 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM898 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM898 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM898 are further described hereinbelow with reference to Table Table1.

[14188] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM898 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14189] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 899 (GAM899) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14190] GAM899 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM899 was detected is described hereinabove with reference to Figs. 2-8.

[14191] GAM899 gene, herein designated GAM GENE, and GAM899 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14192] GAM899 gene, herein designated GAM GENE, encodes a GAM899 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM899 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM899 precursor RNA is designated SEQ ID:872, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:872 is located at position 7441109 relative to contig NT_011520.8, on chromosome 22.

[14193] GAM899 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM899 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14194] An enzyme complex designated DICER COMPLEX, dices the GAM899 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM899 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM899 RNA is designated SEQ ID:2548, and is provided hereinbelow with reference to the sequence listing part.

[14195] GAM899 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM899 target RNA, herein designated GAM TARGET RNA.
GAM899 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14196] GAM899 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM899 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM899 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM899 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM899 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14197] The complementary binding of GAM899 RNA, herein designated GAM RNA, to target binding sites on GAM899 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM899 target RNA, herein designated GAM TARGET RNA, into GAM899 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14198] It is appreciated that GAM899 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM899 target genes. The mRNA of each one of this plurality of GAM899 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM899 RNA, herein designated GAM RNA, and which when bound by GAM899 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM899 target proteins.

[14199] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM899 gene, herein designated GAM GENE, on one or more GAM899 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14200] It is yet further appreciated that specific functions, and accordingly utilities, of GAM899 correlate with, and may be deduced from, the identity of the target genes which GAM899 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14201] Nucleotide sequences of the GAM899 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM899 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM899 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM899 are further described hereinbelow with reference to Table Table1.

[14202] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM899 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14203] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 900 (GAM900) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14204] GAM900 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM900 was detected is described hereinabove with reference to Figs. 2-8.

[14205] GAM900 gene, herein designated GAM GENE, and GAM900 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14206] GAM900 gene, herein designated GAM GENE, encodes a GAM900 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM900 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM900 precursor RNA is desig-

nated SEQ ID:873, and is provided hereinbelow with reference to the sequence listing part.

[14207] GAM900 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM900 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14208] An enzyme complex designated DICER COMPLEX, dices the GAM900 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM900 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM900 RNA is designated SEQ ID:2549, and is provided hereinbelow with reference to the sequence listing part.

[14209] GAM900 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM900 target RNA, herein designated GAM TARGET RNA. GAM900 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14210] GAM900 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM900 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM900 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM900 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM900

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14211] The complementary binding of GAM900 RNA, herein designated GAM RNA, to target binding sites on GAM900 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM900 target RNA, herein designated GAM TARGET RNA, into GAM900 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14212] It is appreciated that GAM900 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM900 target genes. The mRNA of each one of this plurality of GAM900 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM900 RNA, herein designated GAM RNA, and which when bound by GAM900 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM900 target proteins.

[14213] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM900 gene, herein designated GAM GENE, on one or more GAM900 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14214] It is yet further appreciated that specific functions, and accordingly utilities, of GAM900 correlate with, and may be deduced from, the identity of the target genes which GAM900 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14215] Nucleotide sequences of the GAM900 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM900 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM900 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM900 are further described hereinbelow with reference to Table Table1.

[14216] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM900 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14217] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 901 (GAM901) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14218] GAM901 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM901 was detected is described hereinabove with reference to Figs. 2-8.

[14219] GAM901 gene, herein designated GAM GENE, and GAM901 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[14220] GAM901 gene, herein designated GAM GENE, encodes a GAM901 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM901 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM901 precursor RNA is designated SEQ ID:874, and is provided hereinbelow with reference to the sequence listing part.

[14221] GAM901 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM901 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14222] An enzyme complex designated DICER COMPLEX, dices the GAM901 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM901 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM901 RNA is designated SEQ ID:2550, and is provided hereinbelow with reference to the sequence listing part.

[14223] GAM901 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM901 target RNA, herein designated GAM TARGET RNA. GAM901 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14224] GAM901 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM901 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM901 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM901 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM901 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14225] The complementary binding of GAM901 RNA, herein designated GAM RNA, to target binding sites on GAM901 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM901 target RNA, herein designated GAM TARGET RNA, into GAM901 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14226] It is appreciated that GAM901 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM901 target genes. The mRNA of each one of this plurality of GAM901 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM901 RNA, herein designated GAM RNA, and which when bound by GAM901 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM901 target proteins.

[14227] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM901 gene, herein designated GAM GENE, on one or more GAM901 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[14228] It is yet further appreciated that specific functions, and accordingly utilities, of GAM901 correlate with, and may be deduced from, the identity of the target genes which GAM901 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14229] Nucleotide sequences of the GAM901 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM901 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM901 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM901 are further described hereinbelow with reference to Table Table1.

[14230] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM901 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14231] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 902 (GAM902) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[14232] GAM902 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM902 was detected is described hereinabove with reference to Figs. 2-8.

[14233] GAM902 gene, herein designated GAM GENE, and GAM902 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14234] GAM902 gene, herein designated GAM GENE, encodes a GAM902 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM902 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM902 precursor RNA is designated SEQ ID:875, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:875 is located at position 1822711 relative to contig NT_022423.12, on chromosome 3.

[14235] GAM902 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM902 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14236] An enzyme complex designated DICER COMPLEX, dices the GAM902 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM902 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM902 RNA is designated SEQ ID:2551, and is provided hereinbelow with reference to the sequence listing part.

[14237] GAM902 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM902 target RNA, herein designated GAM TARGET RNA. GAM902 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14238] GAM902 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM902 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM902 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM902 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM902 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14239] The complementary binding of GAM902 RNA, herein designated GAM RNA, to target binding sites on GAM902 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM902 target RNA, herein designated GAM TARGET RNA, into GAM902 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14240] It is appreciated that GAM902 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM902 target genes. The mRNA of each one of this plurality of GAM902 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM902 RNA, herein designated GAM RNA, and which when bound by GAM902 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM902 target proteins.

[14241] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM902 gene, herein designated GAM GENE, on one or more GAM902 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14242] It is yet further appreciated that specific functions, and accordingly utilities, of GAM902 correlate with, and may be deduced from, the identity of the target genes which GAM902 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14243] Nucleotide sequences of the GAM902 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM902 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM902 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM902 are further described hereinbelow with reference to Table Table1.

[14244] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM902 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14245] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 903 (GAM903) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14246] GAM903 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM903 was detected is described hereinabove with reference to Figs. 2-8.

[14247] GAM903 gene, herein designated GAM GENE, and GAM903 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14248] GAM903 gene, herein designated GAM GENE, encodes a GAM903 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM903 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM903 precursor RNA is designated SEQ ID:876, and is provided hereinbelow with reference to the sequence listing part.

[14249] GAM903 has 12 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[14250] SEQ ID:99451 detected in mouse EST Accession AA144398.1.

[14251] SEQ ID:99452 detected in mouse EST Accession AI264984.1.

[14252] SEQ ID:99453 detected in mouse EST Accession AI156313.1.

[14253] SEQ ID:99454 detected in mouse EST Accession AW230495.1.

[14254] SEQ ID:99455 detected in mouse EST Accession BG970816.1.

[14255] SEQ ID:99456 detected in mouse EST Accession BF144364.1.

[14256] SEQ ID:99457 detected in mouse EST Accession

BG864461.1.

[14257] SEQ ID:99458 detected in mouse EST Accession BG974532.1.

[14258] SEQ ID:99459 detected in mouse EST Accession BG870381.1.

[14259] SEQ ID:99460 detected in mouse EST Accession BG973293.1.

[14260] SEQ ID:99461 detected in mouse EST Accession BI153175.1.

[14261] SEQ ID:99462 detected in mouse EST Accession BF146992.1.

[14262] GAM903 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM903 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14263] An enzyme complex designated DICER COMPLEX, dices the GAM903 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM903 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM903 RNA is designated SEQ ID:2552, and is provided hereinbelow with reference to the sequence listing part.

[14264] GAM903 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM903 target RNA, herein designated GAM TARGET RNA. GAM903 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14265] GAM903 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM903 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM903 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM903 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM903 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14266] The complementary binding of GAM903 RNA, herein designated GAM RNA, to target binding sites on GAM903 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM903 target RNA, herein designated GAM TARGET RNA, into GAM903 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14267] It is appreciated that GAM903 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM903 target genes. The mRNA of each one of this plurality of GAM903 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM903 RNA, herein designated GAM RNA, and which when bound by GAM903 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM903 target proteins.

[14268] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM903 gene, herein designated GAM GENE, on one or more GAM903 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14269] It is yet further appreciated that specific functions, and accordingly utilities, of GAM903 correlate with, and may be deduced from, the identity of the target genes which GAM903 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14270] Nucleotide sequences of the GAM903 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM903 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM903 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM903 are further described hereinbelow with reference to Table Table1.

[14271] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM903 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14272] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

904 (GAM904) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14273] GAM904 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM904 was detected is described hereinabove with reference to Figs. 2-8.

[14274] GAM904 gene, herein designated GAM GENE, and GAM904 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14275] GAM904 gene, herein designated GAM GENE, encodes a GAM904 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM904 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM904 precursor RNA is designated SEQ ID:877, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:877 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[14276] GAM904 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM904 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14277] An enzyme complex designated DICER COMPLEX, dices the GAM904 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM904 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM904 RNA is designated SEQ ID:2553, and is provided hereinbelow with reference to the sequence listing part.

[14278] GAM904 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM904 target RNA, herein designated GAM TARGET RNA. GAM904 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14279] GAM904 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM904 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM904 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM904 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM904 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[14280] The complementary binding of GAM904 RNA, herein designated GAM RNA, to target binding sites on GAM904 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM904 target RNA, herein designated GAM TARGET RNA, into GAM904 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14281] It is appreciated that GAM904 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM904 target genes. The mRNA of each one of this plurality of GAM904 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM904 RNA, herein designated GAM RNA, and which when bound by GAM904 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM904 target proteins.

[14282] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM904 gene, herein designated GAM GENE, on one or

more GAM904 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14283] It is yet further appreciated that specific functions, and accordingly utilities, of GAM904 correlate with, and may be deduced from, the identity of the target genes which GAM904 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14284] Nucleotide sequences of the GAM904 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM904 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM904 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM904 are further de-

scribed hereinbelow with reference to Table Table1.

[14285] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM904 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14286] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 905 (GAM905) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14287] GAM905 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM905 was detected is described hereinabove with reference to Figs. 2-8.

[14288] GAM905 gene, herein designated GAM GENE, and GAM905 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14289] GAM905 gene, herein designated GAM GENE, encodes a GAM905 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM905 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM905 precursor RNA is designated SEQ ID:878, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:878 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[14290] GAM905 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM905 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14291] An enzyme complex designated DICER COMPLEX, dices the GAM905 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM905 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM905 RNA is designated SEQ ID:2554, and is provided hereinbelow with reference to the sequence listing part.

[14292] GAM905 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM905 target RNA, herein designated GAM TARGET RNA. GAM905 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14293] GAM905 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM905 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM905 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM905 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM905 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14294] The complementary binding of GAM905 RNA, herein designated GAM RNA, to target binding sites on GAM905 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM905 target RNA, herein designated GAM TARGET RNA, into GAM905 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14295] It is appreciated that GAM905 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM905 target genes. The mRNA of each one of this plurality of GAM905 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM905 RNA, herein designated GAM RNA, and which when bound by GAM905 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM905 target proteins.

[14296] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM905 gene, herein designated GAM GENE, on one or more GAM905 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14297] It is yet further appreciated that specific functions, and accordingly utilities, of GAM905 correlate with, and may be deduced from, the identity of the target genes which GAM905 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14298] Nucleotide sequences of the GAM905 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM905 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM905 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM905 are further described hereinbelow with reference to Table Table1.

[14299] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM905 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14300] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 906 (GAM906) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14301] GAM906 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM906 was detected is described hereinabove with reference to Figs. 2-8.

[14302] GAM906 gene, herein designated GAM GENE, and GAM906 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14303] GAM906 gene, herein designated GAM GENE, encodes a GAM906 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM906 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM906 precursor RNA is desig-

nated SEQ ID:879, and is provided hereinbelow with reference to the sequence listing part.

[14304] GAM906 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM906 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14305] An enzyme complex designated DICER COMPLEX, dices the GAM906 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM906 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM906 RNA is designated SEQ ID:2555, and is provided hereinbelow with reference to the sequence listing part.

[14306] GAM906 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM906 target RNA, herein designated GAM TARGET RNA. GAM906 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14307] GAM906 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM906 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM906 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM906 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM906

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14308] The complementary binding of GAM906 RNA, herein designated GAM RNA, to target binding sites on GAM906 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM906 target RNA, herein designated GAM TARGET RNA, into GAM906 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14309] It is appreciated that GAM906 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM906 target genes. The mRNA of each one of this plurality of GAM906 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM906 RNA, herein designated GAM RNA, and which when bound by GAM906 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM906 target proteins.

[14310] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM906 gene, herein designated GAM GENE, on one or more GAM906 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14311] It is yet further appreciated that specific functions, and accordingly utilities, of GAM906 correlate with, and may be deduced from, the identity of the target genes which GAM906 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14312] Nucleotide sequences of the GAM906 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM906 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM906 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM906 are further described hereinbelow with reference to Table Table1.

[14313] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM906 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14314] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 907 (GAM907) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14315] GAM907 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM907 was detected is described hereinabove with reference to Figs. 2-8.

[14316] GAM907 gene, herein designated GAM GENE, and GAM907 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[14317] GAM907 gene, herein designated GAM GENE, encodes a GAM907 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM907 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM907 precursor RNA is designated SEQ ID:880, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:880 is located at position 515071 relative to contig NT_005567.11, on chromosome 3.

[14318] GAM907 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM907 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14319] An enzyme complex designated DICER COMPLEX, dices

the GAM907 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM907 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM907 RNA is designated SEQ ID:2556, and is provided hereinbelow with reference to the sequence listing part.

[14320] GAM907 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM907 target RNA, herein designated GAM TARGET RNA. GAM907 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14321] GAM907 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM907 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM907

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM907 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM907 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14322] The complementary binding of GAM907 RNA, herein designated GAM RNA, to target binding sites on GAM907 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM907 target RNA, herein designated GAM TARGET RNA, into GAM907 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14323] It is appreciated that GAM907 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM907 target genes. The mRNA of each one of this plurality of GAM907 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM907 RNA, herein designated GAM RNA, and which when bound by GAM907 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM907 target proteins.

[14324] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM907 gene, herein designated GAM GENE, on one or more GAM907 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14325] It is yet further appreciated that specific functions, and accordingly utilities, of GAM907 correlate with, and may be deduced from, the identity of the target genes which GAM907 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14326] Nucleotide sequences of the GAM907 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM907 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM907 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM907 are further described hereinbelow with reference to Table Table1.

[14327] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM907 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14328] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 908 (GAM908) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14329] GAM908 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM908 was detected is described hereinabove with reference to Figs. 2-8.

[14330] GAM908 gene, herein designated GAM GENE, and GAM908 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14331] GAM908 gene, herein designated GAM GENE, encodes a GAM908 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM908 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM908 precursor RNA is designated SEQ ID:881, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:881 is located at position 5664059 relative to contig NT_010966.11, on chromosome 18.

[14332] GAM908 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM908 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14333] An enzyme complex designated DICER COMPLEX, dices the GAM908 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM908 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM908 RNA is designated SEQ ID:2557, and is provided hereinbelow with reference to the sequence listing part.

[14334] GAM908 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM908 target RNA, herein designated GAM TARGET RNA.

GAM908 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14335] GAM908 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM908 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM908 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM908 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM908 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14336] The complementary binding of GAM908 RNA, herein designated GAM RNA, to target binding sites on GAM908 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM908 target RNA, herein designated GAM TARGET RNA, into GAM908 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14337] It is appreciated that GAM908 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM908 target genes. The mRNA of each one of this plurality of GAM908 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM908 RNA, herein designated GAM RNA, and which when bound by GAM908 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM908 target proteins.

[14338] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM908 gene, herein designated GAM GENE, on one or more GAM908 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14339] It is yet further appreciated that specific functions, and accordingly utilities, of GAM908 correlate with, and may be deduced from, the identity of the target genes which GAM908 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14340] Nucleotide sequences of the GAM908 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM908 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM908 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM908 are further described hereinbelow with reference to Table Table1.

[14341] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM908 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14342] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 909 (GAM909) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14343] GAM909 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM909 was detected is described hereinabove with reference to Figs. 2-8.

[14344] GAM909 gene, herein designated GAM GENE, and GAM909 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14345] GAM909 gene, herein designated GAM GENE, encodes a GAM909 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM909 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM909 precursor RNA is designated SEQ ID:882, and is provided hereinbelow with reference to the sequence listing part.

[14346] GAM909 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM909 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14347] An enzyme complex designated DICER COMPLEX, dices the GAM909 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM909 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM909 RNA is designated SEQ ID:2558, and is provided hereinbelow with reference to the sequence listing part.

[14348] GAM909 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM909 target RNA, herein designated GAM TARGET RNA. GAM909 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14349] GAM909 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM909 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM909 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM909 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM909 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14350] The complementary binding of GAM909 RNA, herein designated GAM RNA, to target binding sites on GAM909 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM909 target RNA, herein designated GAM TARGET RNA, into GAM909 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14351] It is appreciated that GAM909 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM909 target genes. The mRNA of each one of this plurality of GAM909 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM909 RNA, herein designated GAM RNA, and which when bound by GAM909 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM909 target proteins.

[14352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM909 gene, herein designated GAM GENE, on one or more GAM909 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14353] It is yet further appreciated that specific functions, and accordingly utilities, of GAM909 correlate with, and may

be deduced from, the identity of the target genes which GAM909 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14354] Nucleotide sequences of the GAM909 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM909 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM909 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM909 are further described hereinbelow with reference to Table Table1.

[14355] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM909 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14356] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 910 (GAM910) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14357] GAM910 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM910 was detected is described hereinabove with reference to Figs. 2-8.

[14358] GAM910 gene, herein designated GAM GENE, and GAM910 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14359] GAM910 gene, herein designated GAM GENE, encodes a GAM910 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM910 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM910 precursor RNA is designated SEQ ID:883, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:883 is located at position 4851362 relative to contig NT_022517.13, on chromosome 3.

[14360] GAM910 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM910 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14361] An enzyme complex designated DICER COMPLEX, dices the GAM910 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM910 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM910 RNA is designated SEQ ID:2559, and is provided hereinbelow with reference to the sequence listing part.

[14362] GAM910 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM910 target RNA, herein designated GAM TARGET RNA. GAM910 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14363] GAM910 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM910 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM910 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM910 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM910 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14364] The complementary binding of GAM910 RNA, herein designated GAM RNA, to target binding sites on GAM910 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM910 target RNA, herein designated GAM TARGET RNA, into GAM910 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14365] It is appreciated that GAM910 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM910 target genes. The mRNA of each one of this plurality of GAM910 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM910 RNA, herein designated GAM RNA, and which when bound by GAM910 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM910 target proteins.

[14366] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM910 gene, herein designated GAM GENE, on one or more GAM910 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14367] It is yet further appreciated that specific functions, and accordingly utilities, of GAM910 correlate with, and may be deduced from, the identity of the target genes which GAM910 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14368] Nucleotide sequences of the GAM910 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM910 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM910 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM910 are further described hereinbelow with reference to Table Table1.

[14369] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM910 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14370] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 911 (GAM911) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14371] GAM911 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM911 was detected is described hereinabove with reference to Figs. 2-8.

[14372] GAM911 gene, herein designated GAM GENE, and GAM911 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14373] GAM911 gene, herein designated GAM GENE, encodes a GAM911 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM911 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM911 precursor RNA is desig-

nated SEQ ID:884, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:884 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[14374] GAM911 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14375] An enzyme complex designated DICER COMPLEX, dices the GAM911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM911 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM911 RNA is designated SEQ ID:2560, and is provided hereinbelow with reference to the sequence listing part.

[14376] GAM911 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM911 target RNA, herein designated GAM TARGET RNA. GAM911 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14377] GAM911 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM911 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM911 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM911 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM911 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14378] The complementary binding of GAM911 RNA, herein designated GAM RNA, to target binding sites on GAM911 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM911 target RNA, herein designated GAM TARGET RNA, into GAM911 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14379] It is appreciated that GAM911 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM911 target genes. The mRNA of each one of this plurality of GAM911 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM911 RNA, herein designated GAM RNA, and which when bound by GAM911 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM911 target proteins.

[14380] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM911 gene, herein designated GAM GENE, on one or more GAM911 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14381] It is yet further appreciated that specific functions, and accordingly utilities, of GAM911 correlate with, and may be deduced from, the identity of the target genes which GAM911 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14382] Nucleotide sequences of the GAM911 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM911 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM911 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM911 are further described hereinbelow with reference to Table Table1.

[14383] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM911 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14384] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 912 (GAM912) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14385] GAM912 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM912 was detected is described hereinabove with reference to Figs. 2-8.

[14386] GAM912 gene, herein designated GAM GENE, and GAM912 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14387] GAM912 gene, herein designated GAM GENE, encodes a GAM912 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM912 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM912 precursor RNA is designated SEQ ID:885, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:885 is located at position 9102844 relative to contig NT_017568.11, on chromosome 9.

[14388] GAM912 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM912 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[14389] An enzyme complex designated DICER COMPLEX, dices the GAM912 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM912 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM912 RNA is designated SEQ ID:2561, and is provided hereinbelow with reference to the sequence listing part.

[14390] GAM912 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM912 target RNA, herein designated GAM TARGET RNA. GAM912 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14391] GAM912 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM912 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM912 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM912 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM912 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14392] The complementary binding of GAM912 RNA, herein designated GAM RNA, to target binding sites on GAM912 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM912 target RNA, herein designated GAM TARGET RNA, into GAM912 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14393] It is appreciated that GAM912 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM912 target genes. The mRNA of each one of this plurality of GAM912 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM912 RNA, herein designated GAM RNA, and which when bound by GAM912 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM912 target proteins.

[14394] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM912 gene, herein designated GAM GENE, on one or more GAM912 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14395] It is yet further appreciated that specific functions, and accordingly utilities, of GAM912 correlate with, and may be deduced from, the identity of the target genes which GAM912 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14396] Nucleotide sequences of the GAM912 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM912 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM912 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM912 are further described hereinbelow with reference to Table Table1.

[14397] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM912 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14398] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 913 (GAM913) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14399] GAM913 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM913 was detected is described hereinabove with reference to Figs. 2-8.

[14400] GAM913 gene, herein designated GAM GENE, and GAM913 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14401] GAM913 gene, herein designated GAM GENE, encodes a GAM913 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM913 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM913 precursor RNA is designated SEQ ID:886, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:886 is located at position 2742456 relative to con-

tig NT_033951.3, on chromosome 6.

[14402] GAM913 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14403] An enzyme complex designated DICER COMPLEX, dices the GAM913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM913 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM913 RNA is designated SEQ ID:2562, and is provided hereinbelow with reference to the sequence listing part.

[14404] GAM913 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM913 target RNA, herein designated GAM TARGET RNA.

GAM913 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14405] GAM913 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM913 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM913 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM913 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM913 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14406] The complementary binding of GAM913 RNA, herein designated GAM RNA, to target binding sites on GAM913 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM913 target RNA, herein designated GAM TARGET RNA, into GAM913 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14407] It is appreciated that GAM913 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM913 target genes. The mRNA of each one of this plurality of GAM913 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM913 RNA, herein designated GAM RNA, and which when bound by GAM913 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM913 target proteins.

[14408] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM913 gene, herein designated GAM GENE, on one or more GAM913 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14409] It is yet further appreciated that specific functions, and accordingly utilities, of GAM913 correlate with, and may be deduced from, the identity of the target genes which GAM913 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14410] Nucleotide sequences of the GAM913 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM913 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM913 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM913 are further described hereinbelow with reference to Table Table1.

[14411] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM913 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14412] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 914 (GAM914) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14413] GAM914 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM914 was detected is described hereinabove with reference to Figs. 2-8.

[14414] GAM914 gene, herein designated GAM GENE, and GAM914 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14415] GAM914 gene, herein designated GAM GENE, encodes a GAM914 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM914 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM914 precursor RNA is designated SEQ ID:887, and is provided hereinbelow with reference to the sequence listing part.

[14416] GAM914 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14417] An enzyme complex designated DICER COMPLEX, dices the GAM914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM914 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM914 RNA is designated SEQ ID:2563, and is provided hereinbelow with reference to the sequence listing part.

[14418] GAM914 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM914 target RNA, herein designated GAM TARGET RNA. GAM914 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14419] GAM914 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM914 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM914 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM914 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM914 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14420] The complementary binding of GAM914 RNA, herein designated GAM RNA, to target binding sites on GAM914 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM914 target RNA, herein designated GAM TARGET RNA, into GAM914 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14421] It is appreciated that GAM914 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM914 target genes. The mRNA of each one of this plu-

rality of GAM914 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM914 RNA, herein designated GAM RNA, and which when bound by GAM914 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM914 target proteins.

[14422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM914 gene, herein designated GAM GENE, on one or more GAM914 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14423] It is yet further appreciated that specific functions, and accordingly utilities, of GAM914 correlate with, and may be deduced from, the identity of the target genes which GAM914 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14424] Nucleotide sequences of the GAM914 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM914 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM914 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM914 are further described hereinbelow with reference to Table Table1.

[14425] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM914 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14426] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 915 (GAM915) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[14427] GAM915 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM915 was detected is described hereinabove with reference to Figs. 2-8.

[14428] GAM915 gene, herein designated GAM GENE, and GAM915 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14429] GAM915 gene, herein designated GAM GENE, encodes a GAM915 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM915 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM915 precursor RNA is designated SEQ ID:888, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:888 is located at position 11442844 relative to contig NT_007914.10, on chromosome 7.

[14430] GAM915 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM915 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14431] An enzyme complex designated DICER COMPLEX, dices the GAM915 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM915 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM915 RNA is designated SEQ ID:2564, and is provided hereinbelow with reference to the sequence listing part.

[14432] GAM915 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM915 target RNA, herein designated GAM TARGET RNA. GAM915 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14433] GAM915 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM915 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM915 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM915 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM915 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14434] The complementary binding of GAM915 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM915 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM915 target RNA, herein designated GAM TARGET RNA, into GAM915 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14435] It is appreciated that GAM915 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM915 target genes. The mRNA of each one of this plurality of GAM915 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM915 RNA, herein designated GAM RNA, and which when bound by GAM915 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM915 target proteins.

[14436] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM915 gene, herein designated GAM GENE, on one or more GAM915 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14437] It is yet further appreciated that specific functions, and accordingly utilities, of GAM915 correlate with, and may be deduced from, the identity of the target genes which GAM915 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14438] Nucleotide sequences of the GAM915 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM915 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM915 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM915 are further described hereinbelow with reference to Table Table1.

[14439] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM915 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14440] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 916 (GAM916) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14441] GAM916 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM916 was detected is described hereinabove with reference to Figs. 2-8.

[14442] GAM916 gene, herein designated GAM GENE, and GAM916 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14443] GAM916 gene, herein designated GAM GENE, encodes a GAM916 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM916 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM916 precursor RNA is designated SEQ ID:889, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:889 is located at position 3434864 relative to contig NT_009714.13, on chromosome 12.

[14444] GAM916 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99808, which mouse homolog is detected in mouse EST accession BG288438.1.

[14445] GAM916 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM916 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14446] An enzyme complex designated DICER COMPLEX, dices the GAM916 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM916 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM916 RNA is designated SEQ ID:2565, and is provided hereinbelow with reference to the sequence listing part.

[14447] GAM916 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM916 target RNA, herein designated GAM TARGET RNA. GAM916 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14448] GAM916 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM916 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM916 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM916 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM916 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14449] The complementary binding of GAM916 RNA, herein designated GAM RNA, to target binding sites on GAM916 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM916 target RNA, herein designated GAM TARGET RNA, into GAM916 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14450] It is appreciated that GAM916 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM916 target genes. The mRNA of each one of this plurality of GAM916 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM916 RNA, herein designated GAM RNA, and which when bound by GAM916 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM916 target proteins.

[14451] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM916 gene, herein designated GAM GENE, on one or more GAM916 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14452] It is yet further appreciated that specific functions, and accordingly utilities, of GAM916 correlate with, and may be deduced from, the identity of the target genes which GAM916 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14453] Nucleotide sequences of the GAM916 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM916 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM916 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM916 are further described hereinbelow with reference to Table Table1.

[14454] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM916 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14455] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

917 (GAM917) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14456] GAM917 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM917 was detected is described hereinabove with reference to Figs. 2-8.

[14457] GAM917 gene, herein designated GAM GENE, and GAM917 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14458] GAM917 gene, herein designated GAM GENE, encodes a GAM917 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM917 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM917 precursor RNA is designated SEQ ID:890, and is provided hereinbelow with reference to the sequence listing part.

[14459] GAM917 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM917 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14460] An enzyme complex designated DICER COMPLEX, dices the GAM917 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM917 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM917 RNA is designated SEQ ID:2566, and is provided hereinbelow with reference to the sequence listing part.

[14461] GAM917 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM917 target RNA, herein designated GAM TARGET RNA. GAM917 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14462] GAM917 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM917 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM917 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM917 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM917 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14463] The complementary binding of GAM917 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM917 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM917 target RNA, herein designated GAM TARGET RNA, into GAM917 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14464] It is appreciated that GAM917 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM917 target genes. The mRNA of each one of this plurality of GAM917 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM917 RNA, herein designated GAM RNA, and which when bound by GAM917 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM917 target proteins.

[14465] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM917 gene, herein designated GAM GENE, on one or more GAM917 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14466] It is yet further appreciated that specific functions, and accordingly utilities, of GAM917 correlate with, and may be deduced from, the identity of the target genes which GAM917 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14467] Nucleotide sequences of the GAM917 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM917 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM917 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM917 are further described hereinbelow with reference to Table Table1.

[14468] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM917 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14469] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 918 (GAM918) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14470] GAM918 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM918 was detected is described hereinabove with reference to Figs. 2-8.

[14471] GAM918 gene, herein designated GAM GENE, and GAM918 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14472] GAM918 gene, herein designated GAM GENE, encodes a GAM918 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM918 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM918 precursor RNA is designated SEQ ID:891, and is provided hereinbelow with reference to the sequence listing part.

[14473] GAM918 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM918 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14474] An enzyme complex designated DICER COMPLEX, dices the GAM918 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM918 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM918 RNA is designated SEQ ID:2567, and is provided hereinbelow with reference to the sequence listing part.

[14475] GAM918 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM918 target RNA, herein designated GAM TARGET RNA. GAM918 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14476] GAM918 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM918 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM918 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM918 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM918 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14477] The complementary binding of GAM918 RNA, herein designated GAM RNA, to target binding sites on GAM918 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM918 target RNA, herein designated GAM TARGET RNA, into GAM918 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14478] It is appreciated that GAM918 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM918 target genes. The mRNA of each one of this plurality of GAM918 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM918 RNA, herein designated GAM RNA, and which when bound by GAM918 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM918 target proteins.

[14479] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM918 gene, herein designated GAM GENE, on one or more GAM918 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14480] It is yet further appreciated that specific functions, and accordingly utilities, of GAM918 correlate with, and may be deduced from, the identity of the target genes which GAM918 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14481] Nucleotide sequences of the GAM918 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM918 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM918 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM918 are further described hereinbelow with reference to Table Table1.

[14482] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM918 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14483] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 919 (GAM919) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14484] GAM919 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM919 was detected is described hereinabove with reference to Figs. 2-8.

[14485] GAM919 gene, herein designated GAM GENE, and GAM919 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14486] GAM919 gene, herein designated GAM GENE, encodes a GAM919 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM919 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM919 precursor RNA is designated SEQ ID:892, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:892 is located at position 990016 relative to contig NT_009458.12, on chromosome 12.

[14487] GAM919 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM919 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[14488] An enzyme complex designated DICER COMPLEX, dices the GAM919 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM919 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM919 RNA is designated SEQ ID:2568, and is provided hereinbelow with reference to the sequence listing part.

[14489] GAM919 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM919 target RNA, herein designated GAM TARGET RNA. GAM919 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14490] GAM919 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM919 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM919 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM919 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM919 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14491] The complementary binding of GAM919 RNA, herein designated GAM RNA, to target binding sites on GAM919 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM919 target RNA, herein designated GAM TARGET RNA, into GAM919 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14492] It is appreciated that GAM919 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM919 target genes. The mRNA of each one of this plurality of GAM919 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM919 RNA, herein designated GAM RNA, and which when bound by GAM919 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM919 target proteins.

[14493] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM919 gene, herein designated GAM GENE, on one or more GAM919 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14494] It is yet further appreciated that specific functions, and accordingly utilities, of GAM919 correlate with, and may be deduced from, the identity of the target genes which GAM919 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14495] Nucleotide sequences of the GAM919 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM919 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM919 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM919 are further described hereinbelow with reference to Table Table1.

[14496] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM919 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14497] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 920 (GAM920) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14498] GAM920 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM920 was detected is described hereinabove with reference to Figs. 2-8.

[14499] GAM920 gene, herein designated GAM GENE, and GAM920 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14500] GAM920 gene, herein designated GAM GENE, encodes a GAM920 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM920 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM920 precursor RNA is designated SEQ ID:893, and is provided hereinbelow with reference to the sequence listing part.

[14501] GAM920 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM920 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14502] An enzyme complex designated DICER COMPLEX, dices the GAM920 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM920 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM920 RNA is designated SEQ ID:2569, and is provided hereinbelow with reference to the sequence listing part.

[14503] GAM920 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM920 target RNA, herein designated GAM TARGET RNA.

GAM920 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14504] GAM920 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM920 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM920 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM920 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM920 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14505] The complementary binding of GAM920 RNA, herein designated GAM RNA, to target binding sites on GAM920 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM920 target RNA, herein designated GAM TARGET RNA, into GAM920 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14506] It is appreciated that GAM920 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM920 target genes. The mRNA of each one of this plurality of GAM920 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM920 RNA, herein designated GAM RNA, and which when bound by GAM920 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM920 target proteins.

[14507] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM920 gene, herein designated GAM GENE, on one or more GAM920 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14508] It is yet further appreciated that specific functions, and accordingly utilities, of GAM920 correlate with, and may be deduced from, the identity of the target genes which GAM920 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14509] Nucleotide sequences of the GAM920 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM920 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM920 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM920 are further described hereinbelow with reference to Table Table1.

[14510] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM920 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14511] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 921 (GAM921) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14512] GAM921 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM921 was detected is described hereinabove with reference to Figs. 2-8.

[14513] GAM921 gene, herein designated GAM GENE, and GAM921 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14514] GAM921 gene, herein designated GAM GENE, encodes a GAM921 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM921 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM921 precursor RNA is designated SEQ ID:894, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:894 is located at position 31728536 relative to contig NT_007933.10, on chromosome 7.

[14515] GAM921 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM921 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14516] An enzyme complex designated DICER COMPLEX, dices the GAM921 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM921 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM921 RNA is designated SEQ ID:2570, and is provided hereinbelow with reference to the sequence listing part.

[14517] GAM921 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM921 target RNA, herein designated GAM TARGET RNA. GAM921 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14518] GAM921 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM921 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM921 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM921 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM921 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14519] The complementary binding of GAM921 RNA, herein designated GAM RNA, to target binding sites on GAM921 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM921 target RNA, herein designated GAM TARGET RNA, into GAM921 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14520] It is appreciated that GAM921 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM921 target genes. The mRNA of each one of this plu-

rality of GAM921 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM921 RNA, herein designated GAM RNA, and which when bound by GAM921 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM921 target proteins.

[14521] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM921 gene, herein designated GAM GENE, on one or more GAM921 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14522] It is yet further appreciated that specific functions, and accordingly utilities, of GAM921 correlate with, and may be deduced from, the identity of the target genes which GAM921 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14523] Nucleotide sequences of the GAM921 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM921 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM921 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM921 are further described hereinbelow with reference to Table Table1.

[14524] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM921 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14525] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 922 (GAM922) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[14526] GAM922 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM922 was detected is described hereinabove with reference to Figs. 2-8.

[14527] GAM922 gene, herein designated GAM GENE, and GAM922 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14528] GAM922 gene, herein designated GAM GENE, encodes a GAM922 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM922 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM922 precursor RNA is designated SEQ ID:895, and is provided hereinbelow with reference to the sequence listing part.

[14529] GAM922 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM922 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14530] An enzyme complex designated DICER COMPLEX, dices the GAM922 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM922 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM922 RNA is designated SEQ ID:2571, and is provided hereinbelow with reference to the sequence listing part.

[14531] GAM922 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM922 target RNA, herein designated GAM TARGET RNA.
GAM922 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14532] GAM922 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM922 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM922 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM922 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM922 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14533] The complementary binding of GAM922 RNA, herein designated GAM RNA, to target binding sites on GAM922 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM922 target RNA, herein designated GAM TARGET RNA, into GAM922 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14534] It is appreciated that GAM922 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM922 target genes. The mRNA of each one of this plurality of GAM922 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM922 RNA, herein designated GAM RNA, and which when bound by GAM922 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM922 target proteins.

[14535] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM922 gene, herein designated GAM GENE, on one or more GAM922 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14536] It is yet further appreciated that specific functions, and accordingly utilities, of GAM922 correlate with, and may be deduced from, the identity of the target genes which GAM922 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14537] Nucleotide sequences of the GAM922 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM922 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM922 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM922 are further described hereinbelow with reference to Table Table1.

[14538] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM922 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14539] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 923 (GAM923) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14540] GAM923 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM923 was detected is described hereinabove with reference to Figs. 2-8.

[14541] GAM923 gene, herein designated GAM GENE, and GAM923 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14542] GAM923 gene, herein designated GAM GENE, encodes a GAM923 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM923 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM923 precursor RNA is desig-

nated SEQ ID:896, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:896 is located at position 3102838 relative to contig NT_011109.13, on chromosome 19.

[14543] GAM923 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM923 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14544] An enzyme complex designated DICER COMPLEX, dices the GAM923 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM923 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM923 RNA is designated SEQ ID:2572, and is provided hereinbelow with reference to the sequence listing part.

[14545] GAM923 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM923 target RNA, herein designated GAM TARGET RNA. GAM923 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14546] GAM923 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM923 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM923 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM923 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM923 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14547] The complementary binding of GAM923 RNA, herein designated GAM RNA, to target binding sites on GAM923 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM923 target RNA, herein designated GAM TARGET RNA, into GAM923 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14548] It is appreciated that GAM923 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM923 target genes. The mRNA of each one of this plurality of GAM923 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM923 RNA, herein designated GAM RNA, and which when bound by GAM923 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM923 target proteins.

[14549] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM923 gene, herein designated GAM GENE, on one or more GAM923 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14550] It is yet further appreciated that specific functions, and accordingly utilities, of GAM923 correlate with, and may be deduced from, the identity of the target genes which GAM923 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14551] Nucleotide sequences of the GAM923 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM923 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM923 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM923 are further described hereinbelow with reference to Table Table1.

[14552] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM923 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14553] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 924 (GAM924) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14554] GAM924 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM924 was detected is described hereinabove with reference to Figs. 2-8.

[14555] GAM924 gene, herein designated GAM GENE, and GAM924 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14556] GAM924 gene, herein designated GAM GENE, encodes a GAM924 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM924 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM924 precursor RNA is designated SEQ ID:897, and is provided hereinbelow with reference to the sequence listing part.

[14557] GAM924 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM924 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14558] An enzyme complex designated DICER COMPLEX, dices

the GAM924 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM924 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM924 RNA is designated SEQ ID:2573, and is provided hereinbelow with reference to the sequence listing part.

[14559] GAM924 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM924 target RNA, herein designated GAM TARGET RNA.

GAM924 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14560] GAM924 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM924 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM924

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM924 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM924 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14561] The complementary binding of GAM924 RNA, herein designated GAM RNA, to target binding sites on GAM924 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM924 target RNA, herein designated GAM TARGET RNA, into GAM924 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14562] It is appreciated that GAM924 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM924 target genes. The mRNA of each one of this plurality of GAM924 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM924 RNA, herein designated GAM RNA, and which when bound by GAM924 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM924 target proteins.

[14563] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM924 gene, herein designated GAM GENE, on one or more GAM924 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14564] It is yet further appreciated that specific functions, and accordingly utilities, of GAM924 correlate with, and may be deduced from, the identity of the target genes which GAM924 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14565] Nucleotide sequences of the GAM924 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM924 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM924 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM924 are further described hereinbelow with reference to Table Table1.

[14566] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM924 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14567] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 925 (GAM925) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14568] GAM925 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM925 was detected is described hereinabove with reference to Figs. 2-8.

[14569] GAM925 gene, herein designated GAM GENE, and GAM925 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14570] GAM925 gene, herein designated GAM GENE, encodes a GAM925 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM925 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM925 precursor RNA is designated SEQ ID:898, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:898 is located at position 1364370 relative to contig NT_035014.2, on chromosome 9.

[14571] GAM925 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM925 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14572] An enzyme complex designated DICER COMPLEX, dices the GAM925 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM925 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM925 RNA is designated SEQ ID:2574, and is provided hereinbelow with reference to the sequence listing part.

[14573] GAM925 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM925 target RNA, herein designated GAM TARGET RNA.

GAM925 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14574] GAM925 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM925 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM925 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM925 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM925 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14575] The complementary binding of GAM925 RNA, herein designated GAM RNA, to target binding sites on GAM925 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM925 target RNA, herein designated GAM TARGET RNA, into GAM925 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14576] It is appreciated that GAM925 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM925 target genes. The mRNA of each one of this plurality of GAM925 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM925 RNA, herein designated GAM RNA, and which when bound by GAM925 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM925 target proteins.

[14577] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM925 gene, herein designated GAM GENE, on one or more GAM925 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14578] It is yet further appreciated that specific functions, and accordingly utilities, of GAM925 correlate with, and may be deduced from, the identity of the target genes which GAM925 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14579] Nucleotide sequences of the GAM925 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM925 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM925 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM925 are further described hereinbelow with reference to Table Table1.

[14580] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM925 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14581] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 926 (GAM926) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14582] GAM926 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM926 was detected is described hereinabove with reference to Figs. 2-8.

[14583] GAM926 gene, herein designated GAM GENE, and GAM926 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14584] GAM926 gene, herein designated GAM GENE, encodes a GAM926 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM926 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM926 precursor RNA is designated SEQ ID:899, and is provided hereinbelow with reference to the sequence listing part.

[14585] GAM926 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99174, which mouse homolog is detected in mouse EST accession BE571903.1.

[14586] GAM926 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM926 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14587] An enzyme complex designated DICER COMPLEX, dices

the GAM926 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM926 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM926 RNA is designated SEQ ID:2575, and is provided hereinbelow with reference to the sequence listing part.

[14588] GAM926 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM926 target RNA, herein designated GAM TARGET RNA. GAM926 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14589] GAM926 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM926 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM926

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM926 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM926 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14590] The complementary binding of GAM926 RNA, herein designated GAM RNA, to target binding sites on GAM926 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM926 target RNA, herein designated GAM TARGET RNA, into GAM926 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14591] It is appreciated that GAM926 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM926 target genes. The mRNA of each one of this plurality of GAM926 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM926 RNA, herein designated GAM RNA, and which when bound by GAM926 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM926 target proteins.

[14592] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM926 gene, herein designated GAM GENE, on one or more GAM926 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14593] It is yet further appreciated that specific functions, and accordingly utilities, of GAM926 correlate with, and may be deduced from, the identity of the target genes which GAM926 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14594] Nucleotide sequences of the GAM926 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM926 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM926 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM926 are further described hereinbelow with reference to Table Table1.

[14595] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM926 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14596] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 927 (GAM927) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14597] GAM927 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM927 was detected is described hereinabove with reference to Figs. 2-8.

[14598] GAM927 gene, herein designated GAM GENE, and GAM927 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14599] GAM927 gene, herein designated GAM GENE, encodes a GAM927 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM927 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM927 precursor RNA is designated SEQ ID:900, and is provided hereinbelow with reference to the sequence listing part.

[14600] GAM927 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14601] An enzyme complex designated DICER COMPLEX, dices the GAM927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM927 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM927 RNA is designated SEQ ID:2576, and is provided hereinbelow with reference to the sequence listing part.

[14602] GAM927 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM927 target RNA, herein designated GAM TARGET RNA. GAM927 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14603] GAM927 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM927 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM927 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM927 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM927 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14604] The complementary binding of GAM927 RNA, herein designated GAM RNA, to target binding sites on GAM927 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM927 target RNA, herein designated GAM TARGET RNA, into GAM927 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14605] It is appreciated that GAM927 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM927 target genes. The mRNA of each one of this plurality of GAM927 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM927 RNA, herein designated GAM RNA, and which when bound by GAM927 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM927 target proteins.

[14606] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM927 gene, herein designated GAM GENE, on one or more GAM927 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14607] It is yet further appreciated that specific functions, and accordingly utilities, of GAM927 correlate with, and may be deduced from, the identity of the target genes which GAM927 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14608] Nucleotide sequences of the GAM927 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM927 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM927 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM927 are further described hereinbelow with reference to Table Table1.

[14609] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM927 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14610] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 928 (GAM928) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14611] GAM928 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM928 was detected is described hereinabove with reference to Figs. 2-8.

[14612] GAM928 gene, herein designated GAM GENE, and GAM928 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14613] GAM928 gene, herein designated GAM GENE, encodes a GAM928 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM928 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM928 precursor RNA is designated SEQ ID:901, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:901 is located at position 6507022 relative to contig NT_022792.13, on chromosome 4.

[14614] GAM928 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM928 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14615] An enzyme complex designated DICER COMPLEX, dices the GAM928 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM928 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM928 RNA is designated SEQ ID:2577, and is provided hereinbelow with reference to the sequence listing part.

[14616] GAM928 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM928 target RNA, herein designated GAM TARGET RNA. GAM928 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14617] GAM928 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM928 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM928 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM928 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM928 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14618] The complementary binding of GAM928 RNA, herein designated GAM RNA, to target binding sites on GAM928 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM928 target RNA, herein designated GAM TARGET RNA, into GAM928 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14619] It is appreciated that GAM928 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM928 target genes. The mRNA of each one of this plurality of GAM928 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM928 RNA, herein designated GAM RNA, and which when bound by GAM928 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM928 target proteins.

[14620] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM928 gene, herein designated GAM GENE, on one or more GAM928 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14621] It is yet further appreciated that specific functions, and accordingly utilities, of GAM928 correlate with, and may

be deduced from, the identity of the target genes which GAM928 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14622] Nucleotide sequences of the GAM928 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM928 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM928 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM928 are further described hereinbelow with reference to Table Table1.

[14623] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM928 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14624] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 929 (GAM929) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14625] GAM929 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM929 was detected is described hereinabove with reference to Figs. 2-8.

[14626] GAM929 gene, herein designated GAM GENE, and GAM929 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14627] GAM929 gene, herein designated GAM GENE, encodes a GAM929 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM929 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM929 precursor RNA is designated SEQ ID:902, and is provided hereinbelow with reference to the sequence listing part.

[14628] GAM929 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM929 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-

reversed sequence of the nucleotide sequence of the second half thereof.

[14629] An enzyme complex designated DICER COMPLEX, dices the GAM929 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM929 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM929 RNA is designated SEQ ID:2578, and is provided hereinbelow with reference to the sequence listing part.

[14630] GAM929 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM929 target RNA, herein designated GAM TARGET RNA.
GAM929 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14631] GAM929 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM929 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM929 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM929 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM929 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14632] The complementary binding of GAM929 RNA, herein designated GAM RNA, to target binding sites on GAM929 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM929 target RNA, herein desig-

nated GAM TARGET RNA, into GAM929 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14633] It is appreciated that GAM929 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM929 target genes. The mRNA of each one of this plurality of GAM929 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM929 RNA, herein designated GAM RNA, and which when bound by GAM929 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM929 target proteins.

[14634] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM929 gene, herein designated GAM GENE, on one or more GAM929 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14635] It is yet further appreciated that specific functions, and accordingly utilities, of GAM929 correlate with, and may be deduced from, the identity of the target genes which GAM929 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14636] Nucleotide sequences of the GAM929 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM929 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM929 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM929 are further described hereinbelow with reference to Table Table1.

[14637] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM929 RNA, herein designated GAM RNA, are described

hereinbelow with reference to Table Table2.

[14638] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 930 (GAM930) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14639] GAM930 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM930 was detected is described hereinabove with reference to Figs. 2-8.

[14640] GAM930 gene, herein designated GAM GENE, and GAM930 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14641] GAM930 gene, herein designated GAM GENE, encodes a GAM930 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM930 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM930 precursor RNA is designated SEQ ID:903, and is provided hereinbelow with reference to the sequence listing part.

[14642] GAM930 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM930 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14643] An enzyme complex designated DICER COMPLEX, dices the GAM930 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM930 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM930 RNA is designated SEQ ID:2579, and is provided hereinbelow with reference to the sequence listing part.

[14644] GAM930 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM930

target RNA, herein designated GAM TARGET RNA.

GAM930 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14645] GAM930 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM930 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM930 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM930 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM930 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14646] The complementary binding of GAM930 RNA, herein designated GAM RNA, to target binding sites on GAM930 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM930 target RNA, herein designated GAM TARGET RNA, into GAM930 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14647] It is appreciated that GAM930 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM930 target genes. The mRNA of each one of this plurality of GAM930 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM930 RNA, herein designated GAM RNA, and which when bound by GAM930 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM930 target proteins.

[14648] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM930 gene, herein designated GAM GENE, on one or more GAM930 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14649] It is yet further appreciated that specific functions, and accordingly utilities, of GAM930 correlate with, and may be deduced from, the identity of the target genes which GAM930 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14650] Nucleotide sequences of the GAM930 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM930 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM930 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM930 are further described hereinbelow with reference to Table Table1.

[14651] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM930 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14652] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 931 (GAM931) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14653] GAM931 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM931 was detected is described hereinabove with reference to Figs. 2-8.

[14654] GAM931 gene, herein designated GAM GENE, and GAM931 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14655] GAM931 gene, herein designated GAM GENE, encodes a

GAM931 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM931 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM931 precursor RNA is designated SEQ ID:904, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:904 is located at position 362037 relative to contig NT_035014.2, on chromosome 9.

[14656] GAM931 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14657] An enzyme complex designated DICER COMPLEX, dices the GAM931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM931 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM931 RNA is designated SEQ ID:2580, and is provided hereinbelow with reference to the sequence listing part.

[14658] GAM931 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM931 target RNA, herein designated GAM TARGET RNA.
GAM931 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14659] GAM931 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM931 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM931 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM931 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM931 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14660] The complementary binding of GAM931 RNA, herein designated GAM RNA, to target binding sites on GAM931 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM931 target RNA, herein designated GAM TARGET RNA, into GAM931 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14661] It is appreciated that GAM931 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM931 target genes. The mRNA of each one of this plurality of GAM931 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM931 RNA, herein designated GAM RNA, and which when bound by GAM931 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM931 target proteins.

[14662] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM931 gene, herein designated GAM GENE, on one or more GAM931 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[14663] It is yet further appreciated that specific functions, and accordingly utilities, of GAM931 correlate with, and may be deduced from, the identity of the target genes which GAM931 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14664] Nucleotide sequences of the GAM931 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM931 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM931 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM931 are further described hereinbelow with reference to Table Table1.

[14665] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM931 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14666] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 932 (GAM932) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[14667] GAM932 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM932 was detected is described hereinabove with reference to Figs. 2-8.

[14668] GAM932 gene, herein designated GAM GENE, and GAM932 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14669] GAM932 gene, herein designated GAM GENE, encodes a GAM932 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM932 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM932 precursor RNA is designated SEQ ID:905, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:905 is located at position 1259564 relative to contig NT_025965.9, on chromosome X.

[14670] GAM932 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR

RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14671] An enzyme complex designated DICER COMPLEX, dices the GAM932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM932 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM932 RNA is designated SEQ ID:2581, and is provided hereinbelow with reference to the sequence listing part.

[14672] GAM932 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM932 target RNA, herein designated GAM TARGET RNA. GAM932 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a

protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14673] GAM932 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM932 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM932 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM932 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM932 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14674] The complementary binding of GAM932 RNA, herein designated GAM RNA, to target binding sites on GAM932 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM932 target RNA, herein designated GAM TARGET RNA, into GAM932 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14675] It is appreciated that GAM932 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM932 target genes. The mRNA of each one of this plurality of GAM932 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM932 RNA, herein designated GAM RNA, and which when bound by GAM932 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM932 target proteins.

[14676] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM932 gene, herein designated GAM GENE, on one or more GAM932 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14677] It is yet further appreciated that specific functions, and accordingly utilities, of GAM932 correlate with, and may be deduced from, the identity of the target genes which GAM932 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14678] Nucleotide sequences of the GAM932 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM932 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM932 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM932 are further described hereinbelow with reference to Table Table1.

[14679] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM932 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14680] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 933 (GAM933) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14681] GAM933 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM933 was detected is described hereinabove with reference to Figs. 2-8.

[14682] GAM933 gene, herein designated GAM GENE, and GAM933 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14683] GAM933 gene, herein designated GAM GENE, encodes a GAM933 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM933 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM933 precursor RNA is designated SEQ ID:906, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:906 is located at position 2934168 relative to contig NT_009458.12, on chromosome 12.

[14684] GAM933 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[14685] SEQ ID:99561 detected in mouse EST Accession AA692083.1.

[14686] SEQ ID:99562 detected in mouse EST Accession BI202421.1.

[14687] GAM933 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14688] An enzyme complex designated DICER COMPLEX, dices the GAM933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM933 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM933 RNA is designated SEQ ID:2582, and is provided hereinbelow with reference to the sequence listing part.

[14689] GAM933 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM933 target RNA, herein designated GAM TARGET RNA.
GAM933 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14690] GAM933 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM933 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM933 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM933 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM933 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14691] The complementary binding of GAM933 RNA, herein designated GAM RNA, to target binding sites on GAM933 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM933 target RNA, herein designated GAM TARGET RNA, into GAM933 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14692] It is appreciated that GAM933 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM933 target genes. The mRNA of each one of this plurality of GAM933 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM933 RNA, herein designated GAM RNA, and which when bound by GAM933 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM933 target proteins.

[14693] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM933 gene, herein designated GAM GENE, on one or more GAM933 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14694] It is yet further appreciated that specific functions, and accordingly utilities, of GAM933 correlate with, and may be deduced from, the identity of the target genes which GAM933 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14695] Nucleotide sequences of the GAM933 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM933 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM933 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM933 are further described hereinbelow with reference to Table Table1.

[14696] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM933 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14697] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 934 (GAM934) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14698] GAM934 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM934 was detected is described hereinabove with reference to Figs. 2-8.

[14699] GAM934 gene, herein designated GAM GENE, and GAM934 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14700] GAM934 gene, herein designated GAM GENE, encodes a GAM934 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM934 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM934 precursor RNA is designated SEQ ID:907, and is provided hereinbelow with refer-

ence to the sequence listing part.

[14701] GAM934 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM934 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14702] An enzyme complex designated DICER COMPLEX, dices the GAM934 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM934 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM934 RNA is designated SEQ ID:2583, and is provided hereinbelow with reference to the sequence listing part.

[14703] GAM934 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM934 target RNA, herein designated GAM TARGET RNA.

GAM934 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14704] GAM934 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM934 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM934 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM934 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM934 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14705] The complementary binding of GAM934 RNA, herein designated GAM RNA, to target binding sites on GAM934 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM934 target RNA, herein designated GAM TARGET RNA, into GAM934 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14706] It is appreciated that GAM934 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM934 target genes. The mRNA of each one of this plurality of GAM934 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM934 RNA, herein designated GAM RNA, and which when bound by GAM934 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM934 target proteins.

[14707] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM934 gene, herein designated GAM GENE, on one or more GAM934 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14708] It is yet further appreciated that specific functions, and accordingly utilities, of GAM934 correlate with, and may be deduced from, the identity of the target genes which GAM934 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14709] Nucleotide sequences of the GAM934 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM934 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM934 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM934 are further described hereinbelow with reference to Table Table1.

[14710] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM934 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14711] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 935 (GAM935) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14712] GAM935 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM935 was detected is described hereinabove with reference to Figs. 2-8.

[14713] GAM935 gene, herein designated GAM GENE, and GAM935 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14714] GAM935 gene, herein designated GAM GENE, encodes a GAM935 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM935 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM935 precursor RNA is designated SEQ ID:908, and is provided hereinbelow with reference to the sequence listing part.

[14715] GAM935 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM935 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14716] An enzyme complex designated DICER COMPLEX, dices the GAM935 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM935 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM935 RNA is designated SEQ ID:2584, and is provided hereinbelow with reference to the sequence listing part.

[14717] GAM935 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM935 target RNA, herein designated GAM TARGET RNA. GAM935 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14718] GAM935 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM935 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM935 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM935 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM935 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14719] The complementary binding of GAM935 RNA, herein designated GAM RNA, to target binding sites on GAM935 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM935 target RNA, herein designated GAM TARGET RNA, into GAM935 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14720] It is appreciated that GAM935 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM935 target genes. The mRNA of each one of this plu-

rality of GAM935 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM935 RNA, herein designated GAM RNA, and which when bound by GAM935 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM935 target proteins.

[14721] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM935 gene, herein designated GAM GENE, on one or more GAM935 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14722] It is yet further appreciated that specific functions, and accordingly utilities, of GAM935 correlate with, and may be deduced from, the identity of the target genes which GAM935 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14723] Nucleotide sequences of the GAM935 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM935 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM935 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM935 are further described hereinbelow with reference to Table Table1.

[14724] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM935 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14725] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 936 (GAM936) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[14726] GAM936 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM936 was detected is described hereinabove with reference to Figs. 2-8.

[14727] GAM936 gene, herein designated GAM GENE, and GAM936 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14728] GAM936 gene, herein designated GAM GENE, encodes a GAM936 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM936 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM936 precursor RNA is designated SEQ ID:909, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:909 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[14729] GAM936 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM936 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14730] An enzyme complex designated DICER COMPLEX, dices the GAM936 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM936 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM936 RNA is designated SEQ ID:2585, and is provided hereinbelow with reference to the sequence listing part.

[14731] GAM936 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM936 target RNA, herein designated GAM TARGET RNA. GAM936 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14732] GAM936 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM936 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM936 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM936 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM936 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14733] The complementary binding of GAM936 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM936 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM936 target RNA, herein designated GAM TARGET RNA, into GAM936 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14734] It is appreciated that GAM936 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM936 target genes. The mRNA of each one of this plurality of GAM936 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM936 RNA, herein designated GAM RNA, and which when bound by GAM936 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM936 target proteins.

[14735] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM936 gene, herein designated GAM GENE, on one or more GAM936 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14736] It is yet further appreciated that specific functions, and accordingly utilities, of GAM936 correlate with, and may be deduced from, the identity of the target genes which GAM936 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14737] Nucleotide sequences of the GAM936 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM936 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM936 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM936 are further described hereinbelow with reference to Table Table1.

[14738] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM936 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14739] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 937 (GAM937) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14740] GAM937 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM937 was detected is described hereinabove with reference to Figs. 2-8.

[14741] GAM937 gene, herein designated GAM GENE, and GAM937 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14742] GAM937 gene, herein designated GAM GENE, encodes a GAM937 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM937 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM937 precursor RNA is designated SEQ ID:910, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:910 is located at position 1005831 relative to contig NT_004852.13, on chromosome 1.

[14743] GAM937 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14744] An enzyme complex designated DICER COMPLEX, dices the GAM937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM937 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM937 RNA is designated SEQ ID:2586, and is provided hereinbelow with reference to the sequence listing part.

[14745] GAM937 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM937 target RNA, herein designated GAM TARGET RNA. GAM937 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14746] GAM937 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM937 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM937 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM937 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM937 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14747] The complementary binding of GAM937 RNA, herein designated GAM RNA, to target binding sites on GAM937 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM937 target RNA, herein designated GAM TARGET RNA, into GAM937 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14748] It is appreciated that GAM937 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM937 target genes. The mRNA of each one of this plurality of GAM937 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM937 RNA,

herein designated GAM RNA, and which when bound by GAM937 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM937 target proteins.

[14749] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM937 gene, herein designated GAM GENE, on one or more GAM937 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14750] It is yet further appreciated that specific functions, and accordingly utilities, of GAM937 correlate with, and may be deduced from, the identity of the target genes which

GAM937 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14751] Nucleotide sequences of the GAM937 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM937 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM937 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM937 are further described hereinbelow with reference to Table Table1.

[14752] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM937 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14753] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 938 (GAM938) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14754] GAM938 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM938 was detected is described hereinabove with reference to Figs. 2-8.

[14755] GAM938 gene, herein designated GAM GENE, and GAM938 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14756] GAM938 gene, herein designated GAM GENE, encodes a GAM938 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM938 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM938 precursor RNA is designated SEQ ID:911, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:911 is located at position 1005831 relative to contig NT_004852.13, on chromosome 1.

[14757] GAM938 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM938 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14758] An enzyme complex designated DICER COMPLEX, dices the GAM938 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM938 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM938 RNA is designated SEQ ID:2587, and is provided hereinbelow with reference to the sequence listing part.

[14759] GAM938 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM938 target RNA, herein designated GAM TARGET RNA. GAM938 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14760] GAM938 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM938 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM938 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM938 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM938 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14761] The complementary binding of GAM938 RNA, herein designated GAM RNA, to target binding sites on GAM938 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM938 target RNA, herein designated GAM TARGET RNA, into GAM938 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14762] It is appreciated that GAM938 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM938 target genes. The mRNA of each one of this plurality of GAM938 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM938 RNA, herein designated GAM RNA, and which when bound by GAM938 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM938 target proteins.

[14763] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM938 gene, herein designated GAM GENE, on one or more GAM938 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14764] It is yet further appreciated that specific functions, and accordingly utilities, of GAM938 correlate with, and may be deduced from, the identity of the target genes which GAM938 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14765] Nucleotide sequences of the GAM938 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM938 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM938 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM938 are further described hereinbelow with reference to Table Table1.

[14766] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM938 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14767] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 939 (GAM939) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14768] GAM939 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM939 was detected is described hereinabove with reference to Figs. 2-8.

[14769] GAM939 gene, herein designated GAM GENE, and GAM939 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14770] GAM939 gene, herein designated GAM GENE, encodes a GAM939 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM939 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM939 precursor RNA is designated SEQ ID:912, and is provided hereinbelow with refer-

ence to the sequence listing part.

[14771] GAM939 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM939 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14772] An enzyme complex designated DICER COMPLEX, dices the GAM939 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM939 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM939 RNA is designated SEQ ID:2588, and is provided hereinbelow with reference to the sequence listing part.

[14773] GAM939 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM939 target RNA, herein designated GAM TARGET RNA.

GAM939 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14774] GAM939 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM939 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM939 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM939 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM939 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14775] The complementary binding of GAM939 RNA, herein designated GAM RNA, to target binding sites on GAM939 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM939 target RNA, herein designated GAM TARGET RNA, into GAM939 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14776] It is appreciated that GAM939 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM939 target genes. The mRNA of each one of this plurality of GAM939 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM939 RNA, herein designated GAM RNA, and which when bound by GAM939 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM939 target proteins.

[14777] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM939 gene, herein designated GAM GENE, on one or more GAM939 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14778] It is yet further appreciated that specific functions, and accordingly utilities, of GAM939 correlate with, and may be deduced from, the identity of the target genes which GAM939 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14779] Nucleotide sequences of the GAM939 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM939 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM939 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM939 are further described hereinbelow with reference to Table Table1.

[14780] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM939 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14781] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 940 (GAM940) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14782] GAM940 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM940 was detected is described hereinabove with reference to Figs. 2-8.

[14783] GAM940 gene, herein designated GAM GENE, and GAM940 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14784] GAM940 gene, herein designated GAM GENE, encodes a GAM940 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM940 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM940 precursor RNA is designated SEQ ID:913, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:913 is located at position 298713 relative to contig NT_024997.9, on chromosome 18.

[14785] GAM940 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM940 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14786] An enzyme complex designated DICER COMPLEX, dices the GAM940 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM940 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM940 RNA is designated SEQ ID:2589, and is provided hereinbelow with reference to the sequence listing part.

[14787] GAM940 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM940 target RNA, herein designated GAM TARGET RNA. GAM940 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14788] GAM940 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM940 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM940 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM940 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM940 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14789] The complementary binding of GAM940 RNA, herein designated GAM RNA, to target binding sites on GAM940 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM940 target RNA, herein designated GAM TARGET RNA, into GAM940 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14790] It is appreciated that GAM940 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM940 target genes. The mRNA of each one of this plurality of GAM940 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM940 RNA, herein designated GAM RNA, and which when bound by GAM940 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM940 target proteins.

[14791] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM940 gene, herein designated GAM GENE, on one or more GAM940 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14792] It is yet further appreciated that specific functions, and accordingly utilities, of GAM940 correlate with, and may be deduced from, the identity of the target genes which GAM940 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14793] Nucleotide sequences of the GAM940 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM940 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM940 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM940 are further described hereinbelow with reference to Table Table1.

[14794] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM940 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14795] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

941 (GAM941) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14796] GAM941 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM941 was detected is described hereinabove with reference to Figs. 2-8.

[14797] GAM941 gene, herein designated GAM GENE, and GAM941 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14798] GAM941 gene, herein designated GAM GENE, encodes a GAM941 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM941 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM941 precursor RNA is designated SEQ ID:914, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:914 is located at position 10833520 relative to contig NT_010783.11, on chromosome 17.

[14799] GAM941 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's.

Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[14800] SEQ ID:99175 detected in mouse EST Accession AW913089.1.

[14801] SEQ ID:99186 detected in mouse EST Accession AW909330.1.

[14802] SEQ ID:99187 detected in mouse EST Accession AI153235.1.

[14803] GAM941 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM941 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14804] An enzyme complex designated DICER COMPLEX, dices the GAM941 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM941 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA

segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 97%) nucleotide sequence of GAM941 RNA is designated SEQ ID:2590, and is provided hereinbelow with reference to the sequence listing part.

[14805] GAM941 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM941 target RNA, herein designated GAM TARGET RNA. GAM941 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14806] GAM941 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM941 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM941 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM941 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM941 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14807] The complementary binding of GAM941 RNA, herein designated GAM RNA, to target binding sites on GAM941 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM941 target RNA, herein designated GAM TARGET RNA, into GAM941 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14808] It is appreciated that GAM941 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM941 target genes. The mRNA of each one of this plu-

rality of GAM941 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM941 RNA, herein designated GAM RNA, and which when bound by GAM941 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM941 target proteins.

[14809] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM941 gene, herein designated GAM GENE, on one or more GAM941 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14810] It is yet further appreciated that specific functions, and accordingly utilities, of GAM941 correlate with, and may be deduced from, the identity of the target genes which GAM941 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14811] Nucleotide sequences of the GAM941 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM941 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM941 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM941 are further described hereinbelow with reference to Table Table1.

[14812] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM941 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14813] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 942 (GAM942) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[14814] GAM942 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM942 was detected is described hereinabove with reference to Figs. 2-8.

[14815] GAM942 gene, herein designated GAM GENE, and GAM942 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14816] GAM942 gene, herein designated GAM GENE, encodes a GAM942 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM942 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM942 precursor RNA is designated SEQ ID:915, and is provided hereinbelow with reference to the sequence listing part.

[14817] GAM942 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14818] An enzyme complex designated DICER COMPLEX, dices the GAM942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM942 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM942 RNA is designated SEQ ID:2591, and is provided hereinbelow with reference to the sequence listing part.

[14819] GAM942 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM942 target RNA, herein designated GAM TARGET RNA.
GAM942 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14820] GAM942 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM942 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM942 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM942 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM942 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14821] The complementary binding of GAM942 RNA, herein designated GAM RNA, to target binding sites on GAM942 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM942 target RNA, herein designated GAM TARGET RNA, into GAM942 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14822] It is appreciated that GAM942 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM942 target genes. The mRNA of each one of this plurality of GAM942 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM942 RNA, herein designated GAM RNA, and which when bound by GAM942 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM942 target proteins.

[14823] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM942 gene, herein designated GAM GENE, on one or more GAM942 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14824] It is yet further appreciated that specific functions, and accordingly utilities, of GAM942 correlate with, and may be deduced from, the identity of the target genes which GAM942 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14825] Nucleotide sequences of the GAM942 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM942 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM942 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM942 are further described hereinbelow with reference to Table Table1.

[14826] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM942 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14827] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 943 (GAM943) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14828] GAM943 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM943 was detected is described hereinabove with reference to Figs. 2-8.

[14829] GAM943 gene, herein designated GAM GENE, and GAM943 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14830] GAM943 gene, herein designated GAM GENE, encodes a GAM943 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM943 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM943 precursor RNA is desig-

nated SEQ ID:916, and is provided hereinbelow with reference to the sequence listing part.

[14831] GAM943 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM943 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14832] An enzyme complex designated DICER COMPLEX, dices the GAM943 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM943 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM943 RNA is designated SEQ ID:2592, and is provided hereinbelow with reference to the sequence listing part.

[14833] GAM943 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM943 target RNA, herein designated GAM TARGET RNA. GAM943 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14834] GAM943 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM943 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM943 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM943 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM943

target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14835] The complementary binding of GAM943 RNA, herein designated GAM RNA, to target binding sites on GAM943 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM943 target RNA, herein designated GAM TARGET RNA, into GAM943 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14836] It is appreciated that GAM943 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM943 target genes. The mRNA of each one of this plurality of GAM943 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM943 RNA, herein designated GAM RNA, and which when bound by GAM943 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM943 target proteins.

[14837] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM943 gene, herein designated GAM GENE, on one or more GAM943 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14838] It is yet further appreciated that specific functions, and accordingly utilities, of GAM943 correlate with, and may be deduced from, the identity of the target genes which GAM943 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14839] Nucleotide sequences of the GAM943 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM943 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM943 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM943 are further described hereinbelow with reference to Table Table1.

[14840] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM943 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14841] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 944 (GAM944) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14842] GAM944 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM944 was detected is described hereinabove with reference to Figs. 2-8.

[14843] GAM944 gene, herein designated GAM GENE, and GAM944 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[14844] GAM944 gene, herein designated GAM GENE, encodes a GAM944 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM944 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM944 precursor RNA is designated SEQ ID:917, and is provided hereinbelow with reference to the sequence listing part.

[14845] GAM944 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM944 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14846] An enzyme complex designated DICER COMPLEX, dices the GAM944 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM944 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM944 RNA is designated SEQ ID:2593, and is provided hereinbelow with reference to the sequence listing part.

[14847] GAM944 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM944 target RNA, herein designated GAM TARGET RNA. GAM944 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14848] GAM944 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM944 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM944 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM944 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM944 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14849] The complementary binding of GAM944 RNA, herein designated GAM RNA, to target binding sites on GAM944 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM944 target RNA, herein designated GAM TARGET RNA, into GAM944 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14850] It is appreciated that GAM944 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM944 target genes. The mRNA of each one of this plurality of GAM944 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM944 RNA, herein designated GAM RNA, and which when bound by GAM944 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM944 target proteins.

[14851] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM944 gene, herein designated GAM GENE, on one or more GAM944 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[14852] It is yet further appreciated that specific functions, and accordingly utilities, of GAM944 correlate with, and may be deduced from, the identity of the target genes which GAM944 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14853] Nucleotide sequences of the GAM944 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM944 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM944 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM944 are further described hereinbelow with reference to Table Table1.

[14854] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM944 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14855] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 945 (GAM945) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[14856] GAM945 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM945 was detected is described hereinabove with reference to Figs. 2-8.

[14857] GAM945 gene, herein designated GAM GENE, and GAM945 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14858] GAM945 gene, herein designated GAM GENE, encodes a GAM945 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM945 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM945 precursor RNA is designated SEQ ID:918, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:918 is located at position 1235100 relative to contig NT_009526.11, on chromosome 12.

[14859] GAM945 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences

of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[14860] SEQ ID:98089 detected in mouse EST Accession BI965972.1.

[14861] SEQ ID:98090 detected in mouse EST Accession AI326210.1.

[14862] SEQ ID:98091 detected in mouse EST Accession BI965652.1.

[14863] GAM945 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM945 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14864] An enzyme complex designated DICER COMPLEX, dices the GAM945 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM945 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM945 RNA is designated SEQ ID:2594, and is provided hereinbelow with reference to the sequence listing part.

[14865] GAM945 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM945 target RNA, herein designated GAM TARGET RNA. GAM945 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14866] GAM945 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM945 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM945 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM945 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM945 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14867] The complementary binding of GAM945 RNA, herein designated GAM RNA, to target binding sites on GAM945 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM945 target RNA, herein designated GAM TARGET RNA, into GAM945 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14868] It is appreciated that GAM945 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM945 target genes. The mRNA of each one of this plurality of GAM945 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM945 RNA, herein designated GAM RNA, and which when bound by GAM945 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM945 target proteins.

[14869] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM945 gene, herein designated GAM GENE, on one or more GAM945 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14870] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM945 correlate with, and may be deduced from, the identity of the target genes which GAM945 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14871] Nucleotide sequences of the GAM945 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM945 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM945 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM945 are further described hereinbelow with reference to Table Table1.

[14872] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM945 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14873] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 946 (GAM946) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14874] GAM946 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM946 was detected is described hereinabove with reference to Figs. 2-8.

[14875] GAM946 gene, herein designated GAM GENE, and GAM946 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14876] GAM946 gene, herein designated GAM GENE, encodes a GAM946 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM946 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM946 precursor RNA is designated SEQ ID:919, and is provided hereinbelow with reference to the sequence listing part.

[14877] GAM946 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14878] An enzyme complex designated DICER COMPLEX, dices the GAM946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM946 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM946 RNA is designated SEQ ID:2595, and is provided hereinbelow with reference to the sequence listing part.

[14879] GAM946 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM946 target RNA, herein designated GAM TARGET RNA. GAM946 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14880] GAM946 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM946 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM946 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM946 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM946 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14881] The complementary binding of GAM946 RNA, herein designated GAM RNA, to target binding sites on GAM946 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM946 target RNA, herein designated GAM TARGET RNA, into GAM946 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14882] It is appreciated that GAM946 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM946 target genes. The mRNA of each one of this plurality of GAM946 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM946 RNA, herein designated GAM RNA, and which when bound by GAM946 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM946 target proteins.

[14883] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM946 gene, herein designated GAM GENE, on one or more GAM946 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14884] It is yet further appreciated that specific functions, and accordingly utilities, of GAM946 correlate with, and may be deduced from, the identity of the target genes which GAM946 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14885] Nucleotide sequences of the GAM946 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM946 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM946 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM946 are further described hereinbelow with reference to Table Table1.

[14886] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM946 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14887] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 947 (GAM947) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14888] GAM947 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM947 was detected is described hereinabove with reference to Figs. 2-8.

[14889] GAM947 gene, herein designated GAM GENE, and GAM947 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14890] GAM947 gene, herein designated GAM GENE, encodes a GAM947 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM947 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM947 precursor RNA is designated SEQ ID:920, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:920 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[14891] GAM947 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM947 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14892] An enzyme complex designated DICER COMPLEX, dices the GAM947 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM947 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM947 RNA is designated SEQ ID:2596, and is provided

hereinbelow with reference to the sequence listing part.

[14893] GAM947 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM947 target RNA, herein designated GAM TARGET RNA.

GAM947 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14894] GAM947 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM947 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM947 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM947 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM947 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14895] The complementary binding of GAM947 RNA, herein designated GAM RNA, to target binding sites on GAM947 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM947 target RNA, herein designated GAM TARGET RNA, into GAM947 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14896] It is appreciated that GAM947 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM947 target genes. The mRNA of each one of this plurality of GAM947 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM947 RNA, herein designated GAM RNA, and which when bound by GAM947 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM947 tar-

get proteins.

[14897] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM947 gene, herein designated GAM GENE, on one or more GAM947 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14898] It is yet further appreciated that specific functions, and accordingly utilities, of GAM947 correlate with, and may be deduced from, the identity of the target genes which GAM947 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14899] Nucleotide sequences of the GAM947 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM947 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM947 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM947 are further described hereinbelow with reference to Table Table1.

[14900] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM947 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14901] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 948 (GAM948) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14902] GAM948 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM948 was detected is described hereinabove with reference to Figs. 2-8.

[14903] GAM948 gene, herein designated GAM GENE, and

GAM948 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14904] GAM948 gene, herein designated GAM GENE, encodes a GAM948 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM948 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM948 precursor RNA is designated SEQ ID:921, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:921 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[14905] GAM948 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM948 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14906] An enzyme complex designated DICER COMPLEX, dices the GAM948 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM948 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM948 RNA is designated SEQ ID:2597, and is provided hereinbelow with reference to the sequence listing part.

[14907] GAM948 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM948 target RNA, herein designated GAM TARGET RNA. GAM948 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14908] GAM948 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM948 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM948 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM948 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM948 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14909] The complementary binding of GAM948 RNA, herein designated GAM RNA, to target binding sites on GAM948 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM948 target RNA, herein designated GAM TARGET RNA, into GAM948 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[14910] It is appreciated that GAM948 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM948 target genes. The mRNA of each one of this plurality of GAM948 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM948 RNA, herein designated GAM RNA, and which when bound by GAM948 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM948 target proteins.

[14911] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM948 gene, herein designated GAM GENE, on one or more GAM948 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14912] It is yet further appreciated that specific functions, and accordingly utilities, of GAM948 correlate with, and may be deduced from, the identity of the target genes which GAM948 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14913] Nucleotide sequences of the GAM948 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM948 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM948 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM948 are further described hereinbelow with reference to Table Table1.

[14914] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM948 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14915] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 949 (GAM949) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14916] GAM949 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM949 was detected is described hereinabove with reference to Figs. 2-8.

[14917] GAM949 gene, herein designated GAM GENE, and GAM949 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14918] GAM949 gene, herein designated GAM GENE, encodes a GAM949 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM949 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM949 precursor RNA is designated SEQ ID:922, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:922 is located at position 3686942 relative to contig NT_010799.11, on chromosome 17.

[14919] GAM949 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98767, which mouse homolog is detected in mouse EST accession AW476216.1.

[14920] GAM949 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM949 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14921] An enzyme complex designated DICER COMPLEX, dices the GAM949 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM949 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM949 RNA is designated SEQ ID:2598, and is provided hereinbelow with reference to the sequence listing part.

[14922] GAM949 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM949 target RNA, herein designated GAM TARGET RNA. GAM949 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14923] GAM949 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM949 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM949 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM949 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM949 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14924] The complementary binding of GAM949 RNA, herein designated GAM RNA, to target binding sites on GAM949 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM949 target RNA, herein designated GAM TARGET RNA, into GAM949 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14925] It is appreciated that GAM949 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM949 target genes. The mRNA of each one of this plurality of GAM949 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM949 RNA, herein designated GAM RNA, and which when bound by

GAM949 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM949 target proteins.

[14926] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM949 gene, herein designated GAM GENE, on one or more GAM949 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14927] It is yet further appreciated that specific functions, and accordingly utilities, of GAM949 correlate with, and may be deduced from, the identity of the target genes which GAM949 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[14928] Nucleotide sequences of the GAM949 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM949 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM949 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM949 are further described hereinbelow with reference to Table Table1.

[14929] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM949 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14930] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 950 (GAM950) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14931] GAM950 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM950 was detected is described hereinabove

with reference to Figs. 2-8.

[14932] GAM950 gene, herein designated GAM GENE, and GAM950 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14933] GAM950 gene, herein designated GAM GENE, encodes a GAM950 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM950 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM950 precursor RNA is designated SEQ ID:923, and is provided hereinbelow with reference to the sequence listing part.

[14934] GAM950 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14935] An enzyme complex designated DICER COMPLEX, dices the GAM950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM950 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM950 RNA is designated SEQ ID:2599, and is provided hereinbelow with reference to the sequence listing part.

[14936] GAM950 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM950 target RNA, herein designated GAM TARGET RNA.
GAM950 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14937] GAM950 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM950 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM950 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM950 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM950 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14938] The complementary binding of GAM950 RNA, herein designated GAM RNA, to target binding sites on GAM950 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM950 target RNA, herein designated GAM TARGET RNA, into GAM950 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[14939] It is appreciated that GAM950 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM950 target genes. The mRNA of each one of this plurality of GAM950 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM950 RNA, herein designated GAM RNA, and which when bound by GAM950 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM950 target proteins.

[14940] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM950 gene, herein designated GAM GENE, on one or more GAM950 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14941] It is yet further appreciated that specific functions, and accordingly utilities, of GAM950 correlate with, and may be deduced from, the identity of the target genes which GAM950 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14942] Nucleotide sequences of the GAM950 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM950 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM950 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM950 are further described hereinbelow with reference to Table Table1.

[14943] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM950 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14944] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 951 (GAM951) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14945] GAM951 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM951 was detected is described hereinabove with reference to Figs. 2-8.

[14946] GAM951 gene, herein designated GAM GENE, and GAM951 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14947] GAM951 gene, herein designated GAM GENE, encodes a GAM951 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM951 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM951 precursor RNA is designated SEQ ID:924, and is provided hereinbelow with reference to the sequence listing part.

[14948] GAM951 has 13 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's.

Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[14949] SEQ ID:98932 detected in mouse EST Accession AI157515.1.

[14950] SEQ ID:98933 detected in mouse EST Accession W65790.1.

[14951] SEQ ID:98934 detected in mouse EST Accession AA051691.1.

[14952] SEQ ID:98935 detected in mouse EST Accession AA034667.1.

[14953] SEQ ID:98936 detected in mouse EST Accession W54339.1.

[14954] SEQ ID:98937 detected in mouse EST Accession AI613817.1.

[14955] SEQ ID:98938 detected in mouse EST Accession BE625355.1.

[14956] SEQ ID:98939 detected in mouse EST Accession BE861499.1.

[14957] SEQ ID:98940 detected in mouse EST Accession BB667583.1.

[14958] SEQ ID:98941 detected in mouse EST Accession BI145910.1.

[14959] SEQ ID:98942 detected in mouse EST Accession BI101177.1.

[14960] SEQ ID:98943 detected in mouse EST Accession AV284000.1.

[14961] SEQ ID:98950 detected in mouse EST Accession BF780369.1.

[14962] GAM951 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM951 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14963] An enzyme complex designated DICER COMPLEX, dices the GAM951 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM951 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM951 RNA is designated SEQ ID:2600, and is provided hereinbelow with reference to the sequence listing part.

[14964] GAM951 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM951 target RNA, herein designated GAM TARGET RNA. GAM951 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14965] GAM951 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM951 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM951 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM951 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM951 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14966] The complementary binding of GAM951 RNA, herein designated GAM RNA, to target binding sites on GAM951 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM951 target RNA, herein designated GAM TARGET RNA, into GAM951 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14967] It is appreciated that GAM951 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM951 target genes. The mRNA of each one of this plurality of GAM951 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM951 RNA,

herein designated GAM RNA, and which when bound by GAM951 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM951 target proteins.

[14968] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM951 gene, herein designated GAM GENE, on one or more GAM951 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14969] It is yet further appreciated that specific functions, and accordingly utilities, of GAM951 correlate with, and may be deduced from, the identity of the target genes which

GAM951 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14970] Nucleotide sequences of the GAM951 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM951 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM951 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM951 are further described hereinbelow with reference to Table Table1.

[14971] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM951 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14972] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 952 (GAM952) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14973] GAM952 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM952 was detected is described hereinabove with reference to Figs. 2-8.

[14974] GAM952 gene, herein designated GAM GENE, and GAM952 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14975] GAM952 gene, herein designated GAM GENE, encodes a GAM952 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM952 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM952 precursor RNA is designated SEQ ID:925, and is provided hereinbelow with reference to the sequence listing part.

[14976] GAM952 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99285, which mouse homolog is detected in mouse EST accession AI181854.1.

[14977] GAM952 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM952 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14978] An enzyme complex designated DICER COMPLEX, dices the GAM952 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM952 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM952 RNA is designated SEQ ID:2601, and is provided hereinbelow with reference to the sequence listing part.

[14979] GAM952 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM952 target RNA, herein designated GAM TARGET RNA. GAM952 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14980] GAM952 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM952 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM952 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM952 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM952 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14981] The complementary binding of GAM952 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM952 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM952 target RNA, herein designated GAM TARGET RNA, into GAM952 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14982] It is appreciated that GAM952 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM952 target genes. The mRNA of each one of this plurality of GAM952 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM952 RNA, herein designated GAM RNA, and which when bound by GAM952 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM952 target proteins.

[14983] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM952 gene, herein designated GAM GENE, on one or more GAM952 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14984] It is yet further appreciated that specific functions, and accordingly utilities, of GAM952 correlate with, and may be deduced from, the identity of the target genes which GAM952 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14985] Nucleotide sequences of the GAM952 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM952 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM952 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM952 are further described hereinbelow with reference to Table Table1.

[14986] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM952 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[14987] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 953 (GAM953) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[14988] GAM953 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM953 was detected is described hereinabove with reference to Figs. 2-8.

[14989] GAM953 gene, herein designated GAM GENE, and GAM953 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[14990] GAM953 gene, herein designated GAM GENE, encodes a GAM953 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM953 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM953 precursor RNA is designated SEQ ID:926, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:926 is located at position 19527613 relative to contig NT_007933.10, on chromosome 7.

[14991] GAM953 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM953 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[14992] An enzyme complex designated DICER COMPLEX, dices the GAM953 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM953 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM953 RNA is designated SEQ ID:2602, and is provided hereinbelow with reference to the sequence listing part.

[14993] GAM953 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM953 target RNA, herein designated GAM TARGET RNA. GAM953 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[14994] GAM953 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM953 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM953 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM953 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM953 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[14995] The complementary binding of GAM953 RNA, herein designated GAM RNA, to target binding sites on GAM953 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM953 target RNA, herein designated GAM TARGET RNA, into GAM953 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[14996] It is appreciated that GAM953 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM953 target genes. The mRNA of each one of this plurality of GAM953 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM953 RNA,

herein designated GAM RNA, and which when bound by GAM953 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM953 target proteins.

[14997] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM953 gene, herein designated GAM GENE, on one or more GAM953 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[14998] It is yet further appreciated that specific functions, and accordingly utilities, of GAM953 correlate with, and may be deduced from, the identity of the target genes which

GAM953 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[14999] Nucleotide sequences of the GAM953 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM953 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM953 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM953 are further described hereinbelow with reference to Table Table1.

[15000] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM953 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15001] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 954 (GAM954) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15002] GAM954 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM954 was detected is described hereinabove with reference to Figs. 2-8.

[15003] GAM954 gene, herein designated GAM GENE, and GAM954 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15004] GAM954 gene, herein designated GAM GENE, encodes a GAM954 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM954 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM954 precursor RNA is designated SEQ ID:927, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:927 is located at position 3533624 relative to contig NT_022171.11, on chromosome 2.

[15005] GAM954 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM954 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15006] An enzyme complex designated DICER COMPLEX, dices the GAM954 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM954 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM954 RNA is designated SEQ ID:2603, and is provided hereinbelow with reference to the sequence listing part.

[15007] GAM954 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM954 target RNA, herein designated GAM TARGET RNA. GAM954 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15008] GAM954 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM954 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM954 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM954 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM954 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15009] The complementary binding of GAM954 RNA, herein designated GAM RNA, to target binding sites on GAM954 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM954 target RNA, herein designated GAM TARGET RNA, into GAM954 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15010] It is appreciated that GAM954 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM954 target genes. The mRNA of each one of this plurality of GAM954 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM954 RNA, herein designated GAM RNA, and which when bound by GAM954 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM954 target proteins.

[15011] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM954 gene, herein designated GAM GENE, on one or more GAM954 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15012] It is yet further appreciated that specific functions, and accordingly utilities, of GAM954 correlate with, and may be deduced from, the identity of the target genes which GAM954 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15013] Nucleotide sequences of the GAM954 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM954 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM954 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM954 are further described hereinbelow with reference to Table Table1.

[15014] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM954 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15015] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 955 (GAM955) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15016] GAM955 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM955 was detected is described hereinabove with reference to Figs. 2-8.

[15017] GAM955 gene, herein designated GAM GENE, and GAM955 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15018] GAM955 gene, herein designated GAM GENE, encodes a GAM955 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM955 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM955 precursor RNA is designated SEQ ID:928, and is provided hereinbelow with refer-

ence to the sequence listing part.

[15019] GAM955 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM955 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15020] An enzyme complex designated DICER COMPLEX, dices the GAM955 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM955 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM955 RNA is designated SEQ ID:2604, and is provided hereinbelow with reference to the sequence listing part.

[15021] GAM955 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM955 target RNA, herein designated GAM TARGET RNA.

GAM955 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15022] GAM955 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM955 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM955 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM955 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM955 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15023] The complementary binding of GAM955 RNA, herein designated GAM RNA, to target binding sites on GAM955 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM955 target RNA, herein designated GAM TARGET RNA, into GAM955 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15024] It is appreciated that GAM955 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM955 target genes. The mRNA of each one of this plurality of GAM955 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM955 RNA, herein designated GAM RNA, and which when bound by GAM955 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM955 target proteins.

[15025] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM955 gene, herein designated GAM GENE, on one or more GAM955 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15026] It is yet further appreciated that specific functions, and accordingly utilities, of GAM955 correlate with, and may be deduced from, the identity of the target genes which GAM955 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15027] Nucleotide sequences of the GAM955 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM955 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM955 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM955 are further described hereinbelow with reference to Table Table1.

[15028] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM955 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15029] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 956 (GAM956) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15030] GAM956 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM956 was detected is described hereinabove with reference to Figs. 2-8.

[15031] GAM956 gene, herein designated GAM GENE, and GAM956 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15032] GAM956 gene, herein designated GAM GENE, encodes a GAM956 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM956 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM956 precursor RNA is designated SEQ ID:929, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:929 is located at position 5359465 relative to contig NT_007819.11, on chromosome 7.

[15033] GAM956 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM956 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15034] An enzyme complex designated DICER COMPLEX, dices the GAM956 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM956 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM956 RNA is designated SEQ ID:2605, and is provided hereinbelow with reference to the sequence listing part.

[15035] GAM956 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM956 target RNA, herein designated GAM TARGET RNA. GAM956 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15036] GAM956 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM956 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM956 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM956 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM956 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15037] The complementary binding of GAM956 RNA, herein designated GAM RNA, to target binding sites on GAM956 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM956 target RNA, herein designated GAM TARGET RNA, into GAM956 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15038] It is appreciated that GAM956 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM956 target genes. The mRNA of each one of this plurality of GAM956 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM956 RNA, herein designated GAM RNA, and which when bound by GAM956 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM956 target proteins.

[15039] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM956 gene, herein designated GAM GENE, on one or more GAM956 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15040] It is yet further appreciated that specific functions, and accordingly utilities, of GAM956 correlate with, and may be deduced from, the identity of the target genes which GAM956 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15041] Nucleotide sequences of the GAM956 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM956 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM956 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM956 are further described hereinbelow with reference to Table Table1.

[15042] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM956 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15043] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

957 (GAM957) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15044] GAM957 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM957 was detected is described hereinabove with reference to Figs. 2-8.

[15045] GAM957 gene, herein designated GAM GENE, and GAM957 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15046] GAM957 gene, herein designated GAM GENE, encodes a GAM957 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM957 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM957 precursor RNA is designated SEQ ID:930, and is provided hereinbelow with reference to the sequence listing part.

[15047] GAM957 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM957 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is

well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15048] An enzyme complex designated DICER COMPLEX, dices the GAM957 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM957 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM957 RNA is designated SEQ ID:2606, and is provided hereinbelow with reference to the sequence listing part.

[15049] GAM957 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM957 target RNA, herein designated GAM TARGET RNA. GAM957 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein

coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15050] GAM957 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM957 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM957 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM957 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM957 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15051] The complementary binding of GAM957 RNA, herein des-

ignated GAM RNA, to target binding sites on GAM957 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM957 target RNA, herein designated GAM TARGET RNA, into GAM957 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15052] It is appreciated that GAM957 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM957 target genes. The mRNA of each one of this plurality of GAM957 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM957 RNA, herein designated GAM RNA, and which when bound by GAM957 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM957 target proteins.

[15053] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM957 gene, herein designated GAM GENE, on one or more GAM957 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15054] It is yet further appreciated that specific functions, and accordingly utilities, of GAM957 correlate with, and may be deduced from, the identity of the target genes which GAM957 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15055] Nucleotide sequences of the GAM957 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM957 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM957 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM957 are further described hereinbelow with reference to Table Table1.

[15056] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM957 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15057] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 958 (GAM958) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15058] GAM958 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM958 was detected is described hereinabove with reference to Figs. 2-8.

[15059] GAM958 gene, herein designated GAM GENE, and GAM958 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15060] GAM958 gene, herein designated GAM GENE, encodes a GAM958 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM958 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of GAM958 precursor RNA is designated SEQ ID:931, and is provided hereinbelow with reference to the sequence listing part.

[15061] GAM958 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15062] An enzyme complex designated DICER COMPLEX, dices the GAM958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM958 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM958 RNA is designated SEQ ID:2607, and is provided hereinbelow with reference to the sequence listing part.

[15063] GAM958 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM958 target RNA, herein designated GAM TARGET RNA. GAM958 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15064] GAM958 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM958 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM958 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM958 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM958 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15065] The complementary binding of GAM958 RNA, herein designated GAM RNA, to target binding sites on GAM958 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM958 target RNA, herein designated GAM TARGET RNA, into GAM958 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15066] It is appreciated that GAM958 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM958 target genes. The mRNA of each one of this plurality of GAM958 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM958 RNA, herein designated GAM RNA, and which when bound by GAM958 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM958 target proteins.

[15067] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM958 gene, herein designated GAM GENE, on one or more GAM958 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15068] It is yet further appreciated that specific functions, and accordingly utilities, of GAM958 correlate with, and may be deduced from, the identity of the target genes which GAM958 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15069] Nucleotide sequences of the GAM958 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM958 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM958 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM958 are further described hereinbelow with reference to Table Table1.

[15070] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM958 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15071] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 959 (GAM959) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15072] GAM959 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM959 was detected is described hereinabove with reference to Figs. 2-8.

[15073] GAM959 gene, herein designated GAM GENE, and GAM959 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15074] GAM959 gene, herein designated GAM GENE, encodes a GAM959 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM959 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM959 precursor RNA is designated SEQ ID:932, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:932 is located at position 6525512 relative to contig NT_034483.2, on chromosome 2.

[15075] GAM959 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM959 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the sec-

ond half thereof.

[15076] An enzyme complex designated DICER COMPLEX, dices the GAM959 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM959 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM959 RNA is designated SEQ ID:2608, and is provided hereinbelow with reference to the sequence listing part.

[15077] GAM959 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM959 target RNA, herein designated GAM TARGET RNA. GAM959 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15078] GAM959 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM959 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM959 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM959 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM959 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15079] The complementary binding of GAM959 RNA, herein designated GAM RNA, to target binding sites on GAM959 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM959 target RNA, herein designated GAM TARGET RNA, into GAM959 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15080] It is appreciated that GAM959 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM959 target genes. The mRNA of each one of this plurality of GAM959 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM959 RNA, herein designated GAM RNA, and which when bound by GAM959 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM959 target proteins.

[15081] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM959 gene, herein designated GAM GENE, on one or more GAM959 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15082] It is yet further appreciated that specific functions, and accordingly utilities, of GAM959 correlate with, and may be deduced from, the identity of the target genes which GAM959 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15083] Nucleotide sequences of the GAM959 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM959 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM959 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM959 are further described hereinbelow with reference to Table Table1.

[15084] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM959 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15085] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 960 (GAM960) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15086] GAM960 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM960 was detected is described hereinabove with reference to Figs. 2-8.

[15087] GAM960 gene, herein designated GAM GENE, and GAM960 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15088] GAM960 gene, herein designated GAM GENE, encodes a GAM960 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM960 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM960 precursor RNA is designated SEQ ID:933, and is provided hereinbelow with reference to the sequence listing part.

[15089] GAM960 precursor RNA, herein designated GAM PRECUR-

SOR RNA, folds onto itself, forming GAM960 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15090] An enzyme complex designated DICER COMPLEX, dices the GAM960 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM960 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM960 RNA is designated SEQ ID:2609, and is provided hereinbelow with reference to the sequence listing part.

[15091] GAM960 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM960 target RNA, herein designated GAM TARGET RNA.

GAM960 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15092] GAM960 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM960 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM960 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM960 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM960 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only

these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15093] The complementary binding of GAM960 RNA, herein designated GAM RNA, to target binding sites on GAM960 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM960 target RNA, herein designated GAM TARGET RNA, into GAM960 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15094] It is appreciated that GAM960 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM960 target genes. The mRNA of each one of this plurality of GAM960 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM960 RNA, herein designated GAM RNA, and which when bound by GAM960 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM960 target proteins.

[15095] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM960 gene, herein designated GAM GENE, on one or more GAM960 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15096] It is yet further appreciated that specific functions, and accordingly utilities, of GAM960 correlate with, and may be deduced from, the identity of the target genes which GAM960 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15097] Nucleotide sequences of the GAM960 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM960 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM960 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM960 are further described hereinbelow with reference to Table Table1.

[15098] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM960 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15099] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 961 (GAM961) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15100] GAM961 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM961 was detected is described hereinabove with reference to Figs. 2-8.

[15101] GAM961 gene, herein designated GAM GENE, and GAM961 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15102] GAM961 gene, herein designated GAM GENE, encodes a GAM961 precursor RNA, herein designated GAM PRECUR-

SOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM961 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM961 precursor RNA is designated SEQ ID:934, and is provided hereinbelow with reference to the sequence listing part.

[15103] GAM961 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15104] An enzyme complex designated DICER COMPLEX, dices the GAM961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM961 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM961 RNA is designated SEQ ID:2610, and is provided hereinbelow with reference to the sequence listing part.

[15105] GAM961 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM961 target RNA, herein designated GAM TARGET RNA. GAM961 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15106] GAM961 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM961 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM961 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM961 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM961 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15107] The complementary binding of GAM961 RNA, herein designated GAM RNA, to target binding sites on GAM961 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM961 target RNA, herein designated GAM TARGET RNA, into GAM961 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15108] It is appreciated that GAM961 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM961 target genes. The mRNA of each one of this plurality of GAM961 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM961 RNA, herein designated GAM RNA, and which when bound by GAM961 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM961 target proteins.

[15109] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM961 gene, herein designated GAM GENE, on one or more GAM961 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15110] It is yet further appreciated that specific functions, and accordingly utilities, of GAM961 correlate with, and may

be deduced from, the identity of the target genes which GAM961 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15111] Nucleotide sequences of the GAM961 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM961 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM961 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM961 are further described hereinbelow with reference to Table Table1.

[15112] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM961 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15113] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 962 (GAM962) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15114] GAM962 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM962 was detected is described hereinabove with reference to Figs. 2-8.

[15115] GAM962 gene, herein designated GAM GENE, and GAM962 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15116] GAM962 gene, herein designated GAM GENE, encodes a GAM962 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM962 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM962 precursor RNA is designated SEQ ID:935, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:935 is located at position 2317445 relative to contig NT_023148.9, on chromosome 5.

[15117] GAM962 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM962 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15118] An enzyme complex designated DICER COMPLEX, dices the GAM962 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM962 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM962 RNA is designated SEQ ID:2611, and is provided hereinbelow with reference to the sequence listing part.

[15119] GAM962 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM962 target RNA, herein designated GAM TARGET RNA. GAM962 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15120] GAM962 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM962 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM962 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM962 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM962 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15121] The complementary binding of GAM962 RNA, herein designated GAM RNA, to target binding sites on GAM962 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM962 target RNA, herein designated GAM TARGET RNA, into GAM962 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15122] It is appreciated that GAM962 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM962 target genes. The mRNA of each one of this plurality of GAM962 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM962 RNA, herein designated GAM RNA, and which when bound by GAM962 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM962 target proteins.

[15123] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM962 gene, herein designated GAM GENE, on one or more GAM962 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15124] It is yet further appreciated that specific functions, and accordingly utilities, of GAM962 correlate with, and may be deduced from, the identity of the target genes which GAM962 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15125] Nucleotide sequences of the GAM962 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM962 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM962 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM962 are further described hereinbelow with reference to Table Table1.

[15126] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM962 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15127] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 963 (GAM963) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15128] GAM963 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM963 was detected is described hereinabove with reference to Figs. 2-8.

[15129] GAM963 gene, herein designated GAM GENE, and GAM963 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15130] GAM963 gene, herein designated GAM GENE, encodes a GAM963 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM963 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM963 precursor RNA is desig-

nated SEQ ID:936, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:936 is located at position 3102342 relative to contig NT_011109.13, on chromosome 19.

[15131] GAM963 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15132] An enzyme complex designated DICER COMPLEX, dices the GAM963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM963 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM963 RNA is designated SEQ ID:2612, and is provided hereinbelow with reference to the sequence listing part.

[15133] GAM963 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM963 target RNA, herein designated GAM TARGET RNA.

GAM963 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15134] GAM963 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM963 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM963 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM963 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM963 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15135] The complementary binding of GAM963 RNA, herein designated GAM RNA, to target binding sites on GAM963 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM963 target RNA, herein designated GAM TARGET RNA, into GAM963 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15136] It is appreciated that GAM963 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM963 target genes. The mRNA of each one of this plurality of GAM963 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM963 RNA, herein designated GAM RNA, and which when bound by GAM963 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM963 target proteins.

[15137] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM963 gene, herein designated GAM GENE, on one or more GAM963 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15138] It is yet further appreciated that specific functions, and accordingly utilities, of GAM963 correlate with, and may be deduced from, the identity of the target genes which GAM963 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15139] Nucleotide sequences of the GAM963 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM963 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM963 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM963 are further described hereinbelow with reference to Table Table1.

[15140] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM963 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15141] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 964 (GAM964) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15142] GAM964 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM964 was detected is described hereinabove with reference to Figs. 2-8.

[15143] GAM964 gene, herein designated GAM GENE, and GAM964 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15144] GAM964 gene, herein designated GAM GENE, encodes a GAM964 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM964 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM964 precursor RNA is designated SEQ ID:937, and is provided hereinbelow with reference to the sequence listing part.

[15145] GAM964 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM964 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15146] An enzyme complex designated DICER COMPLEX, dices

the GAM964 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM964 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM964 RNA is designated SEQ ID:2613, and is provided hereinbelow with reference to the sequence listing part.

[15147] GAM964 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM964 target RNA, herein designated GAM TARGET RNA. GAM964 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15148] GAM964 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM964 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM964

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM964 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM964 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15149] The complementary binding of GAM964 RNA, herein designated GAM RNA, to target binding sites on GAM964 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM964 target RNA, herein designated GAM TARGET RNA, into GAM964 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15150] It is appreciated that GAM964 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM964 target genes. The mRNA of each one of this plurality of GAM964 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM964 RNA, herein designated GAM RNA, and which when bound by GAM964 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM964 target proteins.

[15151] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM964 gene, herein designated GAM GENE, on one or more GAM964 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15152] It is yet further appreciated that specific functions, and accordingly utilities, of GAM964 correlate with, and may be deduced from, the identity of the target genes which GAM964 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15153] Nucleotide sequences of the GAM964 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM964 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM964 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM964 are further described hereinbelow with reference to Table Table1.

[15154] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM964 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15155] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 965 (GAM965) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15156] GAM965 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM965 was detected is described hereinabove with reference to Figs. 2-8.

[15157] GAM965 gene, herein designated GAM GENE, and GAM965 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15158] GAM965 gene, herein designated GAM GENE, encodes a GAM965 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM965 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM965 precursor RNA is designated SEQ ID:938, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:938 is located at position 1235053 relative to contig NT_009526.11, on chromosome 12.

[15159] GAM965 has 3 highly conserved, expressed mouse ho-

mologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[15160] SEQ ID:99273 detected in mouse EST Accession AI326210.1.

[15161] SEQ ID:99274 detected in mouse EST Accession BI965652.1.

[15162] SEQ ID:100225 detected in mouse EST Accession BI965972.1.

[15163] GAM965 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15164] An enzyme complex designated DICER COMPLEX, dices the GAM965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM965 RNA, herein

designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM965 RNA is designated SEQ ID:2614, and is provided hereinbelow with reference to the sequence listing part.

[15165] GAM965 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM965 target RNA, herein designated GAM TARGET RNA.
GAM965 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15166] GAM965 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM965 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM965 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM965 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM965 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15167] The complementary binding of GAM965 RNA, herein designated GAM RNA, to target binding sites on GAM965 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM965 target RNA, herein designated GAM TARGET RNA, into GAM965 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15168] It is appreciated that GAM965 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM965 target genes. The mRNA of each one of this plurality of GAM965 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM965 RNA, herein designated GAM RNA, and which when bound by GAM965 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM965 target proteins.

[15169] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM965 gene, herein designated GAM GENE, on one or more GAM965 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[15170] It is yet further appreciated that specific functions, and accordingly utilities, of GAM965 correlate with, and may be deduced from, the identity of the target genes which GAM965 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15171] Nucleotide sequences of the GAM965 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM965 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM965 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM965 are further described hereinbelow with reference to Table Table1.

[15172] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM965 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15173] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 966 (GAM966) gene, which modulates expression of re-

spective target genes thereof, the function and utility of which target genes is known in the art.

[15174] GAM966 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM966 was detected is described hereinabove with reference to Figs. 2-8.

[15175] GAM966 gene, herein designated GAM GENE, and GAM966 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15176] GAM966 gene, herein designated GAM GENE, encodes a GAM966 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM966 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM966 precursor RNA is designated SEQ ID:939, and is provided hereinbelow with reference to the sequence listing part.

[15177] GAM966 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15178] An enzyme complex designated DICER COMPLEX, dices the GAM966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM966 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM966 RNA is designated SEQ ID:2615, and is provided hereinbelow with reference to the sequence listing part.

[15179] GAM966 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM966 target RNA, herein designated GAM TARGET RNA.
GAM966 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[15180] GAM966 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM966 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM966 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM966 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM966 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15181] The complementary binding of GAM966 RNA, herein designated GAM RNA, to target binding sites on GAM966 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM966 target RNA, herein designated GAM TARGET RNA, into GAM966 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15182] It is appreciated that GAM966 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM966 target genes. The mRNA of each one of this plurality of GAM966 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM966 RNA, herein designated GAM RNA, and which when bound by GAM966 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM966 target proteins.

[15183] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM966 gene, herein designated GAM GENE, on one or more GAM966 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15184] It is yet further appreciated that specific functions, and accordingly utilities, of GAM966 correlate with, and may be deduced from, the identity of the target genes which GAM966 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15185] Nucleotide sequences of the GAM966 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM966 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM966 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM966 are further described hereinbelow with reference to Table Table1.

[15186] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM966 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15187] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 967 (GAM967) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15188] GAM967 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM967 was detected is described hereinabove with reference to Figs. 2-8.

[15189] GAM967 gene, herein designated GAM GENE, and GAM967 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15190] GAM967 gene, herein designated GAM GENE, encodes a GAM967 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM967 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM967 precursor RNA is designated SEQ ID:940, and is provided hereinbelow with reference to the sequence listing part.

[15191] GAM967 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM967 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15192] An enzyme complex designated DICER COMPLEX, dices the GAM967 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM967 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM967 RNA is designated SEQ ID:2616, and is provided

hereinbelow with reference to the sequence listing part.

[15193] GAM967 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM967 target RNA, herein designated GAM TARGET RNA.

GAM967 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15194] GAM967 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM967 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM967 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM967 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM967 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15195] The complementary binding of GAM967 RNA, herein designated GAM RNA, to target binding sites on GAM967 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM967 target RNA, herein designated GAM TARGET RNA, into GAM967 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15196] It is appreciated that GAM967 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM967 target genes. The mRNA of each one of this plurality of GAM967 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM967 RNA, herein designated GAM RNA, and which when bound by GAM967 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM967 tar-

get proteins.

[15197] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM967 gene, herein designated GAM GENE, on one or more GAM967 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15198] It is yet further appreciated that specific functions, and accordingly utilities, of GAM967 correlate with, and may be deduced from, the identity of the target genes which GAM967 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15199] Nucleotide sequences of the GAM967 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM967 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM967 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM967 are further described hereinbelow with reference to Table Table1.

[15200] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM967 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15201] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 968 (GAM968) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15202] GAM968 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM968 was detected is described hereinabove with reference to Figs. 2-8.

[15203] GAM968 gene, herein designated GAM GENE, and

GAM968 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15204] GAM968 gene, herein designated GAM GENE, encodes a GAM968 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM968 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM968 precursor RNA is designated SEQ ID:941, and is provided hereinbelow with reference to the sequence listing part.

[15205] GAM968 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM968 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15206] An enzyme complex designated DICER COMPLEX, dices the GAM968 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM968 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM968 RNA is designated SEQ ID:2617, and is provided hereinbelow with reference to the sequence listing part.

[15207] GAM968 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM968 target RNA, herein designated GAM TARGET RNA. GAM968 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15208] GAM968 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM968 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM968 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM968 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM968 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15209] The complementary binding of GAM968 RNA, herein designated GAM RNA, to target binding sites on GAM968 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM968 target RNA, herein designated GAM TARGET RNA, into GAM968 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15210] It is appreciated that GAM968 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM968 target genes. The mRNA of each one of this plurality of GAM968 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM968 RNA, herein designated GAM RNA, and which when bound by GAM968 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM968 target proteins.

[15211] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM968 gene, herein designated GAM GENE, on one or more GAM968 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15212] It is yet further appreciated that specific functions, and accordingly utilities, of GAM968 correlate with, and may be deduced from, the identity of the target genes which GAM968 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15213] Nucleotide sequences of the GAM968 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM968 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM968 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM968 are further described hereinbelow with reference to Table Table1.

[15214] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM968 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15215] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

969 (GAM969) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15216] GAM969 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM969 was detected is described hereinabove with reference to Figs. 2-8.

[15217] GAM969 gene, herein designated GAM GENE, and GAM969 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15218] GAM969 gene, herein designated GAM GENE, encodes a GAM969 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM969 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM969 precursor RNA is designated SEQ ID:942, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:942 is located at position 1813294 relative to contig NT_011574.7, on chromosome X.

[15219] GAM969 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM969 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15220] An enzyme complex designated DICER COMPLEX, dices the GAM969 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM969 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM969 RNA is designated SEQ ID:2618, and is provided hereinbelow with reference to the sequence listing part.

[15221] GAM969 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM969 target RNA, herein designated GAM TARGET RNA. GAM969 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15222] GAM969 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM969 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM969 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM969 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM969 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[15223] The complementary binding of GAM969 RNA, herein designated GAM RNA, to target binding sites on GAM969 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM969 target RNA, herein designated GAM TARGET RNA, into GAM969 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15224] It is appreciated that GAM969 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM969 target genes. The mRNA of each one of this plurality of GAM969 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM969 RNA, herein designated GAM RNA, and which when bound by GAM969 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM969 target proteins.

[15225] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM969 gene, herein designated GAM GENE, on one or

more GAM969 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15226] It is yet further appreciated that specific functions, and accordingly utilities, of GAM969 correlate with, and may be deduced from, the identity of the target genes which GAM969 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15227] Nucleotide sequences of the GAM969 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM969 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM969 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM969 are further de-

scribed hereinbelow with reference to Table Table1.

[15228] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM969 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15229] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 970 (GAM970) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15230] GAM970 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM970 was detected is described hereinabove with reference to Figs. 2-8.

[15231] GAM970 gene, herein designated GAM GENE, and GAM970 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15232] GAM970 gene, herein designated GAM GENE, encodes a GAM970 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM970 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM970 precursor RNA is designated SEQ ID:943, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:943 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[15233] GAM970 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM970 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15234] An enzyme complex designated DICER COMPLEX, dices the GAM970 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM970 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM970 RNA is designated SEQ ID:2619, and is provided hereinbelow with reference to the sequence listing part.

[15235] GAM970 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM970 target RNA, herein designated GAM TARGET RNA. GAM970 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15236] GAM970 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM970 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM970 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM970 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM970 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15237] The complementary binding of GAM970 RNA, herein designated GAM RNA, to target binding sites on GAM970 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM970 target RNA, herein designated GAM TARGET RNA, into GAM970 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15238] It is appreciated that GAM970 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM970 target genes. The mRNA of each one of this plurality of GAM970 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM970 RNA, herein designated GAM RNA, and which when bound by GAM970 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM970 target proteins.

[15239] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM970 gene, herein designated GAM GENE, on one or more GAM970 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15240] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM970 correlate with, and may be deduced from, the identity of the target genes which GAM970 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15241] Nucleotide sequences of the GAM970 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM970 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM970 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM970 are further described hereinbelow with reference to Table Table1.

[15242] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM970 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15243] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 971 (GAM971) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15244] GAM971 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM971 was detected is described hereinabove with reference to Figs. 2-8.

[15245] GAM971 gene, herein designated GAM GENE, and GAM971 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15246] GAM971 gene, herein designated GAM GENE, encodes a GAM971 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM971 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM971 precursor RNA is designated SEQ ID:944, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:944 is located at position 58581 relative to contig NT_004487.13, on chromosome 1.

[15247] GAM971 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15248] An enzyme complex designated DICER COMPLEX, dices the GAM971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM971 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM971 RNA is designated SEQ ID:2620, and is provided hereinbelow with reference to the sequence listing part.

[15249] GAM971 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM971 target RNA, herein designated GAM TARGET RNA.

GAM971 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[15250] GAM971 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM971 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM971 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM971 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM971 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15251] The complementary binding of GAM971 RNA, herein designated GAM RNA, to target binding sites on GAM971 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM971 target RNA, herein designated GAM TARGET RNA, into GAM971 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15252] It is appreciated that GAM971 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM971 target genes. The mRNA of each one of this plurality of GAM971 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM971 RNA, herein designated GAM RNA, and which when bound by GAM971 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM971 target proteins.

[15253] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM971 gene, herein designated GAM GENE, on one or more GAM971 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15254] It is yet further appreciated that specific functions, and accordingly utilities, of GAM971 correlate with, and may be deduced from, the identity of the target genes which GAM971 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15255] Nucleotide sequences of the GAM971 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM971 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM971 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM971 are further described hereinbelow with reference to Table Table1.

[15256] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM971 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15257] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 972 (GAM972) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15258] GAM972 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM972 was detected is described hereinabove with reference to Figs. 2-8.

[15259] GAM972 gene, herein designated GAM GENE, and GAM972 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15260] GAM972 gene, herein designated GAM GENE, encodes a GAM972 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM972 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM972 precursor RNA is designated SEQ ID:945, and is provided hereinbelow with reference to the sequence listing part.

[15261] GAM972 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM972 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15262] An enzyme complex designated DICER COMPLEX, dices the GAM972 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM972 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM972 RNA is designated SEQ ID:2621, and is provided

hereinbelow with reference to the sequence listing part.

[15263] GAM972 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM972 target RNA, herein designated GAM TARGET RNA.

GAM972 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15264] GAM972 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM972 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM972 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM972 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM972 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15265] The complementary binding of GAM972 RNA, herein designated GAM RNA, to target binding sites on GAM972 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM972 target RNA, herein designated GAM TARGET RNA, into GAM972 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15266] It is appreciated that GAM972 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM972 target genes. The mRNA of each one of this plurality of GAM972 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM972 RNA, herein designated GAM RNA, and which when bound by GAM972 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM972 tar-

get proteins.

[15267] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM972 gene, herein designated GAM GENE, on one or more GAM972 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15268] It is yet further appreciated that specific functions, and accordingly utilities, of GAM972 correlate with, and may be deduced from, the identity of the target genes which GAM972 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15269] Nucleotide sequences of the GAM972 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM972 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM972 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM972 are further described hereinbelow with reference to Table Table1.

[15270] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM972 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15271] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 973 (GAM973) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15272] GAM973 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM973 was detected is described hereinabove with reference to Figs. 2-8.

[15273] GAM973 gene, herein designated GAM GENE, and

GAM973 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15274] GAM973 gene, herein designated GAM GENE, encodes a GAM973 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM973 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM973 precursor RNA is designated SEQ ID:946, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:946 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[15275] GAM973 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM973 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15276] An enzyme complex designated DICER COMPLEX, dices the GAM973 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM973 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM973 RNA is designated SEQ ID:2622, and is provided hereinbelow with reference to the sequence listing part.

[15277] GAM973 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM973 target RNA, herein designated GAM TARGET RNA. GAM973 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15278] GAM973 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM973 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM973 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM973 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM973 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15279] The complementary binding of GAM973 RNA, herein designated GAM RNA, to target binding sites on GAM973 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM973 target RNA, herein designated GAM TARGET RNA, into GAM973 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[15280] It is appreciated that GAM973 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM973 target genes. The mRNA of each one of this plurality of GAM973 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM973 RNA, herein designated GAM RNA, and which when bound by GAM973 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM973 target proteins.

[15281] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM973 gene, herein designated GAM GENE, on one or more GAM973 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15282] It is yet further appreciated that specific functions, and accordingly utilities, of GAM973 correlate with, and may be deduced from, the identity of the target genes which GAM973 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15283] Nucleotide sequences of the GAM973 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM973 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM973 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM973 are further described hereinbelow with reference to Table Table1.

[15284] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM973 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15285] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 974 (GAM974) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15286] GAM974 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM974 was detected is described hereinabove with reference to Figs. 2-8.

[15287] GAM974 gene, herein designated GAM GENE, and GAM974 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15288] GAM974 gene, herein designated GAM GENE, encodes a GAM974 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM974 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM974 precursor RNA is designated SEQ ID:947, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:947 is located at position 677944 relative to contig NT_011176.13, on chromosome 19.

[15289] GAM974 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM974 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15290] An enzyme complex designated DICER COMPLEX, dices the GAM974 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM974 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM974 RNA is designated SEQ ID:2623, and is provided hereinbelow with reference to the sequence listing part.

[15291] GAM974 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM974

target RNA, herein designated GAM TARGET RNA.

GAM974 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15292] GAM974 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM974 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM974 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM974 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM974 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15293] The complementary binding of GAM974 RNA, herein designated GAM RNA, to target binding sites on GAM974 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM974 target RNA, herein designated GAM TARGET RNA, into GAM974 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15294] It is appreciated that GAM974 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM974 target genes. The mRNA of each one of this plurality of GAM974 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM974 RNA, herein designated GAM RNA, and which when bound by GAM974 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM974 target proteins.

[15295] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM974 gene, herein designated GAM GENE, on one or more GAM974 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15296] It is yet further appreciated that specific functions, and accordingly utilities, of GAM974 correlate with, and may be deduced from, the identity of the target genes which GAM974 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15297] Nucleotide sequences of the GAM974 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM974 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM974 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM974 are further described hereinbelow with reference to Table Table1.

[15298] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM974 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15299] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 975 (GAM975) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15300] GAM975 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM975 was detected is described hereinabove with reference to Figs. 2-8.

[15301] GAM975 gene, herein designated GAM GENE, and GAM975 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15302] GAM975 gene, herein designated GAM GENE, encodes a

GAM975 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM975 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM975 precursor RNA is designated SEQ ID:948, and is provided hereinbelow with reference to the sequence listing part.

[15303] GAM975 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15304] An enzyme complex designated DICER COMPLEX, dices the GAM975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM975 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM975 RNA is designated SEQ ID:2624, and is provided hereinbelow with reference to the sequence listing part.

[15305] GAM975 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM975 target RNA, herein designated GAM TARGET RNA. GAM975 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15306] GAM975 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM975 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM975 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM975 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM975 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15307] The complementary binding of GAM975 RNA, herein designated GAM RNA, to target binding sites on GAM975 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM975 target RNA, herein designated GAM TARGET RNA, into GAM975 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15308] It is appreciated that GAM975 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM975 target genes. The mRNA of each one of this plurality of GAM975 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM975 RNA, herein designated GAM RNA, and which when bound by GAM975 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM975 target proteins.

[15309] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM975 gene, herein designated GAM GENE, on one or more GAM975 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15310] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM975 correlate with, and may be deduced from, the identity of the target genes which GAM975 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15311] Nucleotide sequences of the GAM975 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM975 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM975 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM975 are further described hereinbelow with reference to Table Table1.

[15312] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM975 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15313] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 976 (GAM976) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15314] GAM976 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM976 was detected is described hereinabove with reference to Figs. 2-8.

[15315] GAM976 gene, herein designated GAM GENE, and GAM976 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15316] GAM976 gene, herein designated GAM GENE, encodes a GAM976 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM976 precursor RNA, herein desig-

nated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM976 precursor RNA is designated SEQ ID:949, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:949 is located at position 20318349 relative to contig NT_011387.8, on chromosome 20.

[15317] GAM976 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15318] An enzyme complex designated DICER COMPLEX, dices the GAM976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM976 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA seg-

ment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM976 RNA is designated SEQ ID:2625, and is provided hereinbelow with reference to the sequence listing part.

[15319] GAM976 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM976 target RNA, herein designated GAM TARGET RNA. GAM976 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15320] GAM976 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM976 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM976 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM976 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM976 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15321] The complementary binding of GAM976 RNA, herein designated GAM RNA, to target binding sites on GAM976 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM976 target RNA, herein designated GAM TARGET RNA, into GAM976 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15322] It is appreciated that GAM976 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM976 target genes. The mRNA of each one of this plurality of GAM976 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM976 RNA, herein designated GAM RNA, and which when bound by GAM976 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM976 target proteins.

[15323] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM976 gene, herein designated GAM GENE, on one or more GAM976 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15324] It is yet further appreciated that specific functions, and accordingly utilities, of GAM976 correlate with, and may

be deduced from, the identity of the target genes which GAM976 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15325] Nucleotide sequences of the GAM976 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM976 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM976 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM976 are further described hereinbelow with reference to Table Table1.

[15326] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM976 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15327] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 977 (GAM977) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15328] GAM977 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM977 was detected is described hereinabove with reference to Figs. 2-8.

[15329] GAM977 gene, herein designated GAM GENE, and GAM977 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15330] GAM977 gene, herein designated GAM GENE, encodes a GAM977 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM977 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM977 precursor RNA is designated SEQ ID:950, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:950 is located at position 1464276 relative to contig NT_005986.13, on chromosome 3.

[15331] GAM977 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM977 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that

the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15332] An enzyme complex designated DICER COMPLEX, dices the GAM977 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM977 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM977 RNA is designated SEQ ID:2626, and is provided hereinbelow with reference to the sequence listing part.

[15333] GAM977 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM977 target RNA, herein designated GAM TARGET RNA. GAM977 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15334] GAM977 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM977 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM977 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM977 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM977 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15335] The complementary binding of GAM977 RNA, herein designated GAM RNA, to target binding sites on GAM977 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM977 target RNA, herein designated GAM TARGET RNA, into GAM977 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15336] It is appreciated that GAM977 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM977 target genes. The mRNA of each one of this plurality of GAM977 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM977 RNA, herein designated GAM RNA, and which when bound by GAM977 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM977 target proteins.

[15337] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM977 gene, herein designated GAM GENE, on one or more GAM977 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15338] It is yet further appreciated that specific functions, and accordingly utilities, of GAM977 correlate with, and may be deduced from, the identity of the target genes which GAM977 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15339] Nucleotide sequences of the GAM977 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM977 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM977 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM977 are further described hereinbelow with reference to Table Table1.

[15340] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM977 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15341] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 978 (GAM978) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15342] GAM978 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM978 was detected is described hereinabove with reference to Figs. 2-8.

[15343] GAM978 gene, herein designated GAM GENE, and GAM978 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15344] GAM978 gene, herein designated GAM GENE, encodes a GAM978 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM978 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM978 precursor RNA is desig-

nated SEQ ID:951, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:951 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[15345] GAM978 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15346] An enzyme complex designated DICER COMPLEX, dices the GAM978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM978 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of

GAM978 RNA is designated SEQ ID:2627, and is provided hereinbelow with reference to the sequence listing part.

[15347] GAM978 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM978 target RNA, herein designated GAM TARGET RNA. GAM978 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15348] GAM978 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM978 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM978 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM978 RNA, herein

designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM978 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15349] The complementary binding of GAM978 RNA, herein designated GAM RNA, to target binding sites on GAM978 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM978 target RNA, herein designated GAM TARGET RNA, into GAM978 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15350] It is appreciated that GAM978 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM978 target genes. The mRNA of each one of this plurality of GAM978 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM978 RNA, herein designated GAM RNA, and which when bound by GAM978 RNA, herein designated GAM RNA, causes inhibi-

tion of translation of respective one or more GAM978 target proteins.

[15351] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM978 gene, herein designated GAM GENE, on one or more GAM978 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15352] It is yet further appreciated that specific functions, and accordingly utilities, of GAM978 correlate with, and may be deduced from, the identity of the target genes which GAM978 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15353] Nucleotide sequences of the GAM978 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM978 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM978 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM978 are further described hereinbelow with reference to Table Table1.

[15354] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM978 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15355] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 979 (GAM979) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15356] GAM979 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM979 was detected is described hereinabove with reference to Figs. 2-8.

[15357] GAM979 gene, herein designated GAM GENE, and GAM979 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15358] GAM979 gene, herein designated GAM GENE, encodes a GAM979 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM979 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM979 precursor RNA is designated SEQ ID:952, and is provided hereinbelow with reference to the sequence listing part.

[15359] GAM979 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[15360] SEQ ID:100639 detected in mouse EST Accession BE369926.1.

[15361] SEQ ID:100640 detected in mouse EST Accession BE371634.1.

[15362] SEQ ID:100641 detected in mouse EST Accession BF162728.1.

[15363] SEQ ID:100642 detected in mouse EST Accession BE572790.1.

[15364] SEQ ID:100643 detected in mouse EST Accession BG964017.1.

[15365] SEQ ID:100645 detected in mouse EST Accession BF450182.1.

[15366] SEQ ID:100646 detected in mouse EST Accession BE291495.1.

[15367] GAM979 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM979 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15368] An enzyme complex designated DICER COMPLEX, dices the GAM979 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM979 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM979 RNA is designated SEQ ID:2628, and is provided hereinbelow with reference to the sequence listing part.

[15369] GAM979 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM979 target RNA, herein designated GAM TARGET RNA. GAM979 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15370] GAM979 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM979 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM979 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM979 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM979 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15371] The complementary binding of GAM979 RNA, herein designated GAM RNA, to target binding sites on GAM979 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM979 target RNA, herein designated GAM TARGET RNA, into GAM979 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15372] It is appreciated that GAM979 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM979 target genes. The mRNA of each one of this plurality of GAM979 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM979 RNA, herein designated GAM RNA, and which when bound by GAM979 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM979 target proteins.

[15373] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM979 gene, herein designated GAM GENE, on one or more GAM979 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15374] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM979 correlate with, and may be deduced from, the identity of the target genes which GAM979 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15375] Nucleotide sequences of the GAM979 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM979 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM979 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM979 are further described hereinbelow with reference to Table Table1.

[15376] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM979 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15377] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 980 (GAM980) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15378] GAM980 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM980 was detected is described hereinabove with reference to Figs. 2-8.

[15379] GAM980 gene, herein designated GAM GENE, and GAM980 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15380] GAM980 gene, herein designated GAM GENE, encodes a GAM980 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM980 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM980 precursor RNA is designated SEQ ID:953, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:953 is located at position 86583 relative to contig NT_011594.9, on chromosome X.

[15381] GAM980 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15382] An enzyme complex designated DICER COMPLEX, dices the GAM980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM980 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM980 RNA is designated SEQ ID:2629, and is provided hereinbelow with reference to the sequence listing part.

[15383] GAM980 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM980 target RNA, herein designated GAM TARGET RNA.
GAM980 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[15384] GAM980 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM980 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM980 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM980 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM980 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15385] The complementary binding of GAM980 RNA, herein designated GAM RNA, to target binding sites on GAM980 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM980 target RNA, herein designated GAM TARGET RNA, into GAM980 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15386] It is appreciated that GAM980 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM980 target genes. The mRNA of each one of this plurality of GAM980 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM980 RNA, herein designated GAM RNA, and which when bound by GAM980 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM980 target proteins.

[15387] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM980 gene, herein designated GAM GENE, on one or more GAM980 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15388] It is yet further appreciated that specific functions, and accordingly utilities, of GAM980 correlate with, and may be deduced from, the identity of the target genes which GAM980 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15389] Nucleotide sequences of the GAM980 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM980 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM980 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM980 are further described hereinbelow with reference to Table Table1.

[15390] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM980 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15391] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 981 (GAM981) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15392] GAM981 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM981 was detected is described hereinabove with reference to Figs. 2-8.

[15393] GAM981 gene, herein designated GAM GENE, and GAM981 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15394] GAM981 gene, herein designated GAM GENE, encodes a GAM981 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM981 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM981 precursor RNA is designated SEQ ID:954, and is provided hereinbelow with reference to the sequence listing part.

[15395] GAM981 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM981 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15396] An enzyme complex designated DICER COMPLEX, dices the GAM981 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM981 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM981 RNA is designated SEQ ID:2630, and is provided

hereinbelow with reference to the sequence listing part.

[15397] GAM981 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM981 target RNA, herein designated GAM TARGET RNA.

GAM981 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15398] GAM981 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM981 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM981 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM981 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM981 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15399] The complementary binding of GAM981 RNA, herein designated GAM RNA, to target binding sites on GAM981 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM981 target RNA, herein designated GAM TARGET RNA, into GAM981 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15400] It is appreciated that GAM981 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM981 target genes. The mRNA of each one of this plurality of GAM981 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM981 RNA, herein designated GAM RNA, and which when bound by GAM981 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM981 tar-

get proteins.

[15401] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM981 gene, herein designated GAM GENE, on one or more GAM981 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15402] It is yet further appreciated that specific functions, and accordingly utilities, of GAM981 correlate with, and may be deduced from, the identity of the target genes which GAM981 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15403] Nucleotide sequences of the GAM981 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM981 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM981 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM981 are further described hereinbelow with reference to Table Table1.

[15404] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM981 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15405] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 982 (GAM982) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15406] GAM982 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM982 was detected is described hereinabove with reference to Figs. 2-8.

[15407] GAM982 gene, herein designated GAM GENE, and

GAM982 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15408] GAM982 gene, herein designated GAM GENE, encodes a GAM982 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM982 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM982 precursor RNA is designated SEQ ID:955, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:955 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[15409] GAM982 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM982 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15410] An enzyme complex designated DICER COMPLEX, dices the GAM982 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM982 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM982 RNA is designated SEQ ID:2631, and is provided hereinbelow with reference to the sequence listing part.

[15411] GAM982 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM982 target RNA, herein designated GAM TARGET RNA. GAM982 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15412] GAM982 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM982 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM982 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM982 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM982 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15413] The complementary binding of GAM982 RNA, herein designated GAM RNA, to target binding sites on GAM982 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM982 target RNA, herein designated GAM TARGET RNA, into GAM982 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[15414] It is appreciated that GAM982 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM982 target genes. The mRNA of each one of this plurality of GAM982 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM982 RNA, herein designated GAM RNA, and which when bound by GAM982 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM982 target proteins.

[15415] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM982 gene, herein designated GAM GENE, on one or more GAM982 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15416] It is yet further appreciated that specific functions, and accordingly utilities, of GAM982 correlate with, and may be deduced from, the identity of the target genes which GAM982 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15417] Nucleotide sequences of the GAM982 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM982 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM982 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM982 are further described hereinbelow with reference to Table Table1.

[15418] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM982 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15419] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 983 (GAM983) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15420] GAM983 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM983 was detected is described hereinabove with reference to Figs. 2-8.

[15421] GAM983 gene, herein designated GAM GENE, and GAM983 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15422] GAM983 gene, herein designated GAM GENE, encodes a GAM983 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM983 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM983 precursor RNA is designated SEQ ID:956, and is provided hereinbelow with reference to the sequence listing part.

[15423] GAM983 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM983 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15424] An enzyme complex designated DICER COMPLEX, dices the GAM983 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM983 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM983 RNA is designated SEQ ID:2632, and is provided hereinbelow with reference to the sequence listing part.

[15425] GAM983 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM983 target RNA, herein designated GAM TARGET RNA. GAM983 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15426] GAM983 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM983 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM983 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM983 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM983 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[15427] The complementary binding of GAM983 RNA, herein designated GAM RNA, to target binding sites on GAM983 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM983 target RNA, herein designated GAM TARGET RNA, into GAM983 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15428] It is appreciated that GAM983 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM983 target genes. The mRNA of each one of this plurality of GAM983 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM983 RNA, herein designated GAM RNA, and which when bound by GAM983 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM983 target proteins.

[15429] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM983 gene, herein designated GAM GENE, on one or

more GAM983 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15430] It is yet further appreciated that specific functions, and accordingly utilities, of GAM983 correlate with, and may be deduced from, the identity of the target genes which GAM983 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15431] Nucleotide sequences of the GAM983 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM983 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM983 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM983 are further de-

scribed hereinbelow with reference to Table Table1.

[15432] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM983 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15433] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 984 (GAM984) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15434] GAM984 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM984 was detected is described hereinabove with reference to Figs. 2-8.

[15435] GAM984 gene, herein designated GAM GENE, and GAM984 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15436] GAM984 gene, herein designated GAM GENE, encodes a GAM984 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM984 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM984 precursor RNA is designated SEQ ID:957, and is provided hereinbelow with reference to the sequence listing part.

[15437] GAM984 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM984 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15438] An enzyme complex designated DICER COMPLEX, dices the GAM984 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM984 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM984 RNA is designated SEQ ID:2633, and is provided hereinbelow with reference to the sequence listing part.

[15439] GAM984 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM984 target RNA, herein designated GAM TARGET RNA. GAM984 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15440] GAM984 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM984 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM984 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM984 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM984 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15441] The complementary binding of GAM984 RNA, herein designated GAM RNA, to target binding sites on GAM984 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM984 target RNA, herein designated GAM TARGET RNA, into GAM984 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15442] It is appreciated that GAM984 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM984 target genes. The mRNA of each one of this plurality of GAM984 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM984 RNA,

herein designated GAM RNA, and which when bound by GAM984 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM984 target proteins.

[15443] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM984 gene, herein designated GAM GENE, on one or more GAM984 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15444] It is yet further appreciated that specific functions, and accordingly utilities, of GAM984 correlate with, and may be deduced from, the identity of the target genes which

GAM984 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15445] Nucleotide sequences of the GAM984 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM984 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM984 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM984 are further described hereinbelow with reference to Table Table1.

[15446] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM984 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15447] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 985 (GAM985) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15448] GAM985 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM985 was detected is described hereinabove with reference to Figs. 2-8.

[15449] GAM985 gene, herein designated GAM GENE, and GAM985 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15450] GAM985 gene, herein designated GAM GENE, encodes a GAM985 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM985 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM985 precursor RNA is designated SEQ ID:958, and is provided hereinbelow with reference to the sequence listing part.

[15451] GAM985 has 48 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[15452] SEQ ID:98508 detected in mouse EST Accession AA517267.1.

[15453] SEQ ID:98509 detected in mouse EST Accession AW488637.1.

[15454] SEQ ID:98510 detected in mouse EST Accession BF730308.1.

[15455] SEQ ID:98511 detected in mouse EST Accession AA770810.1.

[15456] SEQ ID:98512 detected in mouse EST Accession AA142786.1.

[15457] SEQ ID:98513 detected in mouse EST Accession AI788525.1.

[15458] SEQ ID:98514 detected in mouse EST Accession AA691443.1.

[15459] SEQ ID:98515 detected in mouse EST Accession BE626527.1.

[15460] SEQ ID:98516 detected in mouse EST Accession BE623908.1.

[15461] SEQ ID:98517 detected in mouse EST Accession AA672838.1.

[15462] SEQ ID:98518 detected in mouse EST Accession AA624895.1.

[15463] SEQ ID:98519 detected in mouse EST Accession BI714485.1.

[15464] SEQ ID:98520 detected in mouse EST Accession AI390190.1.

[15465] SEQ ID:98521 detected in mouse EST Accession

AA272020.1.

[15466] SEQ ID:98522 detected in mouse EST Accession AA123201.1.

[15467] SEQ ID:98523 detected in mouse EST Accession BE689804.1.

[15468] SEQ ID:98524 detected in mouse EST Accession AA086955.1.

[15469] SEQ ID:98525 detected in mouse EST Accession BG145851.1.

[15470] SEQ ID:98526 detected in mouse EST Accession BE134018.1.

[15471] SEQ ID:98527 detected in mouse EST Accession AW551233.1.

[15472] SEQ ID:98528 detected in mouse EST Accession AA396997.1.

[15473] SEQ ID:98529 detected in mouse EST Accession BE198361.1.

[15474] SEQ ID:98530 detected in mouse EST Accession BE134116.1.

[15475] SEQ ID:98531 detected in mouse EST Accession BB624139.1.

[15476] SEQ ID:98532 detected in mouse EST Accession AA869587.1.

[15477] SEQ ID:98533 detected in mouse EST Accession BG870423.1.

[15478] SEQ ID:98534 detected in mouse EST Accession BE951532.1.

[15479] SEQ ID:98535 detected in mouse EST Accession BI650479.1.

[15480] SEQ ID:98536 detected in mouse EST Accession AA691295.1.

[15481] SEQ ID:98539 detected in mouse EST Accession AA681088.1.

[15482] SEQ ID:98540 detected in mouse EST Accession AA397244.1.

[15483] SEQ ID:98541 detected in mouse EST Accession AA895720.1.

[15484] SEQ ID:98542 detected in mouse EST Accession AA590571.1.

[15485] SEQ ID:98543 detected in mouse EST Accession AA870305.1.

[15486] SEQ ID:98544 detected in mouse EST Accession BF788679.1.

[15487] SEQ ID:98545 detected in mouse EST Accession AA771187.1.

[15488] SEQ ID:98546 detected in mouse EST Accession

BG090143.1.

[15489] SEQ ID:98547 detected in mouse EST Accession AA221182.1.

[15490] SEQ ID:98548 detected in mouse EST Accession BG276809.1.

[15491] SEQ ID:98549 detected in mouse EST Accession BG073645.1.

[15492] SEQ ID:98550 detected in mouse EST Accession AA547023.1.

[15493] SEQ ID:98551 detected in mouse EST Accession AA238167.1.

[15494] SEQ ID:98552 detected in mouse EST Accession AW491159.1.

[15495] SEQ ID:98553 detected in mouse EST Accession AA118820.1.

[15496] SEQ ID:98555 detected in mouse EST Accession BE553328.1.

[15497] SEQ ID:98556 detected in mouse EST Accession BF467940.1.

[15498] SEQ ID:98557 detected in mouse EST Accession BG695432.1.

[15499] SEQ ID:98558 detected in mouse EST Accession BF135327.1.

[15500] GAM985 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM985 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15501] An enzyme complex designated DICER COMPLEX, dices the GAM985 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM985 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM985 RNA is designated SEQ ID:2634, and is provided hereinbelow with reference to the sequence listing part.

[15502] GAM985 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM985

target RNA, herein designated GAM TARGET RNA.

GAM985 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15503] GAM985 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM985 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM985 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM985 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM985 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15504] The complementary binding of GAM985 RNA, herein designated GAM RNA, to target binding sites on GAM985 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM985 target RNA, herein designated GAM TARGET RNA, into GAM985 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15505] It is appreciated that GAM985 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM985 target genes. The mRNA of each one of this plurality of GAM985 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM985 RNA, herein designated GAM RNA, and which when bound by GAM985 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM985 target proteins.

[15506] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM985 gene, herein designated GAM GENE, on one or more GAM985 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15507] It is yet further appreciated that specific functions, and accordingly utilities, of GAM985 correlate with, and may be deduced from, the identity of the target genes which GAM985 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15508] Nucleotide sequences of the GAM985 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM985 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM985 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM985 are further described hereinbelow with reference to Table Table1.

[15509] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM985 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15510] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 986 (GAM986) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15511] GAM986 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM986 was detected is described hereinabove with reference to Figs. 2-8.

[15512] GAM986 gene, herein designated GAM GENE, and GAM986 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15513] GAM986 gene, herein designated GAM GENE, encodes a

GAM986 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM986 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM986 precursor RNA is designated SEQ ID:959, and is provided hereinbelow with reference to the sequence listing part.

[15514] GAM986 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[15515] SEQ ID:98537 detected in mouse EST Accession AA106737.1.

[15516] SEQ ID:98538 detected in mouse EST Accession AA500296.1.

[15517] SEQ ID:98554 detected in mouse EST Accession BE554084.1.

[15518] SEQ ID:98559 detected in mouse EST Accession BG922170.1.

[15519] GAM986 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM986 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15520] An enzyme complex designated DICER COMPLEX, dices the GAM986 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM986 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM986 RNA is designated SEQ ID:2635, and is provided hereinbelow with reference to the sequence listing part.

[15521] GAM986 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM986 target RNA, herein designated GAM TARGET RNA. GAM986 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15522] GAM986 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM986 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM986 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM986 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM986 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[15523] The complementary binding of GAM986 RNA, herein designated GAM RNA, to target binding sites on GAM986 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM986 target RNA, herein designated GAM TARGET RNA, into GAM986 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15524] It is appreciated that GAM986 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM986 target genes. The mRNA of each one of this plurality of GAM986 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM986 RNA, herein designated GAM RNA, and which when bound by GAM986 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM986 target proteins.

[15525] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM986 gene, herein designated GAM GENE, on one or

more GAM986 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15526] It is yet further appreciated that specific functions, and accordingly utilities, of GAM986 correlate with, and may be deduced from, the identity of the target genes which GAM986 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15527] Nucleotide sequences of the GAM986 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM986 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM986 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM986 are further de-

scribed hereinbelow with reference to Table Table1.

[15528] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM986 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15529] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 987 (GAM987) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15530] GAM987 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM987 was detected is described hereinabove with reference to Figs. 2-8.

[15531] GAM987 gene, herein designated GAM GENE, and GAM987 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15532] GAM987 gene, herein designated GAM GENE, encodes a GAM987 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM987 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM987 precursor RNA is designated SEQ ID:960, and is provided hereinbelow with reference to the sequence listing part.

[15533] GAM987 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM987 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15534] An enzyme complex designated DICER COMPLEX, dices the GAM987 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM987 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an

enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM987 RNA is designated SEQ ID:2636, and is provided hereinbelow with reference to the sequence listing part.

[15535] GAM987 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM987 target RNA, herein designated GAM TARGET RNA. GAM987 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15536] GAM987 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM987 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM987 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM987 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM987 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15537] The complementary binding of GAM987 RNA, herein designated GAM RNA, to target binding sites on GAM987 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM987 target RNA, herein designated GAM TARGET RNA, into GAM987 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15538] It is appreciated that GAM987 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM987 target genes. The mRNA of each one of this plurality of GAM987 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM987 RNA,

herein designated GAM RNA, and which when bound by GAM987 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM987 target proteins.

[15539] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM987 gene, herein designated GAM GENE, on one or more GAM987 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15540] It is yet further appreciated that specific functions, and accordingly utilities, of GAM987 correlate with, and may be deduced from, the identity of the target genes which

GAM987 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15541] Nucleotide sequences of the GAM987 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM987 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM987 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM987 are further described hereinbelow with reference to Table Table1.

[15542] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM987 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15543] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 988 (GAM988) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15544] GAM988 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM988 was detected is described hereinabove with reference to Figs. 2-8.

[15545] GAM988 gene, herein designated GAM GENE, and GAM988 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15546] GAM988 gene, herein designated GAM GENE, encodes a GAM988 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM988 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM988 precursor RNA is designated SEQ ID:961, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:961 is located at position 17488561 relative to contig NT_011520.8, on chromosome 22.

[15547] GAM988 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM988 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15548] An enzyme complex designated DICER COMPLEX, dices the GAM988 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM988 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM988 RNA is designated SEQ ID:2637, and is provided hereinbelow with reference to the sequence listing part.

[15549] GAM988 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM988 target RNA, herein designated GAM TARGET RNA. GAM988 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15550] GAM988 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM988 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM988 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM988 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM988 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15551] The complementary binding of GAM988 RNA, herein designated GAM RNA, to target binding sites on GAM988 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM988 target RNA, herein designated GAM TARGET RNA, into GAM988 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15552] It is appreciated that GAM988 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM988 target genes. The mRNA of each one of this plurality of GAM988 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM988 RNA, herein designated GAM RNA, and which when bound by GAM988 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM988 target proteins.

[15553] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM988 gene, herein designated GAM GENE, on one or more GAM988 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15554] It is yet further appreciated that specific functions, and accordingly utilities, of GAM988 correlate with, and may be deduced from, the identity of the target genes which GAM988 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15555] Nucleotide sequences of the GAM988 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM988 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM988 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM988 are further described hereinbelow with reference to Table Table1.

[15556] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM988 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15557] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 989 (GAM989) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15558] GAM989 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM989 was detected is described hereinabove with reference to Figs. 2-8.

[15559] GAM989 gene, herein designated GAM GENE, and GAM989 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15560] GAM989 gene, herein designated GAM GENE, encodes a GAM989 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM989 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM989 precursor RNA is designated SEQ ID:962, and is provided hereinbelow with refer-

ence to the sequence listing part. Nucleotide sequence SEQ ID:962 is located at position 4851368 relative to contig NT_022517.13, on chromosome 3.

[15561] GAM989 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM989 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15562] An enzyme complex designated DICER COMPLEX, dices the GAM989 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM989 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM989 RNA is designated SEQ ID:2638, and is provided

hereinbelow with reference to the sequence listing part.

[15563] GAM989 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM989 target RNA, herein designated GAM TARGET RNA.

GAM989 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15564] GAM989 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM989 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM989 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM989 RNA, herein designated GAM RNA, may have a different number of tar-

get binding sites in untranslated regions of a GAM989 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15565] The complementary binding of GAM989 RNA, herein designated GAM RNA, to target binding sites on GAM989 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM989 target RNA, herein designated GAM TARGET RNA, into GAM989 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15566] It is appreciated that GAM989 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM989 target genes. The mRNA of each one of this plurality of GAM989 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM989 RNA, herein designated GAM RNA, and which when bound by GAM989 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM989 tar-

get proteins.

[15567] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM989 gene, herein designated GAM GENE, on one or more GAM989 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15568] It is yet further appreciated that specific functions, and accordingly utilities, of GAM989 correlate with, and may be deduced from, the identity of the target genes which GAM989 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15569] Nucleotide sequences of the GAM989 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM989 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM989 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM989 are further described hereinbelow with reference to Table Table1.

[15570] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM989 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15571] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 990 (GAM990) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15572] GAM990 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM990 was detected is described hereinabove with reference to Figs. 2-8.

[15573] GAM990 gene, herein designated GAM GENE, and

GAM990 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15574] GAM990 gene, herein designated GAM GENE, encodes a GAM990 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM990 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM990 precursor RNA is designated SEQ ID:963, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:963 is located at position 35563858 relative to contig NT_007819.11, on chromosome 7.

[15575] GAM990 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15576] An enzyme complex designated DICER COMPLEX, dices the GAM990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM990 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM990 RNA is designated SEQ ID:2639, and is provided hereinbelow with reference to the sequence listing part.

[15577] GAM990 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM990 target RNA, herein designated GAM TARGET RNA.
GAM990 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15578] GAM990 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM990 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM990 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM990 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM990 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15579] The complementary binding of GAM990 RNA, herein designated GAM RNA, to target binding sites on GAM990 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM990 target RNA, herein designated GAM TARGET RNA, into GAM990 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[15580] It is appreciated that GAM990 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM990 target genes. The mRNA of each one of this plurality of GAM990 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM990 RNA, herein designated GAM RNA, and which when bound by GAM990 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM990 target proteins.

[15581] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM990 gene, herein designated GAM GENE, on one or more GAM990 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15582] It is yet further appreciated that specific functions, and accordingly utilities, of GAM990 correlate with, and may be deduced from, the identity of the target genes which GAM990 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15583] Nucleotide sequences of the GAM990 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM990 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM990 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM990 are further described hereinbelow with reference to Table Table1.

[15584] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM990 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15585] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 991 (GAM991) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15586] GAM991 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM991 was detected is described hereinabove with reference to Figs. 2-8.

[15587] GAM991 gene, herein designated GAM GENE, and GAM991 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15588] GAM991 gene, herein designated GAM GENE, encodes a GAM991 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM991 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM991 precursor RNA is designated SEQ ID:964, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:964 is located at position 1626042 relative to contig NT_024797.11, on chromosome 16.

[15589] GAM991 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM991 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15590] An enzyme complex designated DICER COMPLEX, dices the GAM991 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM991 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM991 RNA is designated SEQ ID:2640, and is provided hereinbelow with reference to the sequence listing part.

[15591] GAM991 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM991

target RNA, herein designated GAM TARGET RNA.

GAM991 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15592] GAM991 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM991 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM991 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM991 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM991 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding

sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15593] The complementary binding of GAM991 RNA, herein designated GAM RNA, to target binding sites on GAM991 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM991 target RNA, herein designated GAM TARGET RNA, into GAM991 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15594] It is appreciated that GAM991 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM991 target genes. The mRNA of each one of this plurality of GAM991 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM991 RNA, herein designated GAM RNA, and which when bound by GAM991 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM991 target proteins.

[15595] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM991 gene, herein designated GAM GENE, on one or more GAM991 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15596] It is yet further appreciated that specific functions, and accordingly utilities, of GAM991 correlate with, and may be deduced from, the identity of the target genes which GAM991 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15597] Nucleotide sequences of the GAM991 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM991 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM991 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM991 are further described hereinbelow with reference to Table Table1.

[15598] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM991 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15599] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 992 (GAM992) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15600] GAM992 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM992 was detected is described hereinabove with reference to Figs. 2-8.

[15601] GAM992 gene, herein designated GAM GENE, and GAM992 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15602] GAM992 gene, herein designated GAM GENE, encodes a

GAM992 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM992 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM992 precursor RNA is designated SEQ ID:965, and is provided hereinbelow with reference to the sequence listing part.

[15603] GAM992 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM992 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15604] An enzyme complex designated DICER COMPLEX, dices the GAM992 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM992 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM992 RNA is designated SEQ ID:2641, and is provided hereinbelow with reference to the sequence listing part.

[15605] GAM992 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM992 target RNA, herein designated GAM TARGET RNA. GAM992 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15606] GAM992 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM992 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM992 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM992 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM992 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15607] The complementary binding of GAM992 RNA, herein designated GAM RNA, to target binding sites on GAM992 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM992 target RNA, herein designated GAM TARGET RNA, into GAM992 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15608] It is appreciated that GAM992 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM992 target genes. The mRNA of each one of this plurality of GAM992 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM992 RNA, herein designated GAM RNA, and which when bound by GAM992 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM992 target proteins.

[15609] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM992 gene, herein designated GAM GENE, on one or more GAM992 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15610] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM992 correlate with, and may be deduced from, the identity of the target genes which GAM992 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15611] Nucleotide sequences of the GAM992 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM992 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM992 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM992 are further described hereinbelow with reference to Table Table1.

[15612] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM992 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15613] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 993 (GAM993) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15614] GAM993 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM993 was detected is described hereinabove with reference to Figs. 2-8.

[15615] GAM993 gene, herein designated GAM GENE, and GAM993 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15616] GAM993 gene, herein designated GAM GENE, encodes a GAM993 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM993 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM993 precursor RNA is designated SEQ ID:966, and is provided hereinbelow with reference to the sequence listing part.

[15617] GAM993 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM993 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA en-

coded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15618] An enzyme complex designated DICER COMPLEX, dices the GAM993 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM993 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM993 RNA is designated SEQ ID:2642, and is provided hereinbelow with reference to the sequence listing part.

[15619] GAM993 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM993 target RNA, herein designated GAM TARGET RNA. GAM993 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15620] GAM993 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM993 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM993 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM993 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM993 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15621] The complementary binding of GAM993 RNA, herein designated GAM RNA, to target binding sites on GAM993 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM993 target RNA, herein designated GAM TARGET RNA, into GAM993 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15622] It is appreciated that GAM993 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM993 target genes. The mRNA of each one of this plurality of GAM993 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM993 RNA, herein designated GAM RNA, and which when bound by GAM993 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM993 target proteins.

[15623] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM993 gene, herein designated GAM GENE, on one or more GAM993 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15624] It is yet further appreciated that specific functions, and accordingly utilities, of GAM993 correlate with, and may be deduced from, the identity of the target genes which GAM993 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15625] Nucleotide sequences of the GAM993 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM993 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM993 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM993 are further described hereinbelow with reference to Table Table1.

[15626] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM993 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15627] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 994 (GAM994) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15628] GAM994 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM994 was detected is described hereinabove with reference to Figs. 2-8.

[15629] GAM994 gene, herein designated GAM GENE, and GAM994 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15630] GAM994 gene, herein designated GAM GENE, encodes a GAM994 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM994 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM994 precursor RNA is designated SEQ ID:967, and is provided hereinbelow with refer-

ence to the sequence listing part.

[15631] GAM994 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM994 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15632] An enzyme complex designated DICER COMPLEX, dices the GAM994 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM994 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM994 RNA is designated SEQ ID:2643, and is provided hereinbelow with reference to the sequence listing part.

[15633] GAM994 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM994 target RNA, herein designated GAM TARGET RNA.

GAM994 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15634] GAM994 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM994 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM994 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM994 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM994 target RNA, herein designated GAM TARGET RNA. It is fur-

ther appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15635] The complementary binding of GAM994 RNA, herein designated GAM RNA, to target binding sites on GAM994 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM994 target RNA, herein designated GAM TARGET RNA, into GAM994 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15636] It is appreciated that GAM994 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM994 target genes. The mRNA of each one of this plurality of GAM994 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM994 RNA, herein designated GAM RNA, and which when bound by GAM994 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM994 target proteins.

[15637] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM994 gene, herein designated GAM GENE, on one or more GAM994 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15638] It is yet further appreciated that specific functions, and accordingly utilities, of GAM994 correlate with, and may be deduced from, the identity of the target genes which GAM994 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15639] Nucleotide sequences of the GAM994 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM994 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM994 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM994 are further described hereinbelow with reference to Table Table1.

[15640] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM994 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15641] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 995 (GAM995) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15642] GAM995 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM995 was detected is described hereinabove with reference to Figs. 2-8.

[15643] GAM995 gene, herein designated GAM GENE, and GAM995 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15644] GAM995 gene, herein designated GAM GENE, encodes a GAM995 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM995 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM995 precursor RNA is designated SEQ ID:968, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:968 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[15645] GAM995 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM995 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15646] An enzyme complex designated DICER COMPLEX, dices the GAM995 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM995 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM995 RNA is designated SEQ ID:2644, and is provided hereinbelow with reference to the sequence listing part.

[15647] GAM995 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM995 target RNA, herein designated GAM TARGET RNA.

GAM995 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15648] GAM995 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM995 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM995 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM995 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM995 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15649] The complementary binding of GAM995 RNA, herein designated GAM RNA, to target binding sites on GAM995 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM995 target RNA, herein designated GAM TARGET RNA, into GAM995 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15650] It is appreciated that GAM995 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM995 target genes. The mRNA of each one of this plurality of GAM995 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM995 RNA, herein designated GAM RNA, and which when bound by GAM995 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM995 target proteins.

[15651] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM995 gene, herein designated GAM GENE, on one or more GAM995 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15652] It is yet further appreciated that specific functions, and accordingly utilities, of GAM995 correlate with, and may be deduced from, the identity of the target genes which GAM995 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15653] Nucleotide sequences of the GAM995 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM995 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM995 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM995 are further described hereinbelow with reference to Table Table1.

[15654] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM995 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15655] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

996 (GAM996) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15656] GAM996 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM996 was detected is described hereinabove with reference to Figs. 2-8.

[15657] GAM996 gene, herein designated GAM GENE, and GAM996 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15658] GAM996 gene, herein designated GAM GENE, encodes a GAM996 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM996 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM996 precursor RNA is designated SEQ ID:969, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:969 is located at position 2557404 relative to contig NT_035235.2, on chromosome 12.

[15659] GAM996 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM996 folded pre-

cursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15660] An enzyme complex designated DICER COMPLEX, dices the GAM996 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM996 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM996 RNA is designated SEQ ID:2645, and is provided hereinbelow with reference to the sequence listing part.

[15661] GAM996 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM996 target RNA, herein designated GAM TARGET RNA. GAM996 target RNA, herein designated GAM TARGET

RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15662] GAM996 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM996 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM996 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM996 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM996 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR re-

gion, the 5UTR region, or in both 3UTR and 5UTR regions.

[15663] The complementary binding of GAM996 RNA, herein designated GAM RNA, to target binding sites on GAM996 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM996 target RNA, herein designated GAM TARGET RNA, into GAM996 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15664] It is appreciated that GAM996 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM996 target genes. The mRNA of each one of this plurality of GAM996 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM996 RNA, herein designated GAM RNA, and which when bound by GAM996 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM996 target proteins.

[15665] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM996 gene, herein designated GAM GENE, on one or

more GAM996 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15666] It is yet further appreciated that specific functions, and accordingly utilities, of GAM996 correlate with, and may be deduced from, the identity of the target genes which GAM996 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15667] Nucleotide sequences of the GAM996 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM996 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM996 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM996 are further de-

scribed hereinbelow with reference to Table Table1.

[15668] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM996 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15669] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 997 (GAM997) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15670] GAM997 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM997 was detected is described hereinabove with reference to Figs. 2-8.

[15671] GAM997 gene, herein designated GAM GENE, and GAM997 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15672] GAM997 gene, herein designated GAM GENE, encodes a GAM997 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most

ordinary genes, GAM997 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM997 precursor RNA is designated SEQ ID:970, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:970 is located at position 9062046 relative to contig NT_011812.10, on chromosome X.

[15673] GAM997 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15674] An enzyme complex designated DICER COMPLEX, dices the GAM997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM997 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin struc-

tured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM997 RNA is designated SEQ ID:2646, and is provided hereinbelow with reference to the sequence listing part.

[15675] GAM997 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM997 target RNA, herein designated GAM TARGET RNA. GAM997 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15676] GAM997 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM997 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM997 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM997 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM997 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15677] The complementary binding of GAM997 RNA, herein designated GAM RNA, to target binding sites on GAM997 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM997 target RNA, herein designated GAM TARGET RNA, into GAM997 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15678] It is appreciated that GAM997 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM997 target genes. The mRNA of each one of this plurality of GAM997 target genes comprises one or more tar-

get binding sites, each having a nucleotide sequence which is at least partly complementary to GAM997 RNA, herein designated GAM RNA, and which when bound by GAM997 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM997 target proteins.

[15679] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM997 gene, herein designated GAM GENE, on one or more GAM997 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15680] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM997 correlate with, and may be deduced from, the identity of the target genes which GAM997 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15681] Nucleotide sequences of the GAM997 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM997 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM997 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM997 are further described hereinbelow with reference to Table Table1.

[15682] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM997 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15683] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 998 (GAM998) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15684] GAM998 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM998 was detected is described hereinabove with reference to Figs. 2-8.

[15685] GAM998 gene, herein designated GAM GENE, and GAM998 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15686] GAM998 gene, herein designated GAM GENE, encodes a GAM998 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM998 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM998 precursor RNA is designated SEQ ID:971, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:971 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[15687] GAM998 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM998 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of

RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15688] An enzyme complex designated DICER COMPLEX, dices the GAM998 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM998 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM998 RNA is designated SEQ ID:2647, and is provided hereinbelow with reference to the sequence listing part.

[15689] GAM998 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM998 target RNA, herein designated GAM TARGET RNA.
GAM998 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated

5UTR, PROTEIN CODING and 3UTR respectively.

[15690] GAM998 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM998 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM998 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM998 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM998 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15691] The complementary binding of GAM998 RNA, herein designated GAM RNA, to target binding sites on GAM998 tar-

get RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM998 target RNA, herein designated GAM TARGET RNA, into GAM998 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15692] It is appreciated that GAM998 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM998 target genes. The mRNA of each one of this plurality of GAM998 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM998 RNA, herein designated GAM RNA, and which when bound by GAM998 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM998 target proteins.

[15693] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM998 gene, herein designated GAM GENE, on one or more GAM998 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15694] It is yet further appreciated that specific functions, and accordingly utilities, of GAM998 correlate with, and may be deduced from, the identity of the target genes which GAM998 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15695] Nucleotide sequences of the GAM998 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM998 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM998 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM998 are further described hereinbelow with reference to Table Table1.

[15696] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM998 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15697] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 999 (GAM999) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15698] GAM999 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM999 was detected is described hereinabove with reference to Figs. 2-8.

[15699] GAM999 gene, herein designated GAM GENE, and GAM999 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15700] GAM999 gene, herein designated GAM GENE, encodes a GAM999 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM999 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of GAM999 precursor RNA is designated SEQ ID:972, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:972 is located at position 5507938 relative to contig NT_023124.11, on chromosome 5.

[15701] GAM999 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM999 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15702] An enzyme complex designated DICER COMPLEX, dices the GAM999 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM999 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary pro-

teins. A probable (over 89%) nucleotide sequence of GAM999 RNA is designated SEQ ID:2648, and is provided hereinbelow with reference to the sequence listing part.

[15703] GAM999 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM999 target RNA, herein designated GAM TARGET RNA. GAM999 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15704] GAM999 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM999 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM999 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM999 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM999 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15705] The complementary binding of GAM999 RNA, herein designated GAM RNA, to target binding sites on GAM999 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM999 target RNA, herein designated GAM TARGET RNA, into GAM999 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15706] It is appreciated that GAM999 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM999 target genes. The mRNA of each one of this plurality of GAM999 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM999 RNA, herein designated GAM RNA, and which when bound by

GAM999 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM999 target proteins.

[15707] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM999 gene, herein designated GAM GENE, on one or more GAM999 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15708] It is yet further appreciated that specific functions, and accordingly utilities, of GAM999 correlate with, and may be deduced from, the identity of the target genes which GAM999 binds and inhibits, and the function of these tar-

get genes, as elaborated hereinbelow.

[15709] Nucleotide sequences of the GAM999 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM999 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM999 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM999 are further described hereinbelow with reference to Table Table1.

[15710] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM999 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15711] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1000 (GAM1000) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15712] GAM1000 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1000 was detected is described hereinabove

with reference to Figs. 2-8.

[15713] GAM1000 gene, herein designated GAM GENE, and GAM1000 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15714] GAM1000 gene, herein designated GAM GENE, encodes a GAM1000 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1000 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1000 precursor RNA is designated SEQ ID:973, and is provided hereinbelow with reference to the sequence listing part.

[15715] GAM1000 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:100644, which mouse homolog is detected in mouse EST accession AW475121.1.

[15716] GAM1000 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15717] An enzyme complex designated DICER COMPLEX, dices the GAM1000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1000 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1000 RNA is designated SEQ ID:2649, and is provided hereinbelow with reference to the sequence listing part.

[15718] GAM1000 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1000 target RNA, herein designated GAM TARGET RNA. GAM1000 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15719] GAM1000 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1000 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1000 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1000 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1000 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15720] The complementary binding of GAM1000 RNA, herein designated GAM RNA, to target binding sites on GAM1000 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1000 target RNA, herein designated GAM TARGET RNA, into GAM1000 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15721] It is appreciated that GAM1000 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1000 target genes. The mRNA of each one of this plurality of GAM1000 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1000 RNA, herein designated GAM RNA, and which when bound by GAM1000 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1000 target proteins.

[15722] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1000 gene, herein designated GAM GENE, on one or more GAM1000 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15723] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1000 correlate with, and may be deduced from, the identity of the target genes which GAM1000 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15724] Nucleotide sequences of the GAM1000 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1000 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1000 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1000 are further described hereinbelow with reference to Table Table1.

[15725] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1000 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15726] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1001 (GAM1001) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15727] GAM1001 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1001 was detected is described hereinabove with reference to Figs. 2-8.

[15728] GAM1001 gene, herein designated GAM GENE, and GAM1001 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15729] GAM1001 gene, herein designated GAM GENE, encodes a GAM1001 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1001 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1001 precursor RNA is designated SEQ ID:974, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:974 is located at position 182400 relative to contig NT_030685.4, on chromosome 5.

[15730] GAM1001 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1001 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15731] An enzyme complex designated DICER COMPLEX, dices the GAM1001 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1001 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1001 RNA is designated SEQ ID:2650, and is provided hereinbelow with reference to the sequence listing part.

[15732] GAM1001 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1001 target RNA, herein designated GAM TARGET RNA. GAM1001 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15733] GAM1001 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1001 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1001 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1001 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1001 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15734] The complementary binding of GAM1001 RNA, herein designated GAM RNA, to target binding sites on GAM1001 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1001 target RNA, herein designated GAM TARGET RNA, into GAM1001 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15735] It is appreciated that GAM1001 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1001 target genes. The mRNA of each one of this

plurality of GAM1001 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1001 RNA, herein designated GAM RNA, and which when bound by GAM1001 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1001 target proteins.

[15736] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1001 gene, herein designated GAM GENE, on one or more GAM1001 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15737] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1001 correlate with, and may be deduced from, the identity of the target genes which GAM1001 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15738] Nucleotide sequences of the GAM1001 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1001 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1001 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1001 are further described hereinbelow with reference to Table Table1.

[15739] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1001 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15740] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1002 (GAM1002) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[15741] GAM1002 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1002 was detected is described hereinabove with reference to Figs. 2-8.

[15742] GAM1002 gene, herein designated GAM GENE, and GAM1002 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15743] GAM1002 gene, herein designated GAM GENE, encodes a GAM1002 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1002 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1002 precursor RNA is designated SEQ ID:975, and is provided hereinbelow with reference to the sequence listing part.

[15744] GAM1002 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98071, which mouse homolog is detected in mouse EST accession AA118029.1.

[15745] GAM1002 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1002 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15746] An enzyme complex designated DICER COMPLEX, dices the GAM1002 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1002 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1002 RNA is designated SEQ ID:2651, and is provided hereinbelow with reference to the sequence listing part.

[15747] GAM1002 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1002 target RNA, herein designated GAM TARGET RNA. GAM1002 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15748] GAM1002 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1002 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1002 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1002 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1002 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15749] The complementary binding of GAM1002 RNA, herein designated GAM RNA, to target binding sites on GAM1002 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1002 target RNA, herein designated GAM TARGET RNA, into GAM1002 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15750] It is appreciated that GAM1002 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1002 target genes. The mRNA of each one of this plurality of GAM1002 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1002 RNA, herein designated GAM RNA, and which when bound by GAM1002 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1002 target proteins.

[15751] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1002 gene, herein designated GAM GENE, on one or more GAM1002 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15752] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1002 correlate with, and may be deduced from, the identity of the target genes which GAM1002 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15753] Nucleotide sequences of the GAM1002 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1002 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1002 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1002 are further described hereinbelow with reference to Table Table1.

[15754] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1002 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15755] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1003 (GAM1003) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15756] GAM1003 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1003 was detected is described hereinabove with reference to Figs. 2-8.

[15757] GAM1003 gene, herein designated GAM GENE, and GAM1003 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15758] GAM1003 gene, herein designated GAM GENE, encodes a GAM1003 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1003 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1003 precursor RNA is designated SEQ ID:976, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:976 is located at position 9822987 relative to contig NT_007914.10, on chromosome 7.

[15759] GAM1003 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1003 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15760] An enzyme complex designated DICER COMPLEX, dices the GAM1003 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1003 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1003 RNA is designated SEQ ID:2652, and is provided hereinbelow with reference to the sequence listing part.

[15761] GAM1003 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1003 target RNA, herein designated GAM TARGET RNA. GAM1003 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15762] GAM1003 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1003 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1003

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1003 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1003 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15763] The complementary binding of GAM1003 RNA, herein designated GAM RNA, to target binding sites on GAM1003 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1003 target RNA, herein designated GAM TARGET RNA, into GAM1003 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[15764] It is appreciated that GAM1003 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1003 target genes. The mRNA of each one of this plurality of GAM1003 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1003 RNA, herein designated GAM RNA, and which when bound by GAM1003 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1003 target proteins.

[15765] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1003 gene, herein designated GAM GENE, on one or more GAM1003 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15766] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1003 correlate with, and may be deduced from, the identity of the target genes which GAM1003 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15767] Nucleotide sequences of the GAM1003 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1003 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1003 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1003 are further described hereinbelow with reference to Table Table1.

[15768] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1003 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15769] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1004 (GAM1004) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15770] GAM1004 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1004 was detected is described hereinabove with reference to Figs. 2-8.

[15771] GAM1004 gene, herein designated GAM GENE, and GAM1004 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15772] GAM1004 gene, herein designated GAM GENE, encodes a GAM1004 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1004 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1004 precursor RNA is designated SEQ ID:977, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:977 is located at position 1235063 relative to contig NT_009526.11, on chromosome 12.

[15773] GAM1004 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[15774] SEQ ID:100138 detected in mouse EST Accession AI326210.1.

[15775] SEQ ID:100139 detected in mouse EST Accession BI965652.1.

[15776] SEQ ID:100144 detected in mouse EST Accession BI965972.1.

[15777] GAM1004 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1004 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15778] An enzyme complex designated DICER COMPLEX, dices the GAM1004 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1004 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1004 RNA is designated SEQ ID:2653, and is provided hereinbelow with reference to the sequence listing part.

[15779] GAM1004 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1004 target RNA, herein designated GAM TARGET RNA. GAM1004 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15780] GAM1004 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1004 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1004

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1004 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1004 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15781] The complementary binding of GAM1004 RNA, herein designated GAM RNA, to target binding sites on GAM1004 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1004 target RNA, herein designated GAM TARGET RNA, into GAM1004 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[15782] It is appreciated that GAM1004 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1004 target genes. The mRNA of each one of this plurality of GAM1004 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1004 RNA, herein designated GAM RNA, and which when bound by GAM1004 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1004 target proteins.

[15783] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1004 gene, herein designated GAM GENE, on one or more GAM1004 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15784] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1004 correlate with, and may be deduced from, the identity of the target genes which GAM1004 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15785] Nucleotide sequences of the GAM1004 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1004 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1004 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1004 are further described hereinbelow with reference to Table Table1.

[15786] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1004 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15787] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1005 (GAM1005) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15788] GAM1005 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1005 was detected is described hereinabove with reference to Figs. 2-8.

[15789] GAM1005 gene, herein designated GAM GENE, and GAM1005 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15790] GAM1005 gene, herein designated GAM GENE, encodes a GAM1005 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1005 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1005 precursor RNA is designated SEQ ID:978, and is provided hereinbelow with reference to the sequence listing part.

[15791] GAM1005 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1005 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15792] An enzyme complex designated DICER COMPLEX, dices the GAM1005 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1005 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1005 RNA is designated SEQ ID:2654, and is provided hereinbelow with reference to the sequence listing part.

[15793] GAM1005 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1005 target RNA, herein designated GAM TARGET

RNA. GAM1005 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15794] GAM1005 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1005 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1005 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1005 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1005 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15795] The complementary binding of GAM1005 RNA, herein designated GAM RNA, to target binding sites on GAM1005 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1005 target RNA, herein designated GAM TARGET RNA, into GAM1005 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15796] It is appreciated that GAM1005 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1005 target genes. The mRNA of each one of this plurality of GAM1005 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1005 RNA, herein designated GAM RNA, and which when bound by GAM1005 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1005 target proteins.

[15797] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1005 gene, herein designated GAM GENE, on one or more GAM1005 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15798] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1005 correlate with, and may be deduced from, the identity of the target genes which GAM1005 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15799] Nucleotide sequences of the GAM1005 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1005 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1005 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1005 are further described hereinbelow with reference to Table Table1.

[15800] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1005 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15801] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1006 (GAM1006) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15802] GAM1006 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1006 was detected is described hereinabove with reference to Figs. 2-8.

[15803] GAM1006 gene, herein designated GAM GENE, and GAM1006 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15804] GAM1006 gene, herein designated GAM GENE, encodes a

GAM1006 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1006 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1006 precursor RNA is designated SEQ ID:979, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:979 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[15805] GAM1006 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1006 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15806] An enzyme complex designated DICER COMPLEX, dices the GAM1006 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1006 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1006 RNA is designated SEQ ID:2655, and is provided hereinbelow with reference to the sequence listing part.

[15807] GAM1006 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1006 target RNA, herein designated GAM TARGET RNA. GAM1006 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15808] GAM1006 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1006 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1006 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1006 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1006 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15809] The complementary binding of GAM1006 RNA, herein designated GAM RNA, to target binding sites on GAM1006 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1006 target RNA, herein designated GAM TARGET RNA, into GAM1006 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15810] It is appreciated that GAM1006 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1006 target genes. The mRNA of each one of this plurality of GAM1006 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1006 RNA, herein designated GAM RNA, and which when bound by GAM1006 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1006 target proteins.

[15811] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1006 gene, herein designated GAM GENE, on one or more GAM1006 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15812] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1006 correlate with, and may be deduced from, the identity of the target genes which GAM1006 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15813] Nucleotide sequences of the GAM1006 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1006 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1006 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1006 are further described hereinbelow with reference to Table Table1.

[15814] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1006 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15815] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1007 (GAM1007) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15816] GAM1007 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1007 was detected is described hereinabove with reference to Figs. 2-8.

[15817] GAM1007 gene, herein designated GAM GENE, and GAM1007 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15818] GAM1007 gene, herein designated GAM GENE, encodes a GAM1007 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1007 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1007 precursor RNA is designated SEQ ID:980, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:980 is located at position 26456349 relative to contig NT_007819.11, on chromosome 7.

[15819] GAM1007 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1007 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15820] An enzyme complex designated DICER COMPLEX, dices the GAM1007 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1007 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1007 RNA is designated SEQ ID:2656, and is provided hereinbelow with reference to the sequence listing part.

[15821] GAM1007 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1007 target RNA, herein designated GAM TARGET RNA. GAM1007 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15822] GAM1007 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1007 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1007 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1007 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1007 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15823] The complementary binding of GAM1007 RNA, herein designated GAM RNA, to target binding sites on GAM1007 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1007 target RNA, herein designated GAM TARGET RNA, into GAM1007 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15824] It is appreciated that GAM1007 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1007 target genes. The mRNA of each one of this plurality of GAM1007 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1007 RNA, herein designated GAM RNA, and which when bound by GAM1007 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1007 target proteins.

[15825] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1007 gene, herein designated GAM GENE, on one or more GAM1007 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15826] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1007 correlate with, and may be deduced from, the identity of the target genes which GAM1007 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15827] Nucleotide sequences of the GAM1007 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1007 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1007 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1007 are further described hereinbelow with reference to Table Table1.

[15828] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1007 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15829] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1008 (GAM1008) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15830] GAM1008 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1008 was detected is described hereinabove with reference to Figs. 2-8.

[15831] GAM1008 gene, herein designated GAM GENE, and GAM1008 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15832] GAM1008 gene, herein designated GAM GENE, encodes a GAM1008 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1008 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1008 precursor RNA is designated SEQ ID:981, and is provided hereinbelow with reference to the sequence listing part.

[15833] GAM1008 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15834] An enzyme complex designated DICER COMPLEX, dices the GAM1008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1008 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1008 RNA is designated SEQ ID:2657, and is provided hereinbelow with reference to the sequence listing part.

[15835] GAM1008 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1008 target RNA, herein designated GAM TARGET RNA. GAM1008 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15836] GAM1008 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1008 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1008 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1008 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1008 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15837] The complementary binding of GAM1008 RNA, herein designated GAM RNA, to target binding sites on GAM1008 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1008 target RNA, herein designated GAM TARGET RNA, into GAM1008 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15838] It is appreciated that GAM1008 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1008 target genes. The mRNA of each one of this plurality of GAM1008 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1008 RNA, herein designated GAM RNA, and which when bound by GAM1008 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1008 target proteins.

[15839] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1008 gene, herein designated GAM GENE, on one or more GAM1008 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15840] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1008 correlate with, and may be deduced from, the identity of the target genes which GAM1008 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15841] Nucleotide sequences of the GAM1008 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1008 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1008 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1008 are further described hereinbelow with reference to Table Table1.

[15842] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1008 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15843] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1009 (GAM1009) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15844] GAM1009 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1009 was detected is described hereinabove with reference to Figs. 2-8.

[15845] GAM1009 gene, herein designated GAM GENE, and GAM1009 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15846] GAM1009 gene, herein designated GAM GENE, encodes a GAM1009 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1009 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1009 precursor RNA is designated SEQ ID:982, and is provided hereinbelow with reference to the sequence listing part.

[15847] GAM1009 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1009 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15848] An enzyme complex designated DICER COMPLEX, dices the GAM1009 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1009 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1009 RNA is designated SEQ ID:2658, and is provided hereinbelow with reference to the sequence listing part.

[15849] GAM1009 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1009 target RNA, herein designated GAM TARGET RNA. GAM1009 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15850] GAM1009 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1009 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1009 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1009 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1009 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[15851] The complementary binding of GAM1009 RNA, herein designated GAM RNA, to target binding sites on GAM1009 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1009 target RNA, herein designated GAM TARGET RNA, into GAM1009 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15852] It is appreciated that GAM1009 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1009 target genes. The mRNA of each one of this plurality of GAM1009 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1009 RNA, herein designated GAM RNA, and which when bound by GAM1009 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1009 target proteins.

[15853] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1009 gene, herein designated GAM GENE, on one or

more GAM1009 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15854] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1009 correlate with, and may be deduced from, the identity of the target genes which GAM1009 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15855] Nucleotide sequences of the GAM1009 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1009 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1009 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1009 are further de-

scribed hereinbelow with reference to Table Table1.

[15856] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1009 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15857] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1010 (GAM1010) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15858] GAM1010 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1010 was detected is described hereinabove with reference to Figs. 2-8.

[15859] GAM1010 gene, herein designated GAM GENE, and GAM1010 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15860] GAM1010 gene, herein designated GAM GENE, encodes a GAM1010 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1010 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1010 precursor RNA is designated SEQ ID:983, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:983 is located at position 1471884 relative to contig NT_027140.5, on chromosome 13.

[15861] GAM1010 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15862] An enzyme complex designated DICER COMPLEX, dices the GAM1010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1010 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1010 RNA is designated SEQ ID:2659, and is provided hereinbelow with reference to the sequence listing part.

[15863] GAM1010 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1010 target RNA, herein designated GAM TARGET RNA. GAM1010 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15864] GAM1010 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1010 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1010 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1010 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1010 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15865] The complementary binding of GAM1010 RNA, herein designated GAM RNA, to target binding sites on GAM1010 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1010 target RNA, herein designated GAM TARGET RNA, into GAM1010 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15866] It is appreciated that GAM1010 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1010 target genes. The mRNA of each one of this plurality of GAM1010 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1010 RNA, herein designated GAM RNA, and which when bound by GAM1010 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1010 target proteins.

[15867] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1010 gene, herein designated GAM GENE, on one or more GAM1010 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[15868] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1010 correlate with, and may be deduced from, the identity of the target genes which GAM1010 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15869] Nucleotide sequences of the GAM1010 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1010 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1010 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1010 are further described hereinbelow with reference to Table Table1.

[15870] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1010 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15871] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1011 (GAM1011) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[15872] GAM1011 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1011 was detected is described hereinabove with reference to Figs. 2-8.

[15873] GAM1011 gene, herein designated GAM GENE, and GAM1011 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15874] GAM1011 gene, herein designated GAM GENE, encodes a GAM1011 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1011 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1011 precursor RNA is designated SEQ ID:984, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:984 is located at position 1471884 relative to contig NT_027140.5, on chromosome 13.

[15875] GAM1011 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1011 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15876] An enzyme complex designated DICER COMPLEX, dices the GAM1011 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1011 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1011 RNA is designated SEQ ID:2660, and is provided hereinbelow with reference to the sequence listing part.

[15877] GAM1011 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1011 target RNA, herein designated GAM TARGET RNA. GAM1011 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15878] GAM1011 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1011 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1011 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1011 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1011 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15879] The complementary binding of GAM1011 RNA, herein designated GAM RNA, to target binding sites on GAM1011 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1011 target RNA, herein designated GAM TARGET RNA, into GAM1011 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15880] It is appreciated that GAM1011 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1011 target genes. The mRNA of each one of this plurality of GAM1011 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1011 RNA, herein designated GAM RNA, and which when bound by GAM1011 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1011 target proteins.

[15881] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1011 gene, herein designated GAM GENE, on one or more GAM1011 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15882] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1011 correlate with, and may be deduced from, the identity of the target genes which GAM1011 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15883] Nucleotide sequences of the GAM1011 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1011 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1011 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1011 are further described hereinbelow with reference to Table Table1.

[15884] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1011 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15885] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1012 (GAM1012) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15886] GAM1012 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1012 was detected is described hereinabove with reference to Figs. 2-8.

[15887] GAM1012 gene, herein designated GAM GENE, and GAM1012 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15888] GAM1012 gene, herein designated GAM GENE, encodes a GAM1012 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1012 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1012 precursor RNA is designated SEQ ID:985, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:985 is located at position 1471884 relative to contig NT_027140.5, on chromosome 13.

[15889] GAM1012 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1012 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15890] An enzyme complex designated DICER COMPLEX, dices the GAM1012 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1012 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1012 RNA is designated SEQ ID:2661, and is provided hereinbelow with reference to the sequence listing part.

[15891] GAM1012 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1012 target RNA, herein designated GAM TARGET RNA. GAM1012 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15892] GAM1012 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1012 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1012 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1012 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1012 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15893] The complementary binding of GAM1012 RNA, herein designated GAM RNA, to target binding sites on GAM1012 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1012 target RNA, herein designated GAM TARGET RNA, into GAM1012 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15894] It is appreciated that GAM1012 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1012 target genes. The mRNA of each one of this plurality of GAM1012 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1012 RNA, herein designated GAM RNA, and which when bound by GAM1012 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1012 target proteins.

[15895] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1012 gene, herein designated GAM GENE, on one or more GAM1012 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15896] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1012 correlate with, and may be deduced from, the identity of the target genes which GAM1012 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15897] Nucleotide sequences of the GAM1012 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1012 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1012 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1012 are further described hereinbelow with reference to Table Table1.

[15898] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1012 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15899] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1013 (GAM1013) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15900] GAM1013 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1013 was detected is described hereinabove with reference to Figs. 2-8.

[15901] GAM1013 gene, herein designated GAM GENE, and GAM1013 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15902] GAM1013 gene, herein designated GAM GENE, encodes a GAM1013 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1013 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1013 precursor RNA is designated SEQ ID:986, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:986 is located at position 8005268 relative to contig NT_030059.8, on chromosome 10.

[15903] GAM1013 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1013 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15904] An enzyme complex designated DICER COMPLEX, dices the GAM1013 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1013 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1013 RNA is designated SEQ ID:2662, and is provided hereinbelow with reference to the sequence listing part.

[15905] GAM1013 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1013 target RNA, herein designated GAM TARGET

RNA. GAM1013 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15906] GAM1013 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1013 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1013 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1013 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1013 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15907] The complementary binding of GAM1013 RNA, herein designated GAM RNA, to target binding sites on GAM1013 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1013 target RNA, herein designated GAM TARGET RNA, into GAM1013 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15908] It is appreciated that GAM1013 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1013 target genes. The mRNA of each one of this plurality of GAM1013 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1013 RNA, herein designated GAM RNA, and which when bound by GAM1013 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1013 target proteins.

[15909] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1013 gene, herein designated GAM GENE, on one or more GAM1013 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15910] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1013 correlate with, and may be deduced from, the identity of the target genes which GAM1013 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15911] Nucleotide sequences of the GAM1013 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1013 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1013 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1013 are further described hereinbelow with reference to Table Table1.

[15912] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1013 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15913] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1014 (GAM1014) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15914] GAM1014 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1014 was detected is described hereinabove with reference to Figs. 2-8.

[15915] GAM1014 gene, herein designated GAM GENE, and GAM1014 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15916] GAM1014 gene, herein designated GAM GENE, encodes a

GAM1014 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1014 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1014 precursor RNA is designated SEQ ID:987, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:987 is located at position 33703788 relative to contig NT_007592.11, on chromosome 6.

[15917] GAM1014 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15918] An enzyme complex designated DICER COMPLEX, dices the GAM1014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1014 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1014 RNA is designated SEQ ID:2663, and is provided hereinbelow with reference to the sequence listing part.

[15919] GAM1014 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1014 target RNA, herein designated GAM TARGET RNA. GAM1014 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15920] GAM1014 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1014 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1014 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1014 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1014 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15921] The complementary binding of GAM1014 RNA, herein designated GAM RNA, to target binding sites on GAM1014 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1014 target RNA, herein designated GAM TARGET RNA, into GAM1014 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15922] It is appreciated that GAM1014 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1014 target genes. The mRNA of each one of this plurality of GAM1014 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1014 RNA, herein designated GAM RNA, and which when bound by GAM1014 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1014 target proteins.

[15923] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1014 gene, herein designated GAM GENE, on one or more GAM1014 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15924] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1014 correlate with, and may be deduced from, the identity of the target genes which GAM1014 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15925] Nucleotide sequences of the GAM1014 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1014 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1014 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1014 are further described hereinbelow with reference to Table Table1.

[15926] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1014 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15927] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1015 (GAM1015) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15928] GAM1015 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1015 was detected is described hereinabove with reference to Figs. 2-8.

[15929] GAM1015 gene, herein designated GAM GENE, and GAM1015 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15930] GAM1015 gene, herein designated GAM GENE, encodes a GAM1015 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1015 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1015 precursor RNA is designated SEQ ID:988, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:988 is located at position 2419847 relative to contig NT_033944.3, on chromosome 6.

[15931] GAM1015 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1015 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15932] An enzyme complex designated DICER COMPLEX, dices the GAM1015 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1015 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1015 RNA is designated SEQ ID:2664, and is provided hereinbelow with reference to the sequence listing part.

[15933] GAM1015 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1015 target RNA, herein designated GAM TARGET RNA. GAM1015 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15934] GAM1015 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1015 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1015 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1015 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1015 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15935] The complementary binding of GAM1015 RNA, herein designated GAM RNA, to target binding sites on GAM1015 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1015 target RNA, herein designated GAM TARGET RNA, into GAM1015 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15936] It is appreciated that GAM1015 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1015 target genes. The mRNA of each one of this plurality of GAM1015 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1015 RNA, herein designated GAM RNA, and which when bound by GAM1015 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1015 target proteins.

[15937] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1015 gene, herein designated GAM GENE, on one or more GAM1015 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15938] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1015 correlate with, and may be deduced from, the identity of the target genes which GAM1015 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15939] Nucleotide sequences of the GAM1015 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1015 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1015 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1015 are further described hereinbelow with reference to Table Table1.

[15940] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1015 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15941] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1016 (GAM1016) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15942] GAM1016 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1016 was detected is described hereinabove with reference to Figs. 2-8.

[15943] GAM1016 gene, herein designated GAM GENE, and GAM1016 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15944] GAM1016 gene, herein designated GAM GENE, encodes a GAM1016 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1016 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1016 precursor RNA is designated SEQ ID:989, and is provided hereinbelow with reference to the sequence listing part.

[15945] GAM1016 has 9 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[15946] SEQ ID:100046 detected in mouse EST Accession AW227328.1.

[15947] SEQ ID:100047 detected in mouse EST Accession BF151056.1.

[15948] SEQ ID:100048 detected in mouse EST Accession BF232633.1.

[15949] SEQ ID:100049 detected in mouse EST Accession BB627306.1.

[15950] SEQ ID:100050 detected in mouse EST Accession

BI731628.1.

[15951] SEQ ID:100326 detected in mouse EST Accession BF472526.1.

[15952] SEQ ID:100327 detected in mouse EST Accession BB635316.1.

[15953] SEQ ID:100328 detected in mouse EST Accession BE375279.1.

[15954] SEQ ID:100329 detected in mouse EST Accession BF178922.1.

[15955] GAM1016 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1016 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15956] An enzyme complex designated DICER COMPLEX, dices the GAM1016 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1016 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1016 RNA is designated SEQ ID:2665, and is provided hereinbelow with reference to the sequence listing part.

[15957] GAM1016 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1016 target RNA, herein designated GAM TARGET RNA. GAM1016 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15958] GAM1016 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1016 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1016 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1016 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1016 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15959] The complementary binding of GAM1016 RNA, herein designated GAM RNA, to target binding sites on GAM1016 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1016 target RNA, herein designated GAM TARGET RNA, into GAM1016 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15960] It is appreciated that GAM1016 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1016 target genes. The mRNA of each one of this plurality of GAM1016 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1016 RNA, herein designated GAM RNA, and which when bound by GAM1016 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1016 target proteins.

[15961] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1016 gene, herein designated GAM GENE, on one or more GAM1016 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15962] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1016 correlate with, and may be deduced from, the identity of the target genes which GAM1016 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15963] Nucleotide sequences of the GAM1016 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1016 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1016 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1016 are further described hereinbelow with reference to Table Table1.

[15964] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1016 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15965] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1017 (GAM1017) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15966] GAM1017 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1017 was detected is described hereinabove with reference to Figs. 2-8.

[15967] GAM1017 gene, herein designated GAM GENE, and GAM1017 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15968] GAM1017 gene, herein designated GAM GENE, encodes a GAM1017 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1017 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1017 precursor RNA is designated SEQ ID:990, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:990 is located at position 2015247 relative to contig NT_029289.7, on chromosome 5.

[15969] GAM1017 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1017 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15970] An enzyme complex designated DICER COMPLEX, dices the GAM1017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1017 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1017 RNA is designated SEQ ID:2666, and is provided hereinbelow with reference to the sequence listing part.

[15971] GAM1017 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1017 target RNA, herein designated GAM TARGET

RNA. GAM1017 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15972] GAM1017 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1017 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1017 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1017 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1017 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15973] The complementary binding of GAM1017 RNA, herein designated GAM RNA, to target binding sites on GAM1017 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1017 target RNA, herein designated GAM TARGET RNA, into GAM1017 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15974] It is appreciated that GAM1017 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1017 target genes. The mRNA of each one of this plurality of GAM1017 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1017 RNA, herein designated GAM RNA, and which when bound by GAM1017 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1017 target proteins.

[15975] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1017 gene, herein designated GAM GENE, on one or more GAM1017 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[15976] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1017 correlate with, and may be deduced from, the identity of the target genes which GAM1017 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15977] Nucleotide sequences of the GAM1017 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1017 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1017 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1017 are further described hereinbelow with reference to Table Table1.

[15978] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1017 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15979] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1018 (GAM1018) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[15980] GAM1018 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1018 was detected is described hereinabove with reference to Figs. 2-8.

[15981] GAM1018 gene, herein designated GAM GENE, and GAM1018 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15982] GAM1018 gene, herein designated GAM GENE, encodes a

GAM1018 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1018 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1018 precursor RNA is designated SEQ ID:991, and is provided hereinbelow with reference to the sequence listing part.

[15983] GAM1018 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1018 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15984] An enzyme complex designated DICER COMPLEX, dices the GAM1018 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1018 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1018 RNA is designated SEQ ID:2667, and is provided hereinbelow with reference to the sequence listing part.

[15985] GAM1018 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1018 target RNA, herein designated GAM TARGET RNA. GAM1018 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[15986] GAM1018 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1018 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1018 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1018 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1018 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[15987] The complementary binding of GAM1018 RNA, herein designated GAM RNA, to target binding sites on GAM1018 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1018 target RNA, herein designated GAM TARGET RNA, into GAM1018 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[15988] It is appreciated that GAM1018 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1018 target genes. The mRNA of each one of this plurality of GAM1018 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1018 RNA, herein designated GAM RNA, and which when bound by GAM1018 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1018 target proteins.

[15989] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1018 gene, herein designated GAM GENE, on one or more GAM1018 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[15990] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1018 correlate with, and may be deduced from, the identity of the target genes which GAM1018 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[15991] Nucleotide sequences of the GAM1018 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1018 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1018 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1018 are further described hereinbelow with reference to Table Table1.

[15992] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1018 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[15993] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1019 (GAM1019) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[15994] GAM1019 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1019 was detected is described hereinabove with reference to Figs. 2-8.

[15995] GAM1019 gene, herein designated GAM GENE, and GAM1019 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[15996] GAM1019 gene, herein designated GAM GENE, encodes a GAM1019 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1019 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1019 precursor RNA is designated SEQ ID:992, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:992 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[15997] GAM1019 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1019 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[15998] An enzyme complex designated DICER COMPLEX, dices the GAM1019 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1019 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1019 RNA is designated SEQ ID:2668, and is provided hereinbelow with reference to the sequence listing part.

[15999] GAM1019 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1019 target RNA, herein designated GAM TARGET RNA. GAM1019 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16000] GAM1019 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1019 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1019 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1019 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1019 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16001] The complementary binding of GAM1019 RNA, herein designated GAM RNA, to target binding sites on GAM1019 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1019 target RNA, herein designated GAM TARGET RNA, into GAM1019 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16002] It is appreciated that GAM1019 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1019 target genes. The mRNA of each one of this plurality of GAM1019 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1019 RNA, herein designated GAM RNA, and which when bound by GAM1019 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1019 target proteins.

[16003] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1019 gene, herein designated GAM GENE, on one or more GAM1019 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16004] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1019 correlate with, and may be deduced from, the identity of the target genes which GAM1019 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16005] Nucleotide sequences of the GAM1019 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1019 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1019 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1019 are further described hereinbelow with reference to Table Table1.

[16006] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1019 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16007] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1020 (GAM1020) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16008] GAM1020 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1020 was detected is described hereinabove with reference to Figs. 2-8.

[16009] GAM1020 gene, herein designated GAM GENE, and GAM1020 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16010] GAM1020 gene, herein designated GAM GENE, encodes a GAM1020 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1020 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1020 precursor RNA is designated SEQ ID:993, and is provided hereinbelow with reference to the sequence listing part.

[16011] GAM1020 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1020 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16012] An enzyme complex designated DICER COMPLEX, dices the GAM1020 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1020 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1020 RNA is designated SEQ ID:2669, and is provided hereinbelow with reference to the sequence listing part.

[16013] GAM1020 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1020 target RNA, herein designated GAM TARGET RNA. GAM1020 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16014] GAM1020 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1020 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1020 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1020 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1020 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16015] The complementary binding of GAM1020 RNA, herein designated GAM RNA, to target binding sites on GAM1020 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1020 target RNA, herein designated GAM TARGET RNA, into GAM1020 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16016] It is appreciated that GAM1020 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1020 target genes. The mRNA of each one of this

plurality of GAM1020 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1020 RNA, herein designated GAM RNA, and which when bound by GAM1020 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1020 target proteins.

[16017] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1020 gene, herein designated GAM GENE, on one or more GAM1020 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16018] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1020 correlate with, and may be deduced from, the identity of the target genes which GAM1020 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16019] Nucleotide sequences of the GAM1020 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1020 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1020 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1020 are further described hereinbelow with reference to Table Table1.

[16020] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1020 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16021] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1021 (GAM1021) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[16022] GAM1021 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1021 was detected is described hereinabove with reference to Figs. 2-8.

[16023] GAM1021 gene, herein designated GAM GENE, and GAM1021 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16024] GAM1021 gene, herein designated GAM GENE, encodes a GAM1021 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1021 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1021 precursor RNA is designated SEQ ID:994, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:994 is located at position 930096 relative to contig NT_005588.13, on chromosome 3.

[16025] GAM1021 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1021 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16026] An enzyme complex designated DICER COMPLEX, dices the GAM1021 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1021 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1021 RNA is designated SEQ ID:2670, and is provided hereinbelow with reference to the sequence listing part.

[16027] GAM1021 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1021 target RNA, herein designated GAM TARGET RNA. GAM1021 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16028] GAM1021 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1021 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1021 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1021 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1021 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[16029] The complementary binding of GAM1021 RNA, herein designated GAM RNA, to target binding sites on GAM1021 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1021 target RNA, herein designated GAM TARGET RNA, into GAM1021 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16030] It is appreciated that GAM1021 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1021 target genes. The mRNA of each one of this plurality of GAM1021 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1021 RNA, herein designated GAM RNA, and which when bound by GAM1021 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1021 target proteins.

[16031] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1021 gene, herein designated GAM GENE, on one or

more GAM1021 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16032] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1021 correlate with, and may be deduced from, the identity of the target genes which GAM1021 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16033] Nucleotide sequences of the GAM1021 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1021 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1021 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1021 are further de-

scribed hereinbelow with reference to Table Table1.

[16034] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1021 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16035] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1022 (GAM1022) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16036] GAM1022 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1022 was detected is described hereinabove with reference to Figs. 2-8.

[16037] GAM1022 gene, herein designated GAM GENE, and GAM1022 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16038] GAM1022 gene, herein designated GAM GENE, encodes a GAM1022 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1022 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1022 precursor RNA is designated SEQ ID:995, and is provided hereinbelow with reference to the sequence listing part.

[16039] GAM1022 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16040] An enzyme complex designated DICER COMPLEX, dices the GAM1022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1022 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1022 RNA is designated SEQ ID:2671, and is provided hereinbelow with reference to the sequence listing part.

[16041] GAM1022 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1022 target RNA, herein designated GAM TARGET RNA. GAM1022 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16042] GAM1022 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1022 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1022 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1022 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1022 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16043] The complementary binding of GAM1022 RNA, herein designated GAM RNA, to target binding sites on GAM1022 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1022 target RNA, herein designated GAM TARGET RNA, into GAM1022 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16044] It is appreciated that GAM1022 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1022 target genes. The mRNA of each one of this plurality of GAM1022 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1022 RNA, herein designated GAM RNA, and which when bound by GAM1022 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1022 target proteins.

[16045] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1022 gene, herein designated GAM GENE, on one or more GAM1022 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16046] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1022 correlate with, and may be deduced from, the identity of the target genes which GAM1022 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16047] Nucleotide sequences of the GAM1022 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1022 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1022 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1022 are further described hereinbelow with reference to Table Table1.

[16048] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1022 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16049] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1023 (GAM1023) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16050] GAM1023 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1023 was detected is described hereinabove with reference to Figs. 2-8.

[16051] GAM1023 gene, herein designated GAM GENE, and GAM1023 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16052] GAM1023 gene, herein designated GAM GENE, encodes a GAM1023 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1023 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1023 precursor RNA is designated SEQ ID:996, and is provided hereinbelow with reference to the sequence listing part.

[16053] GAM1023 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1023 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16054] An enzyme complex designated DICER COMPLEX, dices the GAM1023 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1023 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1023 RNA is designated SEQ ID:2672, and is provided hereinbelow with reference to the sequence listing part.

[16055] GAM1023 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1023 target RNA, herein designated GAM TARGET RNA. GAM1023 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16056] GAM1023 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1023 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1023 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1023 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1023 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16057] The complementary binding of GAM1023 RNA, herein designated GAM RNA, to target binding sites on GAM1023

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1023 target RNA, herein designated GAM TARGET RNA, into GAM1023 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16058] It is appreciated that GAM1023 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1023 target genes. The mRNA of each one of this plurality of GAM1023 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1023 RNA, herein designated GAM RNA, and which when bound by GAM1023 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1023 target proteins.

[16059] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1023 gene, herein designated GAM GENE, on one or more GAM1023 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16060] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1023 correlate with, and may be deduced from, the identity of the target genes which GAM1023 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16061] Nucleotide sequences of the GAM1023 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1023 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1023 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1023 are further described hereinbelow with reference to Table Table1.

[16062] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1023 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16063] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1024 (GAM1024) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16064] GAM1024 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1024 was detected is described hereinabove with reference to Figs. 2-8.

[16065] GAM1024 gene, herein designated GAM GENE, and GAM1024 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16066] GAM1024 gene, herein designated GAM GENE, encodes a GAM1024 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1024 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1024 precursor RNA is designated SEQ ID:997, and is provided hereinbelow with reference to the sequence listing part.

[16067] GAM1024 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16068] An enzyme complex designated DICER COMPLEX, dices the GAM1024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1024 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1024 RNA is designated SEQ ID:2673, and

is provided hereinbelow with reference to the sequence listing part.

[16069] GAM1024 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1024 target RNA, herein designated GAM TARGET RNA. GAM1024 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16070] GAM1024 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1024 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1024 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1024 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1024 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16071] The complementary binding of GAM1024 RNA, herein designated GAM RNA, to target binding sites on GAM1024 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1024 target RNA, herein designated GAM TARGET RNA, into GAM1024 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16072] It is appreciated that GAM1024 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1024 target genes. The mRNA of each one of this plurality of GAM1024 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1024 RNA, herein designated GAM RNA, and which when bound by

GAM1024 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1024 target proteins.

[16073] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1024 gene, herein designated GAM GENE, on one or more GAM1024 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16074] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1024 correlate with, and may be deduced from, the identity of the target genes which GAM1024 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[16075] Nucleotide sequences of the GAM1024 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1024 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1024 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1024 are further described hereinbelow with reference to Table Table1.

[16076] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1024 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16077] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1025 (GAM1025) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16078] GAM1025 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1025 was detected is described hereinabove

with reference to Figs. 2-8.

[16079] GAM1025 gene, herein designated GAM GENE, and GAM1025 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16080] GAM1025 gene, herein designated GAM GENE, encodes a GAM1025 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1025 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1025 precursor RNA is designated SEQ ID:998, and is provided hereinbelow with reference to the sequence listing part.

[16081] GAM1025 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1025 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16082] An enzyme complex designated DICER COMPLEX, dices the GAM1025 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1025 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1025 RNA is designated SEQ ID:2674, and is provided hereinbelow with reference to the sequence listing part.

[16083] GAM1025 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1025 target RNA, herein designated GAM TARGET RNA. GAM1025 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16084] GAM1025 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1025 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1025 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1025 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1025 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16085] The complementary binding of GAM1025 RNA, herein designated GAM RNA, to target binding sites on GAM1025 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1025 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1025 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16086] It is appreciated that GAM1025 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1025 target genes. The mRNA of each one of this plurality of GAM1025 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1025 RNA, herein designated GAM RNA, and which when bound by GAM1025 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1025 target proteins.

[16087] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1025 gene, herein designated GAM GENE, on one or more GAM1025 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16088] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1025 correlate with, and may be deduced from, the identity of the target genes which GAM1025 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16089] Nucleotide sequences of the GAM1025 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1025 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1025 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1025 are further described hereinbelow with reference to Table Table1.

[16090] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1025 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[16091] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1026 (GAM1026) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16092] GAM1026 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1026 was detected is described hereinabove with reference to Figs. 2-8.

[16093] GAM1026 gene, herein designated GAM GENE, and GAM1026 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16094] GAM1026 gene, herein designated GAM GENE, encodes a GAM1026 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1026 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1026 precursor RNA is designated SEQ ID:999, and is provided hereinbelow with reference to the sequence listing part.

[16095] GAM1026 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1026 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16096] An enzyme complex designated DICER COMPLEX, dices the GAM1026 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1026 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1026 RNA is designated SEQ ID:2675, and is provided hereinbelow with reference to the sequence listing part.

[16097] GAM1026 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1026 target RNA, herein designated GAM TARGET RNA. GAM1026 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16098] GAM1026 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1026 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1026 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1026 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1026 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16099] The complementary binding of GAM1026 RNA, herein designated GAM RNA, to target binding sites on GAM1026 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1026 target RNA, herein designated GAM TARGET RNA, into GAM1026 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16100] It is appreciated that GAM1026 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1026 target genes. The mRNA of each one of this plurality of GAM1026 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1026 RNA, herein designated GAM RNA, and which when bound by GAM1026 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1026 target proteins.

[16101] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1026 gene, herein designated GAM GENE, on one or more GAM1026 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16102] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1026 correlate with, and may be deduced from, the identity of the target genes which GAM1026 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16103] Nucleotide sequences of the GAM1026 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1026 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1026 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1026 are further described hereinbelow with reference to Table Table1.

[16104] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1026 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16105] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1027 (GAM1027) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16106] GAM1027 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1027 was detected is described hereinabove with reference to Figs. 2-8.

[16107] GAM1027 gene, herein designated GAM GENE, and GAM1027 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[16108] GAM1027 gene, herein designated GAM GENE, encodes a GAM1027 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1027 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1027 precursor RNA is designated SEQ ID:1000, and is provided hereinbelow with reference to the sequence listing part.

[16109] GAM1027 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:100348, which mouse homolog is detected in mouse EST accession BI693236.1.

[16110] GAM1027 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16111] An enzyme complex designated DICER COMPLEX, dices the GAM1027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1027 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1027 RNA is designated SEQ ID:2676, and is provided hereinbelow with reference to the sequence listing part.

[16112] GAM1027 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1027 target RNA, herein designated GAM TARGET RNA. GAM1027 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16113] GAM1027 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1027 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1027 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1027 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1027 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16114] The complementary binding of GAM1027 RNA, herein designated GAM RNA, to target binding sites on GAM1027 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1027 target RNA, herein designated GAM TARGET RNA, into GAM1027 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16115] It is appreciated that GAM1027 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1027 target genes. The mRNA of each one of this plurality of GAM1027 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1027 RNA, herein designated GAM RNA, and which when bound by GAM1027 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1027 target proteins.

[16116] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1027 gene, herein designated GAM GENE, on one or more GAM1027 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16117] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1027 correlate with, and may be deduced from, the identity of the target genes which GAM1027 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16118] Nucleotide sequences of the GAM1027 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1027 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1027 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1027 are further described hereinbelow with reference to Table Table1.

[16119] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1027 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16120] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1028 (GAM1028) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16121] GAM1028 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1028 was detected is described hereinabove with reference to Figs. 2-8.

[16122] GAM1028 gene, herein designated GAM GENE, and GAM1028 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16123] GAM1028 gene, herein designated GAM GENE, encodes a GAM1028 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1028 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1028 precursor RNA is

designated SEQ ID:1001, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1001 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[16124] GAM1028 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16125] An enzyme complex designated DICER COMPLEX, dices the GAM1028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1028 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1028 RNA is designated SEQ ID:2677, and is provided hereinbelow with reference to the sequence listing part.

[16126] GAM1028 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1028 target RNA, herein designated GAM TARGET RNA. GAM1028 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16127] GAM1028 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1028 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1028 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1028 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1028 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16128] The complementary binding of GAM1028 RNA, herein designated GAM RNA, to target binding sites on GAM1028 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1028 target RNA, herein designated GAM TARGET RNA, into GAM1028 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16129] It is appreciated that GAM1028 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1028 target genes. The mRNA of each one of this plurality of GAM1028 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1028 RNA,

herein designated GAM RNA, and which when bound by GAM1028 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1028 target proteins.

[16130] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1028 gene, herein designated GAM GENE, on one or more GAM1028 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16131] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1028 correlate with, and may be deduced from, the identity of the target genes which

GAM1028 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16132] Nucleotide sequences of the GAM1028 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1028 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1028 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1028 are further described hereinbelow with reference to Table Table1.

[16133] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1028 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16134] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1029 (GAM1029) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16135] GAM1029 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1029 was detected is described hereinabove with reference to Figs. 2-8.

[16136] GAM1029 gene, herein designated GAM GENE, and GAM1029 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16137] GAM1029 gene, herein designated GAM GENE, encodes a GAM1029 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1029 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1029 precursor RNA is designated SEQ ID:1002, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1002 is located at position 4851363 relative to contig NT_022517.13, on chromosome 3.

[16138] GAM1029 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1029 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16139] An enzyme complex designated DICER COMPLEX, dices the GAM1029 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1029 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1029 RNA is designated SEQ ID:2678, and is provided hereinbelow with reference to the sequence listing part.

[16140] GAM1029 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1029 target RNA, herein designated GAM TARGET RNA. GAM1029 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16141] GAM1029 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1029 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1029 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1029 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1029 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16142] The complementary binding of GAM1029 RNA, herein designated GAM RNA, to target binding sites on GAM1029

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1029 target RNA, herein designated GAM TARGET RNA, into GAM1029 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16143] It is appreciated that GAM1029 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1029 target genes. The mRNA of each one of this plurality of GAM1029 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1029 RNA, herein designated GAM RNA, and which when bound by GAM1029 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1029 target proteins.

[16144] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1029 gene, herein designated GAM GENE, on one or more GAM1029 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16145] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1029 correlate with, and may be deduced from, the identity of the target genes which GAM1029 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16146] Nucleotide sequences of the GAM1029 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1029 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1029 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1029 are further described hereinbelow with reference to Table Table1.

[16147] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1029 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16148] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1030 (GAM1030) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16149] GAM1030 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1030 was detected is described hereinabove with reference to Figs. 2-8.

[16150] GAM1030 gene, herein designated GAM GENE, and GAM1030 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16151] GAM1030 gene, herein designated GAM GENE, encodes a GAM1030 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1030 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1030 precursor RNA is designated SEQ ID:1003, and is provided hereinbelow with reference to the sequence listing part.

[16152] GAM1030 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1030 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16153] An enzyme complex designated DICER COMPLEX, dices the GAM1030 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1030 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1030 RNA is designated SEQ ID:2679, and

is provided hereinbelow with reference to the sequence listing part.

[16154] GAM1030 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1030 target RNA, herein designated GAM TARGET RNA. GAM1030 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16155] GAM1030 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1030 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1030 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1030 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1030 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16156] The complementary binding of GAM1030 RNA, herein designated GAM RNA, to target binding sites on GAM1030 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1030 target RNA, herein designated GAM TARGET RNA, into GAM1030 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16157] It is appreciated that GAM1030 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1030 target genes. The mRNA of each one of this plurality of GAM1030 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1030 RNA, herein designated GAM RNA, and which when bound by

GAM1030 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1030 target proteins.

[16158] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1030 gene, herein designated GAM GENE, on one or more GAM1030 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16159] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1030 correlate with, and may be deduced from, the identity of the target genes which GAM1030 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[16160] Nucleotide sequences of the GAM1030 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1030 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1030 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1030 are further described hereinbelow with reference to Table Table1.

[16161] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1030 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16162] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1031 (GAM1031) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16163] GAM1031 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1031 was detected is described hereinabove

with reference to Figs. 2-8.

[16164] GAM1031 gene, herein designated GAM GENE, and GAM1031 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16165] GAM1031 gene, herein designated GAM GENE, encodes a GAM1031 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1031 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1031 precursor RNA is designated SEQ ID:1004, and is provided hereinbelow with reference to the sequence listing part.

[16166] GAM1031 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16167] An enzyme complex designated DICER COMPLEX, dices the GAM1031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1031 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1031 RNA is designated SEQ ID:2680, and is provided hereinbelow with reference to the sequence listing part.

[16168] GAM1031 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1031 target RNA, herein designated GAM TARGET RNA. GAM1031 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16169] GAM1031 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1031 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1031 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1031 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1031 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16170] The complementary binding of GAM1031 RNA, herein designated GAM RNA, to target binding sites on GAM1031 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1031 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1031 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16171] It is appreciated that GAM1031 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1031 target genes. The mRNA of each one of this plurality of GAM1031 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1031 RNA, herein designated GAM RNA, and which when bound by GAM1031 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1031 target proteins.

[16172] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1031 gene, herein designated GAM GENE, on one or more GAM1031 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16173] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1031 correlate with, and may be deduced from, the identity of the target genes which GAM1031 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16174] Nucleotide sequences of the GAM1031 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1031 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1031 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1031 are further described hereinbelow with reference to Table Table1.

[16175] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1031 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[16176] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1032 (GAM1032) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16177] GAM1032 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1032 was detected is described hereinabove with reference to Figs. 2-8.

[16178] GAM1032 gene, herein designated GAM GENE, and GAM1032 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16179] GAM1032 gene, herein designated GAM GENE, encodes a GAM1032 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1032 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1032 precursor RNA is designated SEQ ID:1005, and is provided hereinbelow with reference to the sequence listing part.

[16180] GAM1032 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:100349, which mouse homolog is detected in mouse EST accession BF165130.1.

[16181] GAM1032 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16182] An enzyme complex designated DICER COMPLEX, dices the GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1032 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1032 RNA is designated SEQ ID:2681, and is provided hereinbelow with reference to the sequence listing part.

[16183] GAM1032 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1032 target RNA, herein designated GAM TARGET RNA. GAM1032 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16184] GAM1032 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1032 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1032 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1032 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1032 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16185] The complementary binding of GAM1032 RNA, herein designated GAM RNA, to target binding sites on GAM1032 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1032 target RNA, herein designated GAM TARGET RNA, into GAM1032 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16186] It is appreciated that GAM1032 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1032 target genes. The mRNA of each one of this plurality of GAM1032 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1032 RNA, herein designated GAM RNA, and which when bound by GAM1032 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1032 target proteins.

[16187] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1032 gene, herein designated GAM GENE, on one or more GAM1032 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16188] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1032 correlate with, and may

be deduced from, the identity of the target genes which GAM1032 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16189] Nucleotide sequences of the GAM1032 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1032 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1032 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1032 are further described hereinbelow with reference to Table Table1.

[16190] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1032 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16191] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1033 (GAM1033) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16192] GAM1033 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1033 was detected is described hereinabove with reference to Figs. 2-8.

[16193] GAM1033 gene, herein designated GAM GENE, and GAM1033 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16194] GAM1033 gene, herein designated GAM GENE, encodes a GAM1033 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1033 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1033 precursor RNA is designated SEQ ID:1006, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1006 is located at position 2349689 relative to contig NT_021907.13, on chromosome 1.

[16195] GAM1033 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16196] An enzyme complex designated DICER COMPLEX, dices the GAM1033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1033 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1033 RNA is designated SEQ ID:2682, and is provided hereinbelow with reference to the sequence listing part.

[16197] GAM1033 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1033 target RNA, herein designated GAM TARGET RNA. GAM1033 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[16198] GAM1033 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1033 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1033 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1033 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1033 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16199] The complementary binding of GAM1033 RNA, herein

designated GAM RNA, to target binding sites on GAM1033 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1033 target RNA, herein designated GAM TARGET RNA, into GAM1033 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16200] It is appreciated that GAM1033 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1033 target genes. The mRNA of each one of this plurality of GAM1033 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1033 RNA, herein designated GAM RNA, and which when bound by GAM1033 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1033 target proteins.

[16201] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1033 gene, herein designated GAM GENE, on one or more GAM1033 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16202] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1033 correlate with, and may be deduced from, the identity of the target genes which GAM1033 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16203] Nucleotide sequences of the GAM1033 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1033 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1033 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1033 are further described hereinbelow with reference to Table Table1.

[16204] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1033 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16205] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1034 (GAM1034) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16206] GAM1034 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1034 was detected is described hereinabove with reference to Figs. 2-8.

[16207] GAM1034 gene, herein designated GAM GENE, and GAM1034 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16208] GAM1034 gene, herein designated GAM GENE, encodes a GAM1034 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1034 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1034 precursor RNA is designated SEQ ID:1007, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1007 is located at position 2624684 relative to contig NT_005825.13, on chromosome 3.

[16209] GAM1034 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1034 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16210] An enzyme complex designated DICER COMPLEX, dices the GAM1034 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1034 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1034 RNA is designated SEQ ID:2683, and is provided hereinbelow with reference to the sequence listing part.

[16211] GAM1034 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1034 target RNA, herein designated GAM TARGET RNA. GAM1034 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16212] GAM1034 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1034 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1034 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1034 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1034 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16213] The complementary binding of GAM1034 RNA, herein designated GAM RNA, to target binding sites on GAM1034 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1034 target RNA, herein designated GAM TARGET RNA, into GAM1034 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16214] It is appreciated that GAM1034 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1034 target genes. The mRNA of each one of this plurality of GAM1034 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1034 RNA, herein designated GAM RNA, and which when bound by GAM1034 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1034 target proteins.

[16215] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1034 gene, herein designated GAM GENE, on one or more GAM1034 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16216] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1034 correlate with, and may be deduced from, the identity of the target genes which GAM1034 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16217] Nucleotide sequences of the GAM1034 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1034 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1034 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1034 are further described hereinbelow with reference to Table Table1.

[16218] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1034 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16219] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1035 (GAM1035) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16220] GAM1035 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1035 was detected is described hereinabove with reference to Figs. 2-8.

[16221] GAM1035 gene, herein designated GAM GENE, and GAM1035 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16222] GAM1035 gene, herein designated GAM GENE, encodes a GAM1035 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1035 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1035 precursor RNA is designated SEQ ID:1008, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1008 is located at position 6650294 relative to contig NT_004559.9, on chromosome 1.

[16223] GAM1035 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16224] SEQ ID:99297 detected in mouse EST Accession AA692084.1.

[16225] SEQ ID:99298 detected in mouse EST Accession AA656927.1.

[16226] GAM1035 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16227] An enzyme complex designated DICER COMPLEX, dices the GAM1035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1035 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide se-

quence of GAM1035 RNA is designated SEQ ID:2684, and is provided hereinbelow with reference to the sequence listing part.

[16228] GAM1035 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1035 target RNA, herein designated GAM TARGET RNA. GAM1035 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16229] GAM1035 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1035 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1035 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1035 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1035 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16230] The complementary binding of GAM1035 RNA, herein designated GAM RNA, to target binding sites on GAM1035 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1035 target RNA, herein designated GAM TARGET RNA, into GAM1035 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16231] It is appreciated that GAM1035 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1035 target genes. The mRNA of each one of this plurality of GAM1035 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1035 RNA,

herein designated GAM RNA, and which when bound by GAM1035 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1035 target proteins.

[16232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1035 gene, herein designated GAM GENE, on one or more GAM1035 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16233] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1035 correlate with, and may be deduced from, the identity of the target genes which

GAM1035 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16234] Nucleotide sequences of the GAM1035 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1035 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1035 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1035 are further described hereinbelow with reference to Table Table1.

[16235] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1035 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16236] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1036 (GAM1036) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16237] GAM1036 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1036 was detected is described hereinabove with reference to Figs. 2-8.

[16238] GAM1036 gene, herein designated GAM GENE, and GAM1036 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16239] GAM1036 gene, herein designated GAM GENE, encodes a GAM1036 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1036 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1036 precursor RNA is designated SEQ ID:1009, and is provided hereinbelow with reference to the sequence listing part.

[16240] GAM1036 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:100161, which mouse homolog is detected in mouse EST accession AV312797.1.

[16241] GAM1036 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1036 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16242] An enzyme complex designated DICER COMPLEX, dices the GAM1036 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1036 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1036 RNA is designated SEQ ID:2685, and is provided hereinbelow with reference to the sequence listing part.

[16243] GAM1036 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1036 target RNA, herein designated GAM TARGET RNA. GAM1036 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16244] GAM1036 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1036 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1036 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1036 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1036 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[16245] The complementary binding of GAM1036 RNA, herein designated GAM RNA, to target binding sites on GAM1036 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1036 target RNA, herein designated GAM TARGET RNA, into GAM1036 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16246] It is appreciated that GAM1036 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1036 target genes. The mRNA of each one of this plurality of GAM1036 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1036 RNA, herein designated GAM RNA, and which when bound by GAM1036 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1036 target proteins.

[16247] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1036 gene, herein designated GAM GENE, on one or

more GAM1036 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16248] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1036 correlate with, and may be deduced from, the identity of the target genes which GAM1036 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16249] Nucleotide sequences of the GAM1036 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1036 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1036 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1036 are further de-

scribed hereinbelow with reference to Table Table1.

[16250] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1036 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16251] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1037 (GAM1037) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16252] GAM1037 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1037 was detected is described hereinabove with reference to Figs. 2-8.

[16253] GAM1037 gene, herein designated GAM GENE, and GAM1037 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16254] GAM1037 gene, herein designated GAM GENE, encodes a GAM1037 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1037 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1037 precursor RNA is designated SEQ ID:1010, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1010 is located at position 598813 relative to contig NT_021979.13, on chromosome 1.

[16255] GAM1037 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16256] SEQ ID:99560 detected in mouse EST Accession BI248882.1.

[16257] SEQ ID:99599 detected in mouse EST Accession AA186155.1.

[16258] SEQ ID:99600 detected in mouse EST Accession BE197124.1.

[16259] SEQ ID:99601 detected in mouse EST Accession BF124611.1.

[16260] GAM1037 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1037 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16261] An enzyme complex designated DICER COMPLEX, dices the GAM1037 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1037 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1037 RNA is designated SEQ ID:2686, and is provided hereinbelow with reference to the sequence listing part.

[16262] GAM1037 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1037 target RNA, herein designated GAM TARGET

RNA. GAM1037 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16263] GAM1037 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1037 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1037 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1037 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1037 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16264] The complementary binding of GAM1037 RNA, herein designated GAM RNA, to target binding sites on GAM1037 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1037 target RNA, herein designated GAM TARGET RNA, into GAM1037 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16265] It is appreciated that GAM1037 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1037 target genes. The mRNA of each one of this plurality of GAM1037 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1037 RNA, herein designated GAM RNA, and which when bound by GAM1037 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1037 target proteins.

[16266] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1037 gene, herein designated GAM GENE, on one or more GAM1037 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16267] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1037 correlate with, and may be deduced from, the identity of the target genes which GAM1037 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16268] Nucleotide sequences of the GAM1037 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1037 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1037 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1037 are further described hereinbelow with reference to Table Table1.

[16269] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1037 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16270] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1038 (GAM1038) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16271] GAM1038 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1038 was detected is described hereinabove with reference to Figs. 2-8.

[16272] GAM1038 gene, herein designated GAM GENE, and GAM1038 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16273] GAM1038 gene, herein designated GAM GENE, encodes a

GAM1038 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1038 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1038 precursor RNA is designated SEQ ID:1011, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1011 is located at position 26544845 relative to contig NT_011512.7, on chromosome 21.

[16274] GAM1038 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1038 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16275] An enzyme complex designated DICER COMPLEX, dices the GAM1038 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1038 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1038 RNA is designated SEQ ID:2687, and is provided hereinbelow with reference to the sequence listing part.

[16276] GAM1038 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1038 target RNA, herein designated GAM TARGET RNA. GAM1038 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16277] GAM1038 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1038 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1038 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1038 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1038 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16278] The complementary binding of GAM1038 RNA, herein designated GAM RNA, to target binding sites on GAM1038 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1038 target RNA, herein designated GAM TARGET RNA, into GAM1038 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16279] It is appreciated that GAM1038 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1038 target genes. The mRNA of each one of this plurality of GAM1038 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1038 RNA, herein designated GAM RNA, and which when bound by GAM1038 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1038 target proteins.

[16280] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1038 gene, herein designated GAM GENE, on one or more GAM1038 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16281] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1038 correlate with, and may be deduced from, the identity of the target genes which GAM1038 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16282] Nucleotide sequences of the GAM1038 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1038 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1038 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1038 are further described hereinbelow with reference to Table Table1.

[16283] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1038 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16284] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1039 (GAM1039) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16285] GAM1039 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1039 was detected is described hereinabove with reference to Figs. 2-8.

[16286] GAM1039 gene, herein designated GAM GENE, and GAM1039 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16287] GAM1039 gene, herein designated GAM GENE, encodes a GAM1039 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1039 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1039 precursor RNA is designated SEQ ID:1012, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1012 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[16288] GAM1039 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1039 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16289] An enzyme complex designated DICER COMPLEX, dices the GAM1039 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1039 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1039 RNA is designated SEQ ID:2688, and is provided hereinbelow with reference to the sequence listing part.

[16290] GAM1039 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1039 target RNA, herein designated GAM TARGET RNA. GAM1039 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16291] GAM1039 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1039 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1039 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1039 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1039 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16292] The complementary binding of GAM1039 RNA, herein designated GAM RNA, to target binding sites on GAM1039 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1039 target RNA, herein designated GAM TARGET RNA, into GAM1039 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16293] It is appreciated that GAM1039 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1039 target genes. The mRNA of each one of this plurality of GAM1039 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1039 RNA, herein designated GAM RNA, and which when bound by GAM1039 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1039 target proteins.

[16294] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1039 gene, herein designated GAM GENE, on one or more GAM1039 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16295] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1039 correlate with, and may be deduced from, the identity of the target genes which GAM1039 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16296] Nucleotide sequences of the GAM1039 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1039 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1039 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1039 are further described hereinbelow with reference to Table Table1.

[16297] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1039 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16298] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1040 (GAM1040) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16299] GAM1040 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1040 was detected is described hereinabove with reference to Figs. 2-8.

[16300] GAM1040 gene, herein designated GAM GENE, and GAM1040 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16301] GAM1040 gene, herein designated GAM GENE, encodes a GAM1040 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1040 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1040 precursor RNA is designated SEQ ID:1013, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1013 is located at position 1259513 relative to contig NT_025965.9, on chromosome X.

[16302] GAM1040 has 12 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16303] SEQ ID:98057 detected in mouse EST Accession AW259242.1.

[16304] SEQ ID:98058 detected in mouse EST Accession BE290074.1.

[16305] SEQ ID:98059 detected in mouse EST Accession BI788766.1.

[16306] SEQ ID:98060 detected in mouse EST Accession

BI789775.1.

[16307] SEQ ID:98061 detected in mouse EST Accession BG807367.1.

[16308] SEQ ID:98062 detected in mouse EST Accession AI098543.1.

[16309] SEQ ID:98063 detected in mouse EST Accession BG915676.1.

[16310] SEQ ID:98064 detected in mouse EST Accession AI115901.1.

[16311] SEQ ID:98065 detected in mouse EST Accession AU067184.1.

[16312] SEQ ID:98066 detected in mouse EST Accession BE371710.1.

[16313] SEQ ID:98067 detected in mouse EST Accession BI789740.1.

[16314] SEQ ID:98068 detected in mouse EST Accession AI151823.1.

[16315] GAM1040 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1040 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16316] An enzyme complex designated DICER COMPLEX, dices the GAM1040 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1040 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1040 RNA is designated SEQ ID:2689, and is provided hereinbelow with reference to the sequence listing part.

[16317] GAM1040 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1040 target RNA, herein designated GAM TARGET RNA. GAM1040 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[16318] GAM1040 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1040 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1040 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1040 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1040 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16319] The complementary binding of GAM1040 RNA, herein

designated GAM RNA, to target binding sites on GAM1040 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1040 target RNA, herein designated GAM TARGET RNA, into GAM1040 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16320] It is appreciated that GAM1040 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1040 target genes. The mRNA of each one of this plurality of GAM1040 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1040 RNA, herein designated GAM RNA, and which when bound by GAM1040 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1040 target proteins.

[16321] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1040 gene, herein designated GAM GENE, on one or more GAM1040 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16322] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1040 correlate with, and may be deduced from, the identity of the target genes which GAM1040 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16323] Nucleotide sequences of the GAM1040 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1040 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1040 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1040 are further described hereinbelow with reference to Table Table1.

[16324] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1040 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16325] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1041 (GAM1041) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16326] GAM1041 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1041 was detected is described hereinabove with reference to Figs. 2-8.

[16327] GAM1041 gene, herein designated GAM GENE, and GAM1041 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16328] GAM1041 gene, herein designated GAM GENE, encodes a GAM1041 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1041 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1041 precursor RNA is designated SEQ ID:1014, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1014 is located at position 2281900 relative to contig NT_024797.11, on chromosome 16.

[16329] GAM1041 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16330] SEQ ID:98956 detected in mouse EST Accession BF134656.1.

[16331] SEQ ID:98957 detected in mouse EST Accession BI149599.1.

[16332] GAM1041 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1041 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16333] An enzyme complex designated DICER COMPLEX, dices the GAM1041 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1041 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1041 RNA is designated SEQ ID:2690, and is provided hereinbelow with reference to the sequence

listing part.

[16334] GAM1041 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1041 target RNA, herein designated GAM TARGET RNA. GAM1041 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16335] GAM1041 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1041 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1041 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1041 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1041 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16336] The complementary binding of GAM1041 RNA, herein designated GAM RNA, to target binding sites on GAM1041 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1041 target RNA, herein designated GAM TARGET RNA, into GAM1041 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16337] It is appreciated that GAM1041 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1041 target genes. The mRNA of each one of this plurality of GAM1041 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1041 RNA, herein designated GAM RNA, and which when bound by GAM1041 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1041 target proteins.

[16338] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1041 gene, herein designated GAM GENE, on one or more GAM1041 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16339] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1041 correlate with, and may be deduced from, the identity of the target genes which GAM1041 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16340] Nucleotide sequences of the GAM1041 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1041 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1041 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1041 are further described hereinbelow with reference to Table Table1.

[16341] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1041 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16342] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1042 (GAM1042) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16343] GAM1042 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1042 was detected is described hereinabove with reference to Figs. 2-8.

[16344] GAM1042 gene, herein designated GAM GENE, and GAM1042 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16345] GAM1042 gene, herein designated GAM GENE, encodes a GAM1042 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1042 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1042 precursor RNA is designated SEQ ID:1015, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1015 is located at position 226062 relative to contig NT_019197.3, on chromosome 22.

[16346] GAM1042 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1042 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[16347] An enzyme complex designated DICER COMPLEX, dices the GAM1042 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1042 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1042 RNA is designated SEQ ID:2691, and is provided hereinbelow with reference to the sequence listing part.

[16348] GAM1042 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1042 target RNA, herein designated GAM TARGET RNA. GAM1042 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16349] GAM1042 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1042 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1042 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1042 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1042 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16350] The complementary binding of GAM1042 RNA, herein designated GAM RNA, to target binding sites on GAM1042 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1042 target RNA, herein designated GAM TARGET RNA, into GAM1042 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16351] It is appreciated that GAM1042 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1042 target genes. The mRNA of each one of this plurality of GAM1042 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1042 RNA, herein designated GAM RNA, and which when bound by GAM1042 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1042 target proteins.

[16352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1042 gene, herein designated GAM GENE, on one or more GAM1042 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16353] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1042 correlate with, and may be deduced from, the identity of the target genes which GAM1042 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16354] Nucleotide sequences of the GAM1042 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1042 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1042 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1042 are further described hereinbelow with reference to Table Table1.

[16355] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1042 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16356] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1043 (GAM1043) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16357] GAM1043 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1043 was detected is described hereinabove with reference to Figs. 2-8.

[16358] GAM1043 gene, herein designated GAM GENE, and GAM1043 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16359] GAM1043 gene, herein designated GAM GENE, encodes a GAM1043 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1043 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1043 precursor RNA is designated SEQ ID:1016, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1016 is located at position 737960 relative to contig NT_010859.10, on chromosome 18.

[16360] GAM1043 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1043 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16361] An enzyme complex designated DICER COMPLEX, dices the GAM1043 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1043 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1043 RNA is designated SEQ ID:2692, and

is provided hereinbelow with reference to the sequence listing part.

[16362] GAM1043 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1043 target RNA, herein designated GAM TARGET RNA. GAM1043 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16363] GAM1043 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1043 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1043 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1043 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1043 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16364] The complementary binding of GAM1043 RNA, herein designated GAM RNA, to target binding sites on GAM1043 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1043 target RNA, herein designated GAM TARGET RNA, into GAM1043 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16365] It is appreciated that GAM1043 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1043 target genes. The mRNA of each one of this plurality of GAM1043 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1043 RNA, herein designated GAM RNA, and which when bound by

GAM1043 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1043 target proteins.

[16366] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1043 gene, herein designated GAM GENE, on one or more GAM1043 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16367] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1043 correlate with, and may be deduced from, the identity of the target genes which GAM1043 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[16368] Nucleotide sequences of the GAM1043 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1043 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1043 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1043 are further described hereinbelow with reference to Table Table1.

[16369] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1043 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16370] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1044 (GAM1044) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16371] GAM1044 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1044 was detected is described hereinabove

with reference to Figs. 2-8.

[16372] GAM1044 gene, herein designated GAM GENE, and GAM1044 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16373] GAM1044 gene, herein designated GAM GENE, encodes a GAM1044 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1044 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1044 precursor RNA is designated SEQ ID:1017, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1017 is located at position 29936963 relative to contig NT_007933.10, on chromosome 7.

[16374] GAM1044 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1044 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16375] An enzyme complex designated DICER COMPLEX, dices the GAM1044 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1044 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1044 RNA is designated SEQ ID:2693, and is provided hereinbelow with reference to the sequence listing part.

[16376] GAM1044 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1044 target RNA, herein designated GAM TARGET RNA. GAM1044 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16377] GAM1044 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1044 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1044 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1044 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1044 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16378] The complementary binding of GAM1044 RNA, herein designated GAM RNA, to target binding sites on GAM1044 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1044 target RNA, herein designated GAM TARGET RNA, into GAM1044 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16379] It is appreciated that GAM1044 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1044 target genes. The mRNA of each one of this plurality of GAM1044 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1044 RNA, herein designated GAM RNA, and which when bound by GAM1044 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1044 target proteins.

[16380] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1044 gene, herein designated GAM GENE, on one or more GAM1044 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16381] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1044 correlate with, and may be deduced from, the identity of the target genes which GAM1044 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16382] Nucleotide sequences of the GAM1044 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1044 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1044 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1044 are further described hereinbelow with reference to Table Table1.

[16383] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1044 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16384] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1045 (GAM1045) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16385] GAM1045 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1045 was detected is described hereinabove with reference to Figs. 2-8.

[16386] GAM1045 gene, herein designated GAM GENE, and GAM1045 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16387] GAM1045 gene, herein designated GAM GENE, encodes a GAM1045 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1045 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1045 precursor RNA is

designated SEQ ID:1018, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1018 is located at position 1259525 relative to contig NT_025965.9, on chromosome X.

[16388] GAM1045 has 12 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16389] SEQ ID:99567 detected in mouse EST Accession BI789740.1.

[16390] SEQ ID:99568 detected in mouse EST Accession AW259242.1.

[16391] SEQ ID:99569 detected in mouse EST Accession AI151823.1.

[16392] SEQ ID:99570 detected in mouse EST Accession BG807367.1.

[16393] SEQ ID:99571 detected in mouse EST Accession AI098543.1.

[16394] SEQ ID:99572 detected in mouse EST Accession BG915676.1.

[16395] SEQ ID:99573 detected in mouse EST Accession AI115901.1.

[16396] SEQ ID:99574 detected in mouse EST Accession AU067184.1.

[16397] SEQ ID:99586 detected in mouse EST Accession BI789775.1.

[16398] SEQ ID:99587 detected in mouse EST Accession BI788766.1.

[16399] SEQ ID:99588 detected in mouse EST Accession BE371710.1.

[16400] SEQ ID:99591 detected in mouse EST Accession BE290074.1.

[16401] GAM1045 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1045 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16402] An enzyme complex designated DICER COMPLEX, dices the GAM1045 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1045 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1045 RNA is designated SEQ ID:2694, and is provided hereinbelow with reference to the sequence listing part.

[16403] GAM1045 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1045 target RNA, herein designated GAM TARGET RNA. GAM1045 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16404] GAM1045 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1045 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1045 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1045 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1045 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16405] The complementary binding of GAM1045 RNA, herein designated GAM RNA, to target binding sites on GAM1045 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1045 target RNA, herein designated GAM TARGET RNA, into GAM1045 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16406] It is appreciated that GAM1045 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1045 target genes. The mRNA of each one of this plurality of GAM1045 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1045 RNA, herein designated GAM RNA, and which when bound by GAM1045 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1045 target proteins.

[16407] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1045 gene, herein designated GAM GENE, on one or more GAM1045 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16408] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1045 correlate with, and may be deduced from, the identity of the target genes which GAM1045 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16409] Nucleotide sequences of the GAM1045 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1045 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1045 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1045 are further described hereinbelow with reference to Table Table1.

[16410] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1045 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16411] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1046 (GAM1046) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16412] GAM1046 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1046 was detected is described hereinabove with reference to Figs. 2-8.

[16413] GAM1046 gene, herein designated GAM GENE, and GAM1046 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16414] GAM1046 gene, herein designated GAM GENE, encodes a GAM1046 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1046 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1046 precursor RNA is designated SEQ ID:1019, and is provided hereinbelow with reference to the sequence listing part.

[16415] GAM1046 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1046 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16416] An enzyme complex designated DICER COMPLEX, dices the GAM1046 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1046 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1046 RNA is designated SEQ ID:2695, and is provided hereinbelow with reference to the sequence listing part.

[16417] GAM1046 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1046 target RNA, herein designated GAM TARGET RNA. GAM1046 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16418] GAM1046 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1046 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1046 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1046 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1046 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16419] The complementary binding of GAM1046 RNA, herein designated GAM RNA, to target binding sites on GAM1046 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1046 target RNA, herein designated GAM TARGET RNA, into GAM1046 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16420] It is appreciated that GAM1046 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1046 target genes. The mRNA of each one of this plurality of GAM1046 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1046 RNA, herein designated GAM RNA, and which when bound by GAM1046 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1046 target proteins.

[16421] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1046 gene, herein designated GAM GENE, on one or more GAM1046 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16422] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1046 correlate with, and may be deduced from, the identity of the target genes which GAM1046 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16423] Nucleotide sequences of the GAM1046 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1046 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1046 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1046 are further described hereinbelow with reference to Table Table1.

[16424] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1046 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16425] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1047 (GAM1047) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16426] GAM1047 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1047 was detected is described hereinabove with reference to Figs. 2-8.

[16427] GAM1047 gene, herein designated GAM GENE, and GAM1047 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16428] GAM1047 gene, herein designated GAM GENE, encodes a GAM1047 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1047 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1047 precursor RNA is designated SEQ ID:1020, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1020 is located at position 476362 relative to contig NT_021937.13, on chromosome 1.

[16429] GAM1047 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16430] An enzyme complex designated DICER COMPLEX, dices the GAM1047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1047 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1047 RNA is designated SEQ ID:2696, and is provided hereinbelow with reference to the sequence listing part.

[16431] GAM1047 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1047 target RNA, herein designated GAM TARGET RNA. GAM1047 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16432] GAM1047 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1047 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1047 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1047 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1047 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16433] The complementary binding of GAM1047 RNA, herein designated GAM RNA, to target binding sites on GAM1047 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1047 target RNA, herein designated GAM TARGET RNA, into GAM1047 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16434] It is appreciated that GAM1047 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1047 target genes. The mRNA of each one of this plurality of GAM1047 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1047 RNA, herein designated GAM RNA, and which when bound by GAM1047 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1047 target proteins.

[16435] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1047 gene, herein designated GAM GENE, on one or more GAM1047 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16436] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1047 correlate with, and may be deduced from, the identity of the target genes which GAM1047 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16437] Nucleotide sequences of the GAM1047 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1047 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1047 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1047 are further described hereinbelow with reference to Table Table1.

[16438] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1047 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16439] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1048 (GAM1048) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16440] GAM1048 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1048 was detected is described hereinabove with reference to Figs. 2-8.

[16441] GAM1048 gene, herein designated GAM GENE, and GAM1048 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16442] GAM1048 gene, herein designated GAM GENE, encodes a GAM1048 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1048 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1048 precursor RNA is designated SEQ ID:1021, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1021 is located at position 7819273 relative to contig NT_023935.13, on chromosome 9.

[16443] GAM1048 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1048 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16444] An enzyme complex designated DICER COMPLEX, dices the GAM1048 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1048 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1048 RNA is designated SEQ ID:2697, and is provided hereinbelow with reference to the sequence listing part.

[16445] GAM1048 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1048 target RNA, herein designated GAM TARGET

RNA. GAM1048 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16446] GAM1048 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1048 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1048 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1048 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1048 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16447] The complementary binding of GAM1048 RNA, herein designated GAM RNA, to target binding sites on GAM1048 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1048 target RNA, herein designated GAM TARGET RNA, into GAM1048 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16448] It is appreciated that GAM1048 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1048 target genes. The mRNA of each one of this plurality of GAM1048 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1048 RNA, herein designated GAM RNA, and which when bound by GAM1048 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1048 target proteins.

[16449] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1048 gene, herein designated GAM GENE, on one or more GAM1048 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16450] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1048 correlate with, and may be deduced from, the identity of the target genes which GAM1048 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16451] Nucleotide sequences of the GAM1048 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1048 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1048 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1048 are further described hereinbelow with reference to Table Table1.

[16452] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1048 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16453] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1049 (GAM1049) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16454] GAM1049 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1049 was detected is described hereinabove with reference to Figs. 2-8.

[16455] GAM1049 gene, herein designated GAM GENE, and GAM1049 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16456] GAM1049 gene, herein designated GAM GENE, encodes a

GAM1049 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1049 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1049 precursor RNA is designated SEQ ID:1022, and is provided hereinbelow with reference to the sequence listing part.

[16457] GAM1049 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1049 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16458] An enzyme complex designated DICER COMPLEX, dices the GAM1049 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1049 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1049 RNA is designated SEQ ID:2698, and is provided hereinbelow with reference to the sequence listing part.

[16459] GAM1049 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1049 target RNA, herein designated GAM TARGET RNA. GAM1049 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16460] GAM1049 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1049 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1049 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1049 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1049 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16461] The complementary binding of GAM1049 RNA, herein designated GAM RNA, to target binding sites on GAM1049 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1049 target RNA, herein designated GAM TARGET RNA, into GAM1049 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16462] It is appreciated that GAM1049 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1049 target genes. The mRNA of each one of this plurality of GAM1049 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1049 RNA, herein designated GAM RNA, and which when bound by GAM1049 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1049 target proteins.

[16463] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1049 gene, herein designated GAM GENE, on one or more GAM1049 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[16464] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1049 correlate with, and may be deduced from, the identity of the target genes which GAM1049 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16465] Nucleotide sequences of the GAM1049 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1049 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1049 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1049 are further described hereinbelow with reference to Table Table1.

[16466] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1049 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16467] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1050 (GAM1050) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[16468] GAM1050 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1050 was detected is described hereinabove with reference to Figs. 2-8.

[16469] GAM1050 gene, herein designated GAM GENE, and GAM1050 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16470] GAM1050 gene, herein designated GAM GENE, encodes a GAM1050 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1050 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1050 precursor RNA is designated SEQ ID:1023, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1023 is located at position 3633453 relative to contig NT_035325.2, on chromosome 15.

[16471] GAM1050 has 21 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences

of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16472] SEQ ID:97978 detected in mouse EST Accession BE862401.1.

[16473] SEQ ID:97979 detected in mouse EST Accession BG277942.1.

[16474] SEQ ID:97980 detected in mouse EST Accession AA413748.1.

[16475] SEQ ID:97981 detected in mouse EST Accession AA238000.1.

[16476] SEQ ID:97982 detected in mouse EST Accession BE374711.1.

[16477] SEQ ID:97983 detected in mouse EST Accession BI692473.1.

[16478] SEQ ID:97987 detected in mouse EST Accession AA792494.1.

[16479] SEQ ID:97988 detected in mouse EST Accession AA413839.1.

[16480] SEQ ID:97989 detected in mouse EST Accession AA647932.1.

[16481] SEQ ID:97990 detected in mouse EST Accession AI036398.1.

[16482] SEQ ID:97991 detected in mouse EST Accession

BI156958.1.

[16483] SEQ ID:97992 detected in mouse EST Accession BB037062.2.

[16484] SEQ ID:97994 detected in mouse EST Accession AA681199.1.

[16485] SEQ ID:97995 detected in mouse EST Accession AI646762.1.

[16486] SEQ ID:98634 detected in mouse EST Accession AA277327.1.

[16487] SEQ ID:98635 detected in mouse EST Accession AW109849.1.

[16488] SEQ ID:98636 detected in mouse EST Accession BI413021.1.

[16489] SEQ ID:98637 detected in mouse EST Accession AW475413.1.

[16490] SEQ ID:98638 detected in mouse EST Accession BI683887.1.

[16491] SEQ ID:98639 detected in mouse EST Accession BG915034.1.

[16492] SEQ ID:98640 detected in mouse EST Accession AA561807.1.

[16493] GAM1050 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1050 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16494] An enzyme complex designated DICER COMPLEX, dices the GAM1050 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1050 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1050 RNA is designated SEQ ID:2699, and is provided hereinbelow with reference to the sequence listing part.

[16495] GAM1050 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1050 target RNA, herein designated GAM TARGET

RNA. GAM1050 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16496] GAM1050 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1050 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1050 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1050 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1050 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16497] The complementary binding of GAM1050 RNA, herein designated GAM RNA, to target binding sites on GAM1050 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1050 target RNA, herein designated GAM TARGET RNA, into GAM1050 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16498] It is appreciated that GAM1050 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1050 target genes. The mRNA of each one of this plurality of GAM1050 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1050 RNA, herein designated GAM RNA, and which when bound by GAM1050 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1050 target proteins.

[16499] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1050 gene, herein designated GAM GENE, on one or more GAM1050 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16500] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1050 correlate with, and may be deduced from, the identity of the target genes which GAM1050 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16501] Nucleotide sequences of the GAM1050 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1050 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1050 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1050 are further described hereinbelow with reference to Table Table1.

[16502] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1050 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16503] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1051 (GAM1051) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16504] GAM1051 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1051 was detected is described hereinabove with reference to Figs. 2-8.

[16505] GAM1051 gene, herein designated GAM GENE, and GAM1051 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16506] GAM1051 gene, herein designated GAM GENE, encodes a

GAM1051 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1051 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1051 precursor RNA is designated SEQ ID:1024, and is provided hereinbelow with reference to the sequence listing part.

[16507] GAM1051 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16508] An enzyme complex designated DICER COMPLEX, dices the GAM1051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1051 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1051 RNA is designated SEQ ID:2700, and is provided hereinbelow with reference to the sequence listing part.

[16509] GAM1051 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1051 target RNA, herein designated GAM TARGET RNA. GAM1051 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16510] GAM1051 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1051 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1051 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1051 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1051 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16511] The complementary binding of GAM1051 RNA, herein designated GAM RNA, to target binding sites on GAM1051 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1051 target RNA, herein designated GAM TARGET RNA, into GAM1051 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16512] It is appreciated that GAM1051 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1051 target genes. The mRNA of each one of this plurality of GAM1051 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1051 RNA, herein designated GAM RNA, and which when bound by GAM1051 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1051 target proteins.

[16513] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1051 gene, herein designated GAM GENE, on one or more GAM1051 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[16514] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1051 correlate with, and may be deduced from, the identity of the target genes which GAM1051 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16515] Nucleotide sequences of the GAM1051 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1051 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1051 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1051 are further described hereinbelow with reference to Table Table1.

[16516] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1051 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16517] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1052 (GAM1052) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[16518] GAM1052 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1052 was detected is described hereinabove with reference to Figs. 2-8.

[16519] GAM1052 gene, herein designated GAM GENE, and GAM1052 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16520] GAM1052 gene, herein designated GAM GENE, encodes a GAM1052 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1052 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1052 precursor RNA is designated SEQ ID:1025, and is provided hereinbelow with reference to the sequence listing part.

[16521] GAM1052 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1052 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16522] An enzyme complex designated DICER COMPLEX, dices the GAM1052 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1052 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1052 RNA is designated SEQ ID:2701, and is provided hereinbelow with reference to the sequence listing part.

[16523] GAM1052 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1052 target RNA, herein designated GAM TARGET RNA. GAM1052 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16524] GAM1052 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1052 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1052 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1052 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1052 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16525] The complementary binding of GAM1052 RNA, herein designated GAM RNA, to target binding sites on GAM1052 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1052 target RNA, herein designated GAM TARGET RNA, into GAM1052 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16526] It is appreciated that GAM1052 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1052 target genes. The mRNA of each one of this plurality of GAM1052 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1052 RNA, herein designated GAM RNA, and which when bound by GAM1052 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1052 target proteins.

[16527] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1052 gene, herein designated GAM GENE, on one or more GAM1052 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16528] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1052 correlate with, and may be deduced from, the identity of the target genes which GAM1052 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16529] Nucleotide sequences of the GAM1052 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1052 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1052 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1052 are further described hereinbelow with reference to Table Table1.

[16530] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1052 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16531] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1053 (GAM1053) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16532] GAM1053 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1053 was detected is described hereinabove with reference to Figs. 2-8.

[16533] GAM1053 gene, herein designated GAM GENE, and GAM1053 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16534] GAM1053 gene, herein designated GAM GENE, encodes a GAM1053 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1053 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1053 precursor RNA is designated SEQ ID:1026, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1026 is located at position 7678827 relative to contig NT_004852.13, on chromosome 1.

[16535] GAM1053 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1053 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16536] An enzyme complex designated DICER COMPLEX, dices the GAM1053 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1053 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1053 RNA is designated SEQ ID:2702, and is provided hereinbelow with reference to the sequence listing part.

[16537] GAM1053 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1053 target RNA, herein designated GAM TARGET RNA. GAM1053 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16538] GAM1053 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1053 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1053 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1053 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1053 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16539] The complementary binding of GAM1053 RNA, herein designated GAM RNA, to target binding sites on GAM1053 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1053 target RNA, herein designated GAM TARGET RNA, into GAM1053 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16540] It is appreciated that GAM1053 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1053 target genes. The mRNA of each one of this

plurality of GAM1053 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1053 RNA, herein designated GAM RNA, and which when bound by GAM1053 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1053 target proteins.

[16541] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1053 gene, herein designated GAM GENE, on one or more GAM1053 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16542] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1053 correlate with, and may be deduced from, the identity of the target genes which GAM1053 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16543] Nucleotide sequences of the GAM1053 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1053 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1053 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1053 are further described hereinbelow with reference to Table Table1.

[16544] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1053 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16545] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1054 (GAM1054) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[16546] GAM1054 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1054 was detected is described hereinabove with reference to Figs. 2-8.

[16547] GAM1054 gene, herein designated GAM GENE, and GAM1054 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16548] GAM1054 gene, herein designated GAM GENE, encodes a GAM1054 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1054 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1054 precursor RNA is designated SEQ ID:1027, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1027 is located at position 33703774 relative to contig NT_007592.11, on chromosome 6.

[16549] GAM1054 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1054 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16550] An enzyme complex designated DICER COMPLEX, dices the GAM1054 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1054 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1054 RNA is designated SEQ ID:2703, and is provided hereinbelow with reference to the sequence listing part.

[16551] GAM1054 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1054 target RNA, herein designated GAM TARGET RNA. GAM1054 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16552] GAM1054 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1054 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1054 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1054 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1054 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[16553] The complementary binding of GAM1054 RNA, herein designated GAM RNA, to target binding sites on GAM1054 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1054 target RNA, herein designated GAM TARGET RNA, into GAM1054 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16554] It is appreciated that GAM1054 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1054 target genes. The mRNA of each one of this plurality of GAM1054 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1054 RNA, herein designated GAM RNA, and which when bound by GAM1054 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1054 target proteins.

[16555] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1054 gene, herein designated GAM GENE, on one or

more GAM1054 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16556] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1054 correlate with, and may be deduced from, the identity of the target genes which GAM1054 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16557] Nucleotide sequences of the GAM1054 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1054 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1054 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1054 are further de-

scribed hereinbelow with reference to Table Table1.

[16558] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1054 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16559] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1055 (GAM1055) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16560] GAM1055 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1055 was detected is described hereinabove with reference to Figs. 2-8.

[16561] GAM1055 gene, herein designated GAM GENE, and GAM1055 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16562] GAM1055 gene, herein designated GAM GENE, encodes a GAM1055 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1055 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1055 precursor RNA is designated SEQ ID:1028, and is provided hereinbelow with reference to the sequence listing part.

[16563] GAM1055 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16564] An enzyme complex designated DICER COMPLEX, dices the GAM1055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1055 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1055 RNA is designated SEQ ID:2704, and is provided hereinbelow with reference to the sequence listing part.

[16565] GAM1055 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1055 target RNA, herein designated GAM TARGET RNA. GAM1055 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16566] GAM1055 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1055 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1055 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1055 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1055 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16567] The complementary binding of GAM1055 RNA, herein designated GAM RNA, to target binding sites on GAM1055 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1055 target RNA, herein designated GAM TARGET RNA, into GAM1055 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16568] It is appreciated that GAM1055 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1055 target genes. The mRNA of each one of this plurality of GAM1055 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1055 RNA, herein designated GAM RNA, and which when bound by GAM1055 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1055 target proteins.

[16569] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1055 gene, herein designated GAM GENE, on one or more GAM1055 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16570] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1055 correlate with, and may be deduced from, the identity of the target genes which GAM1055 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16571] Nucleotide sequences of the GAM1055 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1055 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1055 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1055 are further described hereinbelow with reference to Table Table1.

[16572] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1055 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16573] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1056 (GAM1056) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16574] GAM1056 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1056 was detected is described hereinabove with reference to Figs. 2-8.

[16575] GAM1056 gene, herein designated GAM GENE, and GAM1056 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16576] GAM1056 gene, herein designated GAM GENE, encodes a GAM1056 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1056 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1056 precursor RNA is designated SEQ ID:1029, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1029 is located at position 2349694 relative to contig NT_021907.13, on chromosome 1.

[16577] GAM1056 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1056 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16578] An enzyme complex designated DICER COMPLEX, dices the GAM1056 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1056 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1056 RNA is designated SEQ ID:2705, and is provided hereinbelow with reference to the sequence listing part.

[16579] GAM1056 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1056 target RNA, herein designated GAM TARGET RNA. GAM1056 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16580] GAM1056 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1056 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1056 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1056 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1056 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16581] The complementary binding of GAM1056 RNA, herein designated GAM RNA, to target binding sites on GAM1056 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1056 target RNA, herein designated GAM TARGET RNA, into GAM1056 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16582] It is appreciated that GAM1056 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1056 target genes. The mRNA of each one of this plurality of GAM1056 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1056 RNA, herein designated GAM RNA, and which when bound by GAM1056 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1056 target proteins.

[16583] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1056 gene, herein designated GAM GENE, on one or more GAM1056 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16584] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1056 correlate with, and may be deduced from, the identity of the target genes which GAM1056 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16585] Nucleotide sequences of the GAM1056 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1056 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1056 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1056 are further described hereinbelow with reference to Table Table1.

[16586] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1056 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16587] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1057 (GAM1057) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16588] GAM1057 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1057 was detected is described hereinabove with reference to Figs. 2-8.

[16589] GAM1057 gene, herein designated GAM GENE, and GAM1057 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16590] GAM1057 gene, herein designated GAM GENE, encodes a GAM1057 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1057 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1057 precursor RNA is designated SEQ ID:1030, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1030 is located at position 413152 relative to contig NT_034901.2, on chromosome 8.

[16591] GAM1057 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16592] An enzyme complex designated DICER COMPLEX, dices the GAM1057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1057 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1057 RNA is designated SEQ ID:2706, and is provided hereinbelow with reference to the sequence listing part.

[16593] GAM1057 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1057 target RNA, herein designated GAM TARGET RNA. GAM1057 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16594] GAM1057 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1057 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1057 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1057 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1057 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16595] The complementary binding of GAM1057 RNA, herein designated GAM RNA, to target binding sites on GAM1057 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1057 target RNA, herein designated GAM TARGET RNA, into GAM1057 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16596] It is appreciated that GAM1057 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1057 target genes. The mRNA of each one of this

plurality of GAM1057 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1057 RNA, herein designated GAM RNA, and which when bound by GAM1057 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1057 target proteins.

[16597] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1057 gene, herein designated GAM GENE, on one or more GAM1057 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16598] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1057 correlate with, and may be deduced from, the identity of the target genes which GAM1057 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16599] Nucleotide sequences of the GAM1057 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1057 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1057 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1057 are further described hereinbelow with reference to Table Table1.

[16600] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1057 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16601] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1058 (GAM1058) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[16602] GAM1058 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1058 was detected is described hereinabove with reference to Figs. 2-8.

[16603] GAM1058 gene, herein designated GAM GENE, and GAM1058 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16604] GAM1058 gene, herein designated GAM GENE, encodes a GAM1058 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1058 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1058 precursor RNA is designated SEQ ID:1031, and is provided hereinbelow with reference to the sequence listing part.

[16605] GAM1058 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16606] SEQ ID:99763 detected in mouse EST Accession

AL022643.1.

[16607] SEQ ID:99764 detected in mouse EST Accession BF452099.1.

[16608] SEQ ID:99765 detected in mouse EST Accession BE531895.1.

[16609] SEQ ID:99766 detected in mouse EST Accession AA546767.1.

[16610] SEQ ID:99767 detected in mouse EST Accession BI453661.1.

[16611] SEQ ID:99769 detected in mouse EST Accession AI060752.1.

[16612] SEQ ID:99770 detected in mouse EST Accession AA184326.1.

[16613] GAM1058 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16614] An enzyme complex designated DICER COMPLEX, dices the GAM1058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1058 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1058 RNA is designated SEQ ID:2707, and is provided hereinbelow with reference to the sequence listing part.

[16615] GAM1058 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1058 target RNA, herein designated GAM TARGET RNA. GAM1058 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16616] GAM1058 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1058 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1058 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1058 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1058 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16617] The complementary binding of GAM1058 RNA, herein designated GAM RNA, to target binding sites on GAM1058 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1058 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1058 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16618] It is appreciated that GAM1058 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1058 target genes. The mRNA of each one of this plurality of GAM1058 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1058 RNA, herein designated GAM RNA, and which when bound by GAM1058 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1058 target proteins.

[16619] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1058 gene, herein designated GAM GENE, on one or more GAM1058 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16620] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1058 correlate with, and may be deduced from, the identity of the target genes which GAM1058 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16621] Nucleotide sequences of the GAM1058 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1058 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1058 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1058 are further described hereinbelow with reference to Table Table1.

[16622] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1058 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[16623] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1059 (GAM1059) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16624] GAM1059 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1059 was detected is described hereinabove with reference to Figs. 2-8.

[16625] GAM1059 gene, herein designated GAM GENE, and GAM1059 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16626] GAM1059 gene, herein designated GAM GENE, encodes a GAM1059 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1059 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1059 precursor RNA is designated SEQ ID:1032, and is provided hereinbelow with reference to the sequence listing part.

[16627] GAM1059 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1059 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16628] An enzyme complex designated DICER COMPLEX, dices the GAM1059 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1059 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1059 RNA is designated SEQ ID:2708, and is provided hereinbelow with reference to the sequence listing part.

[16629] GAM1059 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1059 target RNA, herein designated GAM TARGET RNA. GAM1059 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16630] GAM1059 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1059 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1059 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1059 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1059 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16631] The complementary binding of GAM1059 RNA, herein designated GAM RNA, to target binding sites on GAM1059 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1059 target RNA, herein designated GAM TARGET RNA, into GAM1059 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16632] It is appreciated that GAM1059 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1059 target genes. The mRNA of each one of this plurality of GAM1059 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1059 RNA, herein designated GAM RNA, and which when bound by GAM1059 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1059 target proteins.

[16633] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1059 gene, herein designated GAM GENE, on one or more GAM1059 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16634] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1059 correlate with, and may be deduced from, the identity of the target genes which GAM1059 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16635] Nucleotide sequences of the GAM1059 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1059 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1059 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1059 are further described hereinbelow with reference to Table Table1.

[16636] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1059 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16637] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1060 (GAM1060) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16638] GAM1060 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1060 was detected is described hereinabove with reference to Figs. 2-8.

[16639] GAM1060 gene, herein designated GAM GENE, and GAM1060 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[16640] GAM1060 gene, herein designated GAM GENE, encodes a GAM1060 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1060 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1060 precursor RNA is designated SEQ ID:1033, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1033 is located at position 464443 relative to contig NT_010692.9, on chromosome 17.

[16641] GAM1060 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16642] SEQ ID:98376 detected in mouse EST Accession AA068787.1.

[16643] SEQ ID:98377 detected in mouse EST Accession AA823029.1.

[16644] SEQ ID:98378 detected in mouse EST Accession BE625629.1.

[16645] SEQ ID:98379 detected in mouse EST Accession BI792530.1.

[16646] SEQ ID:98380 detected in mouse EST Accession BE380224.1.

[16647] SEQ ID:98381 detected in mouse EST Accession BG296866.1.

[16648] SEQ ID:98382 detected in mouse EST Accession BE309708.1.

[16649] SEQ ID:98383 detected in mouse EST Accession BI100916.1.

[16650] GAM1060 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1060 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16651] An enzyme complex designated DICER COMPLEX, dices the GAM1060 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1060 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 97%) nucleotide sequence of GAM1060 RNA is designated SEQ ID:2709, and is provided hereinbelow with reference to the sequence listing part.

[16652] GAM1060 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1060 target RNA, herein designated GAM TARGET RNA. GAM1060 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16653] GAM1060 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1060 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1060 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1060 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1060 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16654] The complementary binding of GAM1060 RNA, herein designated GAM RNA, to target binding sites on GAM1060 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1060 target RNA, herein designated GAM TARGET RNA, into GAM1060 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16655] It is appreciated that GAM1060 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1060 target genes. The mRNA of each one of this plurality of GAM1060 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1060 RNA, herein designated GAM RNA, and which when bound by GAM1060 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1060 target proteins.

[16656] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1060 gene, herein designated GAM GENE, on one or more GAM1060 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16657] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1060 correlate with, and may be deduced from, the identity of the target genes which GAM1060 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16658] Nucleotide sequences of the GAM1060 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1060 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1060 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1060 are further described hereinbelow with reference to Table Table1.

[16659] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1060 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16660] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1061 (GAM1061) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16661] GAM1061 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1061 was detected is described hereinabove with reference to Figs. 2-8.

[16662] GAM1061 gene, herein designated GAM GENE, and GAM1061 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16663] GAM1061 gene, herein designated GAM GENE, encodes a GAM1061 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1061 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1061 precursor RNA is designated SEQ ID:1034, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1034 is located at position 42810843 relative to contig NT_007592.11, on chromosome 6.

[16664] GAM1061 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16665] An enzyme complex designated DICER COMPLEX, dices the GAM1061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1061 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 96%) nucleotide sequence of GAM1061 RNA is designated SEQ ID:2710, and is provided hereinbelow with reference to the sequence listing part.

[16666] GAM1061 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1061 target RNA, herein designated GAM TARGET RNA. GAM1061 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16667] GAM1061 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1061 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1061 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1061 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1061 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16668] The complementary binding of GAM1061 RNA, herein designated GAM RNA, to target binding sites on GAM1061 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1061 target RNA, herein designated GAM TARGET RNA, into GAM1061 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16669] It is appreciated that GAM1061 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1061 target genes. The mRNA of each one of this plurality of GAM1061 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1061 RNA, herein designated GAM RNA, and which when bound by GAM1061 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1061 target proteins.

[16670] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1061 gene, herein designated GAM GENE, on one or more GAM1061 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16671] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1061 correlate with, and may be deduced from, the identity of the target genes which GAM1061 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16672] Nucleotide sequences of the GAM1061 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1061 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1061 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1061 are further described hereinbelow with reference to Table Table1.

[16673] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1061 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16674] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1062 (GAM1062) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16675] GAM1062 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1062 was detected is described hereinabove with reference to Figs. 2-8.

[16676] GAM1062 gene, herein designated GAM GENE, and GAM1062 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16677] GAM1062 gene, herein designated GAM GENE, encodes a GAM1062 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1062 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1062 precursor RNA is designated SEQ ID:1035, and is provided hereinbelow with reference to the sequence listing part.

[16678] GAM1062 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16679] An enzyme complex designated DICER COMPLEX, dices the GAM1062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1062 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1062 RNA is designated SEQ ID:2711, and is provided hereinbelow with reference to the sequence listing part.

[16680] GAM1062 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1062 target RNA, herein designated GAM TARGET RNA. GAM1062 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16681] GAM1062 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1062 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1062 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1062 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1062 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16682] The complementary binding of GAM1062 RNA, herein designated GAM RNA, to target binding sites on GAM1062 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1062 target RNA, herein designated GAM TARGET RNA, into GAM1062 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16683] It is appreciated that GAM1062 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1062 target genes. The mRNA of each one of this plurality of GAM1062 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1062 RNA, herein designated GAM RNA, and which when bound by GAM1062 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1062 target proteins.

[16684] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1062 gene, herein designated GAM GENE, on one or more GAM1062 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16685] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1062 correlate with, and may be deduced from, the identity of the target genes which GAM1062 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16686] Nucleotide sequences of the GAM1062 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1062 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1062 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1062 are further described hereinbelow with reference to Table Table1.

[16687] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1062 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16688] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1063 (GAM1063) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16689] GAM1063 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1063 was detected is described hereinabove with reference to Figs. 2-8.

[16690] GAM1063 gene, herein designated GAM GENE, and GAM1063 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16691] GAM1063 gene, herein designated GAM GENE, encodes a GAM1063 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1063 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1063 precursor RNA is designated SEQ ID:1036, and is provided hereinbelow with reference to the sequence listing part.

[16692] GAM1063 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1063 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16693] An enzyme complex designated DICER COMPLEX, dices the GAM1063 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1063 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1063 RNA is designated SEQ ID:2712, and is provided hereinbelow with reference to the sequence listing part.

[16694] GAM1063 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1063 target RNA, herein designated GAM TARGET RNA. GAM1063 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16695] GAM1063 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1063 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1063 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1063 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1063 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[16696] The complementary binding of GAM1063 RNA, herein designated GAM RNA, to target binding sites on GAM1063 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1063 target RNA, herein designated GAM TARGET RNA, into GAM1063 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16697] It is appreciated that GAM1063 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1063 target genes. The mRNA of each one of this plurality of GAM1063 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1063 RNA, herein designated GAM RNA, and which when bound by GAM1063 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1063 target proteins.

[16698] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1063 gene, herein designated GAM GENE, on one or

more GAM1063 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16699] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1063 correlate with, and may be deduced from, the identity of the target genes which GAM1063 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16700] Nucleotide sequences of the GAM1063 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1063 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1063 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1063 are further de-

scribed hereinbelow with reference to Table Table1.

[16701] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1063 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16702] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1064 (GAM1064) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16703] GAM1064 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1064 was detected is described hereinabove with reference to Figs. 2-8.

[16704] GAM1064 gene, herein designated GAM GENE, and GAM1064 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16705] GAM1064 gene, herein designated GAM GENE, encodes a GAM1064 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1064 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1064 precursor RNA is designated SEQ ID:1037, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1037 is located at position 2045038 relative to contig NT_011176.13, on chromosome 19.

[16706] GAM1064 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16707] An enzyme complex designated DICER COMPLEX, dices the GAM1064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1064 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1064 RNA is designated SEQ ID:2713, and is provided hereinbelow with reference to the sequence listing part.

[16708] GAM1064 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1064 target RNA, herein designated GAM TARGET RNA. GAM1064 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16709] GAM1064 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1064 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1064 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1064 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1064 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16710] The complementary binding of GAM1064 RNA, herein designated GAM RNA, to target binding sites on GAM1064 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1064 target RNA, herein designated GAM TARGET RNA, into GAM1064 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16711] It is appreciated that GAM1064 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1064 target genes. The mRNA of each one of this plurality of GAM1064 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1064 RNA, herein designated GAM RNA, and which when bound by GAM1064 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1064 target proteins.

[16712] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1064 gene, herein designated GAM GENE, on one or more GAM1064 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[16713] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1064 correlate with, and may be deduced from, the identity of the target genes which GAM1064 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16714] Nucleotide sequences of the GAM1064 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1064 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1064 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1064 are further described hereinbelow with reference to Table Table1.

[16715] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1064 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16716] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1065 (GAM1065) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[16717] GAM1065 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1065 was detected is described hereinabove with reference to Figs. 2-8.

[16718] GAM1065 gene, herein designated GAM GENE, and GAM1065 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16719] GAM1065 gene, herein designated GAM GENE, encodes a GAM1065 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1065 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1065 precursor RNA is designated SEQ ID:1038, and is provided hereinbelow with reference to the sequence listing part.

[16720] GAM1065 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1065 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16721] An enzyme complex designated DICER COMPLEX, dices the GAM1065 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1065 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1065 RNA is designated SEQ ID:2714, and is provided hereinbelow with reference to the sequence listing part.

[16722] GAM1065 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1065 target RNA, herein designated GAM TARGET RNA. GAM1065 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16723] GAM1065 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1065 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1065 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1065 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1065 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16724] The complementary binding of GAM1065 RNA, herein designated GAM RNA, to target binding sites on GAM1065 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1065 target RNA, herein designated GAM TARGET RNA, into GAM1065 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16725] It is appreciated that GAM1065 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1065 target genes. The mRNA of each one of this plurality of GAM1065 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1065 RNA, herein designated GAM RNA, and which when bound by GAM1065 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1065 target proteins.

[16726] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1065 gene, herein designated GAM GENE, on one or more GAM1065 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16727] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1065 correlate with, and may be deduced from, the identity of the target genes which GAM1065 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16728] Nucleotide sequences of the GAM1065 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1065 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1065 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1065 are further described hereinbelow with reference to Table Table1.

[16729] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1065 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16730] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1066 (GAM1066) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16731] GAM1066 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1066 was detected is described hereinabove with reference to Figs. 2-8.

[16732] GAM1066 gene, herein designated GAM GENE, and GAM1066 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16733] GAM1066 gene, herein designated GAM GENE, encodes a GAM1066 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1066 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1066 precursor RNA is designated SEQ ID:1039, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1039 is located at position 1366797 relative to contig NT_028309.8, on chromosome 11.

[16734] GAM1066 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16735] SEQ ID:98373 detected in mouse EST Accession AA517646.1.

[16736] SEQ ID:98374 detected in mouse EST Accession AA516955.1.

[16737] SEQ ID:98375 detected in mouse EST Accession AA516629.1.

[16738] GAM1066 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1066 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16739] An enzyme complex designated DICER COMPLEX, dices the GAM1066 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1066 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1066 RNA is designated SEQ ID:2715, and is provided hereinbelow with reference to the sequence listing part.

[16740] GAM1066 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1066 target RNA, herein designated GAM TARGET RNA. GAM1066 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16741] GAM1066 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1066 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1066 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1066 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1066 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16742] The complementary binding of GAM1066 RNA, herein designated GAM RNA, to target binding sites on GAM1066 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1066 target RNA, herein designated GAM TARGET RNA, into GAM1066 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16743] It is appreciated that GAM1066 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1066 target genes. The mRNA of each one of this plurality of GAM1066 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1066 RNA, herein designated GAM RNA, and which when bound by GAM1066 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1066 target proteins.

[16744] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1066 gene, herein designated GAM GENE, on one or more GAM1066 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16745] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1066 correlate with, and may be deduced from, the identity of the target genes which GAM1066 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16746] Nucleotide sequences of the GAM1066 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1066 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1066 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1066 are further described hereinbelow with reference to Table Table1.

[16747] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1066 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16748] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1067 (GAM1067) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16749] GAM1067 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1067 was detected is described hereinabove with reference to Figs. 2-8.

[16750] GAM1067 gene, herein designated GAM GENE, and GAM1067 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16751] GAM1067 gene, herein designated GAM GENE, encodes a GAM1067 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1067 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1067 precursor RNA is designated SEQ ID:1040, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1040 is located at position 1552122 relative to contig NT_010783.11, on chromosome 17.

[16752] GAM1067 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1067 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16753] An enzyme complex designated DICER COMPLEX, dices the GAM1067 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1067 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1067 RNA is designated SEQ ID:2716, and is provided hereinbelow with reference to the sequence listing part.

[16754] GAM1067 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1067 target RNA, herein designated GAM TARGET RNA. GAM1067 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16755] GAM1067 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1067 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1067 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1067 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1067 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16756] The complementary binding of GAM1067 RNA, herein designated GAM RNA, to target binding sites on GAM1067 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1067 target RNA, herein designated GAM TARGET RNA, into GAM1067 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16757] It is appreciated that GAM1067 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1067 target genes. The mRNA of each one of this

plurality of GAM1067 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1067 RNA, herein designated GAM RNA, and which when bound by GAM1067 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1067 target proteins.

[16758] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1067 gene, herein designated GAM GENE, on one or more GAM1067 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16759] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1067 correlate with, and may be deduced from, the identity of the target genes which GAM1067 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16760] Nucleotide sequences of the GAM1067 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1067 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1067 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1067 are further described hereinbelow with reference to Table Table1.

[16761] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1067 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16762] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1068 (GAM1068) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[16763] GAM1068 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1068 was detected is described hereinabove with reference to Figs. 2-8.

[16764] GAM1068 gene, herein designated GAM GENE, and GAM1068 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16765] GAM1068 gene, herein designated GAM GENE, encodes a GAM1068 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1068 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1068 precursor RNA is designated SEQ ID:1041, and is provided hereinbelow with reference to the sequence listing part.

[16766] GAM1068 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1068 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16767] An enzyme complex designated DICER COMPLEX, dices the GAM1068 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1068 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1068 RNA is designated SEQ ID:2717, and is provided hereinbelow with reference to the sequence listing part.

[16768] GAM1068 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1068 target RNA, herein designated GAM TARGET RNA. GAM1068 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[16769] GAM1068 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1068 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1068 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1068 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1068 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16770] The complementary binding of GAM1068 RNA, herein

designated GAM RNA, to target binding sites on GAM1068 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1068 target RNA, herein designated GAM TARGET RNA, into GAM1068 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16771] It is appreciated that GAM1068 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1068 target genes. The mRNA of each one of this plurality of GAM1068 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1068 RNA, herein designated GAM RNA, and which when bound by GAM1068 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1068 target proteins.

[16772] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1068 gene, herein designated GAM GENE, on one or more GAM1068 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16773] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1068 correlate with, and may be deduced from, the identity of the target genes which GAM1068 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16774] Nucleotide sequences of the GAM1068 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1068 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1068 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1068 are further described hereinbelow with reference to Table Table1.

[16775] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1068 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16776] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1069 (GAM1069) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16777] GAM1069 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1069 was detected is described hereinabove with reference to Figs. 2-8.

[16778] GAM1069 gene, herein designated GAM GENE, and GAM1069 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16779] GAM1069 gene, herein designated GAM GENE, encodes a GAM1069 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1069 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1069 precursor RNA is designated SEQ ID:1042, and is provided hereinbelow with reference to the sequence listing part.

[16780] GAM1069 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1069 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16781] An enzyme complex designated DICER COMPLEX, dices the GAM1069 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1069 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1069 RNA is designated SEQ ID:2718, and is provided hereinbelow with reference to the sequence listing part.

[16782] GAM1069 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1069 target RNA, herein designated GAM TARGET RNA. GAM1069 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16783] GAM1069 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1069 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1069 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1069 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1069 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16784] The complementary binding of GAM1069 RNA, herein designated GAM RNA, to target binding sites on GAM1069 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1069 target RNA, herein designated GAM TARGET RNA, into GAM1069 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16785] It is appreciated that GAM1069 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1069 target genes. The mRNA of each one of this plurality of GAM1069 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1069 RNA,

herein designated GAM RNA, and which when bound by GAM1069 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1069 target proteins.

[16786] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1069 gene, herein designated GAM GENE, on one or more GAM1069 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16787] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1069 correlate with, and may be deduced from, the identity of the target genes which

GAM1069 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16788] Nucleotide sequences of the GAM1069 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1069 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1069 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1069 are further described hereinbelow with reference to Table Table1.

[16789] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1069 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16790] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1070 (GAM1070) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16791] GAM1070 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1070 was detected is described hereinabove with reference to Figs. 2-8.

[16792] GAM1070 gene, herein designated GAM GENE, and GAM1070 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16793] GAM1070 gene, herein designated GAM GENE, encodes a GAM1070 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1070 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1070 precursor RNA is designated SEQ ID:1043, and is provided hereinbelow with reference to the sequence listing part.

[16794] GAM1070 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1070 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[16795] An enzyme complex designated DICER COMPLEX, dices the GAM1070 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1070 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1070 RNA is designated SEQ ID:2719, and is provided hereinbelow with reference to the sequence listing part.

[16796] GAM1070 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1070 target RNA, herein designated GAM TARGET RNA. GAM1070 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16797] GAM1070 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1070 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1070 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1070 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1070 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16798] The complementary binding of GAM1070 RNA, herein designated GAM RNA, to target binding sites on GAM1070 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1070 target RNA, herein designated GAM TARGET RNA, into GAM1070 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16799] It is appreciated that GAM1070 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1070 target genes. The mRNA of each one of this plurality of GAM1070 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1070 RNA, herein designated GAM RNA, and which when bound by GAM1070 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1070 target proteins.

[16800] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1070 gene, herein designated GAM GENE, on one or more GAM1070 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16801] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1070 correlate with, and may be deduced from, the identity of the target genes which GAM1070 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16802] Nucleotide sequences of the GAM1070 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1070 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1070 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1070 are further described hereinbelow with reference to Table Table1.

[16803] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1070 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16804] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1071 (GAM1071) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16805] GAM1071 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1071 was detected is described hereinabove with reference to Figs. 2-8.

[16806] GAM1071 gene, herein designated GAM GENE, and GAM1071 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16807] GAM1071 gene, herein designated GAM GENE, encodes a GAM1071 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1071 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1071 precursor RNA is designated SEQ ID:1044, and is provided hereinbelow with

reference to the sequence listing part.

[16808] GAM1071 has 13 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16809] SEQ ID:98641 detected in mouse EST Accession BI456668.1.

[16810] SEQ ID:98642 detected in mouse EST Accession BI694899.1.

[16811] SEQ ID:98643 detected in mouse EST Accession BI078155.1.

[16812] SEQ ID:98644 detected in mouse EST Accession BF159467.1.

[16813] SEQ ID:98645 detected in mouse EST Accession BI410352.1.

[16814] SEQ ID:98646 detected in mouse EST Accession BI905610.1.

[16815] SEQ ID:98647 detected in mouse EST Accession BI111937.1.

[16816] SEQ ID:98648 detected in mouse EST Accession BG077301.1.

[16817] SEQ ID:98649 detected in mouse EST Accession

BE572346.1.

[16818] SEQ ID:98650 detected in mouse EST Accession BI412346.1.

[16819] SEQ ID:98651 detected in mouse EST Accession BI904719.1.

[16820] SEQ ID:98652 detected in mouse EST Accession BI904322.1.

[16821] SEQ ID:98653 detected in mouse EST Accession BI904491.1.

[16822] GAM1071 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1071 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16823] An enzyme complex designated DICER COMPLEX, dices the GAM1071 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1071 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1071 RNA is designated SEQ ID:2720, and is provided hereinbelow with reference to the sequence listing part.

[16824] GAM1071 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1071 target RNA, herein designated GAM TARGET RNA. GAM1071 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16825] GAM1071 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1071 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1071 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1071 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1071 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16826] The complementary binding of GAM1071 RNA, herein designated GAM RNA, to target binding sites on GAM1071 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1071 target RNA, herein designated GAM TARGET RNA, into GAM1071 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16827] It is appreciated that GAM1071 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1071 target genes. The mRNA of each one of this plurality of GAM1071 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1071 RNA, herein designated GAM RNA, and which when bound by GAM1071 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1071 target proteins.

[16828] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1071 gene, herein designated GAM GENE, on one or more GAM1071 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16829] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1071 correlate with, and may be deduced from, the identity of the target genes which GAM1071 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16830] Nucleotide sequences of the GAM1071 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1071 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1071 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1071 are further described hereinbelow with reference to Table Table1.

[16831] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1071 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16832] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1072 (GAM1072) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16833] GAM1072 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1072 was detected is described hereinabove with reference to Figs. 2-8.

[16834] GAM1072 gene, herein designated GAM GENE, and GAM1072 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16835] GAM1072 gene, herein designated GAM GENE, encodes a GAM1072 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1072 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1072 precursor RNA is designated SEQ ID:1045, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1045 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[16836] GAM1072 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1072 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16837] An enzyme complex designated DICER COMPLEX, dices the GAM1072 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1072 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1072 RNA is designated SEQ ID:2721, and is provided hereinbelow with reference to the sequence listing part.

[16838] GAM1072 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1072 target RNA, herein designated GAM TARGET

RNA. GAM1072 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16839] GAM1072 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1072 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1072 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1072 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1072 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16840] The complementary binding of GAM1072 RNA, herein designated GAM RNA, to target binding sites on GAM1072 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1072 target RNA, herein designated GAM TARGET RNA, into GAM1072 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16841] It is appreciated that GAM1072 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1072 target genes. The mRNA of each one of this plurality of GAM1072 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1072 RNA, herein designated GAM RNA, and which when bound by GAM1072 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1072 target proteins.

[16842] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1072 gene, herein designated GAM GENE, on one or more GAM1072 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16843] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1072 correlate with, and may be deduced from, the identity of the target genes which GAM1072 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16844] Nucleotide sequences of the GAM1072 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1072 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1072 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1072 are further described hereinbelow with reference to Table Table1.

[16845] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1072 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16846] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1073 (GAM1073) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16847] GAM1073 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1073 was detected is described hereinabove with reference to Figs. 2-8.

[16848] GAM1073 gene, herein designated GAM GENE, and GAM1073 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16849] GAM1073 gene, herein designated GAM GENE, encodes a

GAM1073 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1073 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1073 precursor RNA is designated SEQ ID:1046, and is provided hereinbelow with reference to the sequence listing part.

[16850] GAM1073 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1073 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16851] An enzyme complex designated DICER COMPLEX, dices the GAM1073 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1073 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1073 RNA is designated SEQ ID:2722, and is provided hereinbelow with reference to the sequence listing part.

[16852] GAM1073 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1073 target RNA, herein designated GAM TARGET RNA. GAM1073 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16853] GAM1073 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1073 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1073 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1073 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1073 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16854] The complementary binding of GAM1073 RNA, herein designated GAM RNA, to target binding sites on GAM1073 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1073 target RNA, herein designated GAM TARGET RNA, into GAM1073 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16855] It is appreciated that GAM1073 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1073 target genes. The mRNA of each one of this plurality of GAM1073 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1073 RNA, herein designated GAM RNA, and which when bound by GAM1073 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1073 target proteins.

[16856] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1073 gene, herein designated GAM GENE, on one or more GAM1073 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[16857] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1073 correlate with, and may be deduced from, the identity of the target genes which GAM1073 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16858] Nucleotide sequences of the GAM1073 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1073 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1073 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1073 are further described hereinbelow with reference to Table Table1.

[16859] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1073 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16860] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1074 (GAM1074) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[16861] GAM1074 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1074 was detected is described hereinabove with reference to Figs. 2-8.

[16862] GAM1074 gene, herein designated GAM GENE, and GAM1074 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16863] GAM1074 gene, herein designated GAM GENE, encodes a GAM1074 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1074 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1074 precursor RNA is designated SEQ ID:1047, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1047 is located at position 881700 relative to contig NT_024812.8, on chromosome 16.

[16864] GAM1074 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1074 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16865] An enzyme complex designated DICER COMPLEX, dices the GAM1074 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1074 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1074 RNA is designated SEQ ID:2723, and is provided hereinbelow with reference to the sequence listing part.

[16866] GAM1074 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1074 target RNA, herein designated GAM TARGET RNA. GAM1074 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16867] GAM1074 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1074 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1074 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1074 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1074 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16868] The complementary binding of GAM1074 RNA, herein designated GAM RNA, to target binding sites on GAM1074 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1074 target RNA, herein designated GAM TARGET RNA, into GAM1074 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16869] It is appreciated that GAM1074 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1074 target genes. The mRNA of each one of this plurality of GAM1074 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1074 RNA, herein designated GAM RNA, and which when bound by GAM1074 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1074 target proteins.

[16870] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1074 gene, herein designated GAM GENE, on one or more GAM1074 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16871] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1074 correlate with, and may be deduced from, the identity of the target genes which GAM1074 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16872] Nucleotide sequences of the GAM1074 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1074 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1074 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1074 are further described hereinbelow with reference to Table Table1.

[16873] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1074 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16874] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1075 (GAM1075) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16875] GAM1075 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1075 was detected is described hereinabove with reference to Figs. 2-8.

[16876] GAM1075 gene, herein designated GAM GENE, and GAM1075 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16877] GAM1075 gene, herein designated GAM GENE, encodes a GAM1075 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1075 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1075 precursor RNA is designated SEQ ID:1048, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1048 is located at position 2215915 relative to contig NT_004852.13, on chromosome 1.

[16878] GAM1075 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1075 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16879] An enzyme complex designated DICER COMPLEX, dices the GAM1075 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1075 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1075 RNA is designated SEQ ID:2724, and is provided hereinbelow with reference to the sequence listing part.

[16880] GAM1075 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1075 target RNA, herein designated GAM TARGET RNA. GAM1075 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16881] GAM1075 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1075 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1075 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1075 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1075 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16882] The complementary binding of GAM1075 RNA, herein designated GAM RNA, to target binding sites on GAM1075 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1075 target RNA, herein designated GAM TARGET RNA, into GAM1075 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16883] It is appreciated that GAM1075 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1075 target genes. The mRNA of each one of this plurality of GAM1075 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1075 RNA, herein designated GAM RNA, and which when bound by GAM1075 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1075 target proteins.

[16884] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1075 gene, herein designated GAM GENE, on one or more GAM1075 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16885] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1075 correlate with, and may be deduced from, the identity of the target genes which GAM1075 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16886] Nucleotide sequences of the GAM1075 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1075 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1075 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1075 are further described hereinbelow with reference to Table Table1.

[16887] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1075 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16888] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1076 (GAM1076) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16889] GAM1076 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1076 was detected is described hereinabove with reference to Figs. 2-8.

[16890] GAM1076 gene, herein designated GAM GENE, and GAM1076 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16891] GAM1076 gene, herein designated GAM GENE, encodes a GAM1076 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1076 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1076 precursor RNA is designated SEQ ID:1049, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1049 is located at position 5263435 relative to contig NT_007819.11, on chromosome 7.

[16892] GAM1076 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1076 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16893] An enzyme complex designated DICER COMPLEX, dices the GAM1076 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1076 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1076 RNA is designated SEQ ID:2725, and is provided hereinbelow with reference to the sequence listing part.

[16894] GAM1076 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1076 target RNA, herein designated GAM TARGET

RNA. GAM1076 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16895] GAM1076 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1076 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1076 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1076 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1076 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16896] The complementary binding of GAM1076 RNA, herein designated GAM RNA, to target binding sites on GAM1076 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1076 target RNA, herein designated GAM TARGET RNA, into GAM1076 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16897] It is appreciated that GAM1076 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1076 target genes. The mRNA of each one of this plurality of GAM1076 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1076 RNA, herein designated GAM RNA, and which when bound by GAM1076 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1076 target proteins.

[16898] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1076 gene, herein designated GAM GENE, on one or more GAM1076 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16899] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1076 correlate with, and may be deduced from, the identity of the target genes which GAM1076 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16900] Nucleotide sequences of the GAM1076 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1076 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1076 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1076 are further described hereinbelow with reference to Table Table1.

[16901] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1076 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16902] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1077 (GAM1077) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16903] GAM1077 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1077 was detected is described hereinabove with reference to Figs. 2-8.

[16904] GAM1077 gene, herein designated GAM GENE, and GAM1077 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16905] GAM1077 gene, herein designated GAM GENE, encodes a

GAM1077 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1077 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1077 precursor RNA is designated SEQ ID:1050, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1050 is located at position 4467915 relative to contig NT_011109.13, on chromosome 19.

[16906] GAM1077 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16907] An enzyme complex designated DICER COMPLEX, dices the GAM1077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1077 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1077 RNA is designated SEQ ID:2726, and is provided hereinbelow with reference to the sequence listing part.

[16908] GAM1077 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1077 target RNA, herein designated GAM TARGET RNA. GAM1077 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16909] GAM1077 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1077 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1077 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1077 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1077 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16910] The complementary binding of GAM1077 RNA, herein designated GAM RNA, to target binding sites on GAM1077 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1077 target RNA, herein designated GAM TARGET RNA, into GAM1077 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16911] It is appreciated that GAM1077 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1077 target genes. The mRNA of each one of this plurality of GAM1077 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1077 RNA, herein designated GAM RNA, and which when bound by GAM1077 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1077 target proteins.

[16912] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1077 gene, herein designated GAM GENE, on one or more GAM1077 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16913] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1077 correlate with, and may be deduced from, the identity of the target genes which GAM1077 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16914] Nucleotide sequences of the GAM1077 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1077 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1077 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1077 are further described hereinbelow with reference to Table Table1.

[16915] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1077 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16916] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1078 (GAM1078) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16917] GAM1078 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1078 was detected is described hereinabove with reference to Figs. 2-8.

[16918] GAM1078 gene, herein designated GAM GENE, and GAM1078 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16919] GAM1078 gene, herein designated GAM GENE, encodes a GAM1078 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1078 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1078 precursor RNA is designated SEQ ID:1051, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1051 is located at position 2200668 relative to contig NT_010775.11, on chromosome 17.

[16920] GAM1078 has 2 highly conserved, expressed mouse ho-

mologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16921] SEQ ID:100320 detected in mouse EST Accession BB737686.1.

[16922] SEQ ID:100321 detected in mouse EST Accession BB734496.1.

[16923] GAM1078 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16924] An enzyme complex designated DICER COMPLEX, dices the GAM1078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1078 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1078 RNA is designated SEQ ID:2727, and is provided hereinbelow with reference to the sequence listing part.

[16925] GAM1078 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1078 target RNA, herein designated GAM TARGET RNA. GAM1078 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16926] GAM1078 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1078 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1078 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1078 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1078 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16927] The complementary binding of GAM1078 RNA, herein designated GAM RNA, to target binding sites on GAM1078 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1078 target RNA, herein designated GAM TARGET RNA, into GAM1078 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16928] It is appreciated that GAM1078 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1078 target genes. The mRNA of each one of this plurality of GAM1078 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1078 RNA, herein designated GAM RNA, and which when bound by GAM1078 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1078 target proteins.

[16929] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1078 gene, herein designated GAM GENE, on one or more GAM1078 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[16930] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1078 correlate with, and may be deduced from, the identity of the target genes which GAM1078 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16931] Nucleotide sequences of the GAM1078 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1078 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1078 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1078 are further described hereinbelow with reference to Table Table1.

[16932] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1078 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16933] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1079 (GAM1079) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[16934] GAM1079 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1079 was detected is described hereinabove with reference to Figs. 2-8.

[16935] GAM1079 gene, herein designated GAM GENE, and GAM1079 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16936] GAM1079 gene, herein designated GAM GENE, encodes a GAM1079 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1079 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1079 precursor RNA is designated SEQ ID:1052, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1052 is located at position 23535227 relative to contig NT_033899.3, on chromosome 11.

[16937] GAM1079 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences

of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[16938] SEQ ID:98654 detected in mouse EST Accession BE368829.1.

[16939] SEQ ID:98655 detected in mouse EST Accession BI714485.1.

[16940] GAM1079 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1079 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16941] An enzyme complex designated DICER COMPLEX, dices the GAM1079 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1079 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1079 RNA is designated SEQ ID:2728, and is provided hereinbelow with reference to the sequence listing part.

[16942] GAM1079 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1079 target RNA, herein designated GAM TARGET RNA. GAM1079 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16943] GAM1079 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1079 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1079 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1079 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1079 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16944] The complementary binding of GAM1079 RNA, herein designated GAM RNA, to target binding sites on GAM1079 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1079 target RNA, herein designated GAM TARGET RNA, into GAM1079 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16945] It is appreciated that GAM1079 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1079 target genes. The mRNA of each one of this plurality of GAM1079 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1079 RNA, herein designated GAM RNA, and which when bound by GAM1079 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1079 target proteins.

[16946] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1079 gene, herein designated GAM GENE, on one or more GAM1079 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16947] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1079 correlate with, and may be deduced from, the identity of the target genes which GAM1079 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16948] Nucleotide sequences of the GAM1079 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1079 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1079 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1079 are further described hereinbelow with reference to Table Table1.

[16949] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1079 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16950] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1080 (GAM1080) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16951] GAM1080 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1080 was detected is described hereinabove with reference to Figs. 2-8.

[16952] GAM1080 gene, herein designated GAM GENE, and GAM1080 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16953] GAM1080 gene, herein designated GAM GENE, encodes a GAM1080 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1080 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1080 precursor RNA is designated SEQ ID:1053, and is provided hereinbelow with reference to the sequence listing part.

[16954] GAM1080 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16955] An enzyme complex designated DICER COMPLEX, dices the GAM1080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1080 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1080 RNA is designated SEQ ID:2729, and is provided hereinbelow with reference to the sequence listing part.

[16956] GAM1080 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1080 target RNA, herein designated GAM TARGET RNA. GAM1080 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16957] GAM1080 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1080 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1080 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1080 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1080 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16958] The complementary binding of GAM1080 RNA, herein designated GAM RNA, to target binding sites on GAM1080

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1080 target RNA, herein designated GAM TARGET RNA, into GAM1080 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16959] It is appreciated that GAM1080 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1080 target genes. The mRNA of each one of this plurality of GAM1080 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1080 RNA, herein designated GAM RNA, and which when bound by GAM1080 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1080 target proteins.

[16960] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1080 gene, herein designated GAM GENE, on one or more GAM1080 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16961] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1080 correlate with, and may be deduced from, the identity of the target genes which GAM1080 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16962] Nucleotide sequences of the GAM1080 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1080 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1080 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1080 are further described hereinbelow with reference to Table Table1.

[16963] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1080 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16964] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1081 (GAM1081) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16965] GAM1081 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1081 was detected is described hereinabove with reference to Figs. 2-8.

[16966] GAM1081 gene, herein designated GAM GENE, and GAM1081 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16967] GAM1081 gene, herein designated GAM GENE, encodes a GAM1081 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1081 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1081 precursor RNA is designated SEQ ID:1054, and is provided hereinbelow with reference to the sequence listing part.

[16968] GAM1081 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16969] An enzyme complex designated DICER COMPLEX, dices the GAM1081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1081 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1081 RNA is designated SEQ ID:2730, and

is provided hereinbelow with reference to the sequence listing part.

[16970] GAM1081 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1081 target RNA, herein designated GAM TARGET RNA. GAM1081 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16971] GAM1081 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1081 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1081 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1081 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1081 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16972] The complementary binding of GAM1081 RNA, herein designated GAM RNA, to target binding sites on GAM1081 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1081 target RNA, herein designated GAM TARGET RNA, into GAM1081 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16973] It is appreciated that GAM1081 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1081 target genes. The mRNA of each one of this plurality of GAM1081 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1081 RNA, herein designated GAM RNA, and which when bound by

GAM1081 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1081 target proteins.

[16974] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1081 gene, herein designated GAM GENE, on one or more GAM1081 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16975] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1081 correlate with, and may be deduced from, the identity of the target genes which GAM1081 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[16976] Nucleotide sequences of the GAM1081 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1081 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1081 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1081 are further described hereinbelow with reference to Table Table1.

[16977] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1081 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[16978] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1082 (GAM1082) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16979] GAM1082 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1082 was detected is described hereinabove

with reference to Figs. 2-8.

[16980] GAM1082 gene, herein designated GAM GENE, and GAM1082 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16981] GAM1082 gene, herein designated GAM GENE, encodes a GAM1082 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1082 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1082 precursor RNA is designated SEQ ID:1055, and is provided hereinbelow with reference to the sequence listing part.

[16982] GAM1082 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16983] An enzyme complex designated DICER COMPLEX, dices the GAM1082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1082 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1082 RNA is designated SEQ ID:2731, and is provided hereinbelow with reference to the sequence listing part.

[16984] GAM1082 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1082 target RNA, herein designated GAM TARGET RNA. GAM1082 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16985] GAM1082 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1082 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1082 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1082 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1082 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[16986] The complementary binding of GAM1082 RNA, herein designated GAM RNA, to target binding sites on GAM1082 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1082 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1082 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[16987] It is appreciated that GAM1082 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1082 target genes. The mRNA of each one of this plurality of GAM1082 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1082 RNA, herein designated GAM RNA, and which when bound by GAM1082 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1082 target proteins.

[16988] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1082 gene, herein designated GAM GENE, on one or more GAM1082 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[16989] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1082 correlate with, and may be deduced from, the identity of the target genes which GAM1082 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[16990] Nucleotide sequences of the GAM1082 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1082 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1082 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1082 are further described hereinbelow with reference to Table Table1.

[16991] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1082 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[16992] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1083 (GAM1083) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[16993] GAM1083 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1083 was detected is described hereinabove with reference to Figs. 2-8.

[16994] GAM1083 gene, herein designated GAM GENE, and GAM1083 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[16995] GAM1083 gene, herein designated GAM GENE, encodes a GAM1083 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1083 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1083 precursor RNA is designated SEQ ID:1056, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1056 is located at position 5432875 relative to contig NT_034880.2, on chromosome 6.

[16996] GAM1083 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[16997] An enzyme complex designated DICER COMPLEX, dices the GAM1083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1083 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1083 RNA is designated SEQ ID:2732, and is provided hereinbelow with reference to the sequence

listing part.

[16998] GAM1083 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1083 target RNA, herein designated GAM TARGET RNA. GAM1083 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[16999] GAM1083 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1083 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1083 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1083 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1083 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17000] The complementary binding of GAM1083 RNA, herein designated GAM RNA, to target binding sites on GAM1083 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1083 target RNA, herein designated GAM TARGET RNA, into GAM1083 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17001] It is appreciated that GAM1083 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1083 target genes. The mRNA of each one of this plurality of GAM1083 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1083 RNA, herein designated GAM RNA, and which when bound by GAM1083 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1083 target proteins.

[17002] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1083 gene, herein designated GAM GENE, on one or more GAM1083 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17003] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1083 correlate with, and may be deduced from, the identity of the target genes which GAM1083 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17004] Nucleotide sequences of the GAM1083 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1083 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1083 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1083 are further described hereinbelow with reference to Table Table1.

[17005] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1083 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17006] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1084 (GAM1084) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17007] GAM1084 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1084 was detected is described hereinabove with reference to Figs. 2-8.

[17008] GAM1084 gene, herein designated GAM GENE, and GAM1084 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17009] GAM1084 gene, herein designated GAM GENE, encodes a GAM1084 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1084 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1084 precursor RNA is designated SEQ ID:1057, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1057 is located at position 463779 relative to contig NT_011799.10, on chromosome X.

[17010] GAM1084 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1084 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[17011] An enzyme complex designated DICER COMPLEX, dices the GAM1084 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1084 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 97%) nucleotide sequence of GAM1084 RNA is designated SEQ ID:2733, and is provided hereinbelow with reference to the sequence listing part.

[17012] GAM1084 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1084 target RNA, herein designated GAM TARGET RNA. GAM1084 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17013] GAM1084 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1084 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1084 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1084 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1084 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17014] The complementary binding of GAM1084 RNA, herein designated GAM RNA, to target binding sites on GAM1084 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1084 target RNA, herein designated GAM TARGET RNA, into GAM1084 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17015] It is appreciated that GAM1084 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1084 target genes. The mRNA of each one of this plurality of GAM1084 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1084 RNA, herein designated GAM RNA, and which when bound by GAM1084 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1084 target proteins.

[17016] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1084 gene, herein designated GAM GENE, on one or more GAM1084 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17017] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1084 correlate with, and may be deduced from, the identity of the target genes which GAM1084 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17018] Nucleotide sequences of the GAM1084 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1084 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1084 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1084 are further described hereinbelow with reference to Table Table1.

[17019] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1084 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17020] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1085 (GAM1085) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17021] GAM1085 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1085 was detected is described hereinabove with reference to Figs. 2-8.

[17022] GAM1085 gene, herein designated GAM GENE, and GAM1085 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17023] GAM1085 gene, herein designated GAM GENE, encodes a GAM1085 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1085 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1085 precursor RNA is designated SEQ ID:1058, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1058 is located at position 2349689 relative to contig NT_021907.13, on chromosome 1.

[17024] GAM1085 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17025] An enzyme complex designated DICER COMPLEX, dices the GAM1085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1085 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1085 RNA is designated SEQ ID:2734, and

is provided hereinbelow with reference to the sequence listing part.

[17026] GAM1085 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1085 target RNA, herein designated GAM TARGET RNA. GAM1085 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17027] GAM1085 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1085 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1085 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1085 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1085 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17028] The complementary binding of GAM1085 RNA, herein designated GAM RNA, to target binding sites on GAM1085 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1085 target RNA, herein designated GAM TARGET RNA, into GAM1085 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17029] It is appreciated that GAM1085 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1085 target genes. The mRNA of each one of this plurality of GAM1085 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1085 RNA, herein designated GAM RNA, and which when bound by

GAM1085 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1085 target proteins.

[17030] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1085 gene, herein designated GAM GENE, on one or more GAM1085 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17031] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1085 correlate with, and may be deduced from, the identity of the target genes which GAM1085 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[17032] Nucleotide sequences of the GAM1085 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1085 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1085 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1085 are further described hereinbelow with reference to Table Table1.

[17033] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1085 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17034] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1086 (GAM1086) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17035] GAM1086 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1086 was detected is described hereinabove

with reference to Figs. 2-8.

[17036] GAM1086 gene, herein designated GAM GENE, and GAM1086 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17037] GAM1086 gene, herein designated GAM GENE, encodes a GAM1086 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1086 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1086 precursor RNA is designated SEQ ID:1059, and is provided hereinbelow with reference to the sequence listing part.

[17038] GAM1086 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1086 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17039] An enzyme complex designated DICER COMPLEX, dices the GAM1086 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1086 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1086 RNA is designated SEQ ID:2735, and is provided hereinbelow with reference to the sequence listing part.

[17040] GAM1086 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1086 target RNA, herein designated GAM TARGET RNA. GAM1086 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17041] GAM1086 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1086 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1086 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1086 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1086 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17042] The complementary binding of GAM1086 RNA, herein designated GAM RNA, to target binding sites on GAM1086 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1086 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1086 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17043] It is appreciated that GAM1086 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1086 target genes. The mRNA of each one of this plurality of GAM1086 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1086 RNA, herein designated GAM RNA, and which when bound by GAM1086 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1086 target proteins.

[17044] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1086 gene, herein designated GAM GENE, on one or more GAM1086 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17045] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1086 correlate with, and may be deduced from, the identity of the target genes which GAM1086 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17046] Nucleotide sequences of the GAM1086 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1086 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1086 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1086 are further described hereinbelow with reference to Table Table1.

[17047] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1086 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[17048] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1087 (GAM1087) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17049] GAM1087 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1087 was detected is described hereinabove with reference to Figs. 2-8.

[17050] GAM1087 gene, herein designated GAM GENE, and GAM1087 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17051] GAM1087 gene, herein designated GAM GENE, encodes a GAM1087 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1087 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1087 precursor RNA is designated SEQ ID:1060, and is provided hereinbelow with reference to the sequence listing part.

[17052] GAM1087 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17053] An enzyme complex designated DICER COMPLEX, dices the GAM1087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1087 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1087 RNA is designated SEQ ID:2736, and is provided hereinbelow with reference to the sequence listing part.

[17054] GAM1087 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1087 target RNA, herein designated GAM TARGET RNA. GAM1087 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17055] GAM1087 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1087 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1087 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1087 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1087 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17056] The complementary binding of GAM1087 RNA, herein designated GAM RNA, to target binding sites on GAM1087 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1087 target RNA, herein designated GAM TARGET RNA, into GAM1087 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17057] It is appreciated that GAM1087 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1087 target genes. The mRNA of each one of this plurality of GAM1087 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1087 RNA, herein designated GAM RNA, and which when bound by GAM1087 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1087 target proteins.

[17058] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1087 gene, herein designated GAM GENE, on one or more GAM1087 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17059] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1087 correlate with, and may be deduced from, the identity of the target genes which GAM1087 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17060] Nucleotide sequences of the GAM1087 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1087 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1087 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1087 are further described hereinbelow with reference to Table Table1.

[17061] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1087 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17062] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1088 (GAM1088) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17063] GAM1088 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1088 was detected is described hereinabove with reference to Figs. 2-8.

[17064] GAM1088 gene, herein designated GAM GENE, and GAM1088 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[17065] GAM1088 gene, herein designated GAM GENE, encodes a GAM1088 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1088 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1088 precursor RNA is designated SEQ ID:1061, and is provided hereinbelow with reference to the sequence listing part.

[17066] GAM1088 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[17067] SEQ ID:98221 detected in mouse EST Accession BI657852.1.

[17068] SEQ ID:98222 detected in mouse EST Accession AI463876.1.

[17069] GAM1088 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17070] An enzyme complex designated DICER COMPLEX, dices the GAM1088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1088 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1088 RNA is designated SEQ ID:2737, and is provided hereinbelow with reference to the sequence listing part.

[17071] GAM1088 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1088 target RNA, herein designated GAM TARGET RNA. GAM1088 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17072] GAM1088 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1088 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1088 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1088 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1088 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[17073] The complementary binding of GAM1088 RNA, herein designated GAM RNA, to target binding sites on GAM1088 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1088 target RNA, herein designated GAM TARGET RNA, into GAM1088 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17074] It is appreciated that GAM1088 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1088 target genes. The mRNA of each one of this plurality of GAM1088 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1088 RNA, herein designated GAM RNA, and which when bound by GAM1088 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1088 target proteins.

[17075] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1088 gene, herein designated GAM GENE, on one or

more GAM1088 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17076] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1088 correlate with, and may be deduced from, the identity of the target genes which GAM1088 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17077] Nucleotide sequences of the GAM1088 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1088 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1088 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1088 are further de-

scribed hereinbelow with reference to Table Table1.

[17078] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1088 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17079] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1089 (GAM1089) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17080] GAM1089 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1089 was detected is described hereinabove with reference to Figs. 2-8.

[17081] GAM1089 gene, herein designated GAM GENE, and GAM1089 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17082] GAM1089 gene, herein designated GAM GENE, encodes a GAM1089 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1089 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1089 precursor RNA is designated SEQ ID:1062, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1062 is located at position 2145124 relative to contig NT_028310.8, on chromosome 11.

[17083] GAM1089 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17084] An enzyme complex designated DICER COMPLEX, dices the GAM1089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1089 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1089 RNA is designated SEQ ID:2738, and is provided hereinbelow with reference to the sequence listing part.

[17085] GAM1089 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1089 target RNA, herein designated GAM TARGET RNA. GAM1089 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17086] GAM1089 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1089 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1089 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1089 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1089 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17087] The complementary binding of GAM1089 RNA, herein designated GAM RNA, to target binding sites on GAM1089 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1089 target RNA, herein designated GAM TARGET RNA, into GAM1089 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17088] It is appreciated that GAM1089 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1089 target genes. The mRNA of each one of this plurality of GAM1089 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1089 RNA, herein designated GAM RNA, and which when bound by GAM1089 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1089 target proteins.

[17089] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1089 gene, herein designated GAM GENE, on one or more GAM1089 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[17090] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1089 correlate with, and may be deduced from, the identity of the target genes which GAM1089 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17091] Nucleotide sequences of the GAM1089 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1089 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1089 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1089 are further described hereinbelow with reference to Table Table1.

[17092] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1089 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17093] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1090 (GAM1090) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[17094] GAM1090 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1090 was detected is described hereinabove with reference to Figs. 2-8.

[17095] GAM1090 gene, herein designated GAM GENE, and GAM1090 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17096] GAM1090 gene, herein designated GAM GENE, encodes a GAM1090 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1090 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1090 precursor RNA is designated SEQ ID:1063, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1063 is located at position 160795 relative to contig NT_010748.10, on chromosome 17.

[17097] GAM1090 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1090 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17098] An enzyme complex designated DICER COMPLEX, dices the GAM1090 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1090 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1090 RNA is designated SEQ ID:2739, and is provided hereinbelow with reference to the sequence listing part.

[17099] GAM1090 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1090 target RNA, herein designated GAM TARGET RNA. GAM1090 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17100] GAM1090 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1090 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1090 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1090 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1090 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17101] The complementary binding of GAM1090 RNA, herein designated GAM RNA, to target binding sites on GAM1090 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1090 target RNA, herein designated GAM TARGET RNA, into GAM1090 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17102] It is appreciated that GAM1090 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1090 target genes. The mRNA of each one of this plurality of GAM1090 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1090 RNA, herein designated GAM RNA, and which when bound by GAM1090 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1090 target proteins.

[17103] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1090 gene, herein designated GAM GENE, on one or more GAM1090 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17104] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1090 correlate with, and may be deduced from, the identity of the target genes which GAM1090 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17105] Nucleotide sequences of the GAM1090 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1090 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1090 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1090 are further described hereinbelow with reference to Table Table1.

[17106] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1090 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17107] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1091 (GAM1091) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17108] GAM1091 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1091 was detected is described hereinabove with reference to Figs. 2-8.

[17109] GAM1091 gene, herein designated GAM GENE, and GAM1091 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17110] GAM1091 gene, herein designated GAM GENE, encodes a GAM1091 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1091 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1091 precursor RNA is designated SEQ ID:1064, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1064 is located at position 8457428 relative to contig NT_016354.13, on chromosome 4.

[17111] GAM1091 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17112] An enzyme complex designated DICER COMPLEX, dices the GAM1091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1091 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1091 RNA is designated SEQ ID:2740, and is provided hereinbelow with reference to the sequence listing part.

[17113] GAM1091 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1091 target RNA, herein designated GAM TARGET RNA. GAM1091 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17114] GAM1091 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1091 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1091 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1091 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1091 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17115] The complementary binding of GAM1091 RNA, herein designated GAM RNA, to target binding sites on GAM1091 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1091 target RNA, herein designated GAM TARGET RNA, into GAM1091 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17116] It is appreciated that GAM1091 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1091 target genes. The mRNA of each one of this plurality of GAM1091 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1091 RNA, herein designated GAM RNA, and which when bound by GAM1091 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1091 target proteins.

[17117] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1091 gene, herein designated GAM GENE, on one or more GAM1091 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17118] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1091 correlate with, and may be deduced from, the identity of the target genes which GAM1091 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17119] Nucleotide sequences of the GAM1091 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1091 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1091 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1091 are further described hereinbelow with reference to Table Table1.

[17120] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1091 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17121] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1092 (GAM1092) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17122] GAM1092 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1092 was detected is described hereinabove with reference to Figs. 2-8.

[17123] GAM1092 gene, herein designated GAM GENE, and GAM1092 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17124] GAM1092 gene, herein designated GAM GENE, encodes a GAM1092 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1092 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1092 precursor RNA is designated SEQ ID:1065, and is provided hereinbelow with reference to the sequence listing part.

[17125] GAM1092 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1092 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17126] An enzyme complex designated DICER COMPLEX, dices the GAM1092 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1092 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1092 RNA is designated SEQ ID:2741, and is provided hereinbelow with reference to the sequence listing part.

[17127] GAM1092 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1092 target RNA, herein designated GAM TARGET RNA. GAM1092 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17128] GAM1092 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1092 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1092 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1092 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1092 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[17129] The complementary binding of GAM1092 RNA, herein designated GAM RNA, to target binding sites on GAM1092 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1092 target RNA, herein designated GAM TARGET RNA, into GAM1092 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17130] It is appreciated that GAM1092 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1092 target genes. The mRNA of each one of this plurality of GAM1092 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1092 RNA, herein designated GAM RNA, and which when bound by GAM1092 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1092 target proteins.

[17131] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1092 gene, herein designated GAM GENE, on one or

more GAM1092 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17132] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1092 correlate with, and may be deduced from, the identity of the target genes which GAM1092 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17133] Nucleotide sequences of the GAM1092 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1092 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1092 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1092 are further de-

scribed hereinbelow with reference to Table Table1.

[17134] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1092 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17135] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1093 (GAM1093) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17136] GAM1093 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1093 was detected is described hereinabove with reference to Figs. 2-8.

[17137] GAM1093 gene, herein designated GAM GENE, and GAM1093 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17138] GAM1093 gene, herein designated GAM GENE, encodes a GAM1093 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1093 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1093 precursor RNA is designated SEQ ID:1066, and is provided hereinbelow with reference to the sequence listing part.

[17139] GAM1093 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1093 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17140] An enzyme complex designated DICER COMPLEX, dices the GAM1093 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1093 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1093 RNA is designated SEQ ID:2742, and is provided hereinbelow with reference to the sequence listing part.

[17141] GAM1093 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1093 target RNA, herein designated GAM TARGET RNA. GAM1093 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17142] GAM1093 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1093 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1093 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1093 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1093 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17143] The complementary binding of GAM1093 RNA, herein designated GAM RNA, to target binding sites on GAM1093 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1093 target RNA, herein designated GAM TARGET RNA, into GAM1093 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17144] It is appreciated that GAM1093 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1093 target genes. The mRNA of each one of this plurality of GAM1093 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1093 RNA, herein designated GAM RNA, and which when bound by GAM1093 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1093 target proteins.

[17145] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1093 gene, herein designated GAM GENE, on one or more GAM1093 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17146] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1093 correlate with, and may be deduced from, the identity of the target genes which GAM1093 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17147] Nucleotide sequences of the GAM1093 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1093 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1093 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1093 are further described hereinbelow with reference to Table Table1.

[17148] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1093 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17149] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1094 (GAM1094) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17150] GAM1094 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1094 was detected is described hereinabove with reference to Figs. 2-8.

[17151] GAM1094 gene, herein designated GAM GENE, and GAM1094 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17152] GAM1094 gene, herein designated GAM GENE, encodes a GAM1094 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1094 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1094 precursor RNA is designated SEQ ID:1067, and is provided hereinbelow with reference to the sequence listing part.

[17153] GAM1094 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1094 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17154] An enzyme complex designated DICER COMPLEX, dices the GAM1094 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1094 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1094 RNA is designated SEQ ID:2743, and is provided hereinbelow with reference to the sequence listing part.

[17155] GAM1094 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1094 target RNA, herein designated GAM TARGET RNA. GAM1094 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17156] GAM1094 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1094 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1094 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1094 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1094 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17157] The complementary binding of GAM1094 RNA, herein designated GAM RNA, to target binding sites on GAM1094

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1094 target RNA, herein designated GAM TARGET RNA, into GAM1094 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17158] It is appreciated that GAM1094 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1094 target genes. The mRNA of each one of this plurality of GAM1094 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1094 RNA, herein designated GAM RNA, and which when bound by GAM1094 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1094 target proteins.

[17159] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1094 gene, herein designated GAM GENE, on one or more GAM1094 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17160] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1094 correlate with, and may be deduced from, the identity of the target genes which GAM1094 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17161] Nucleotide sequences of the GAM1094 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1094 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1094 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1094 are further described hereinbelow with reference to Table Table1.

[17162] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1094 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17163] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1095 (GAM1095) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17164] GAM1095 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1095 was detected is described hereinabove with reference to Figs. 2-8.

[17165] GAM1095 gene, herein designated GAM GENE, and GAM1095 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17166] GAM1095 gene, herein designated GAM GENE, encodes a GAM1095 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1095 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1095 precursor RNA is designated SEQ ID:1068, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1068 is located at position 1364370 relative to contig NT_035014.2, on chromosome 9.

[17167] GAM1095 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1095 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17168] An enzyme complex designated DICER COMPLEX, dices the GAM1095 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1095 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1095 RNA is designated SEQ ID:2744, and is provided hereinbelow with reference to the sequence listing part.

[17169] GAM1095 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1095 target RNA, herein designated GAM TARGET RNA. GAM1095 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17170] GAM1095 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1095 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1095 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1095 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1095 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17171] The complementary binding of GAM1095 RNA, herein designated GAM RNA, to target binding sites on GAM1095 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1095 target RNA, herein designated GAM TARGET RNA, into GAM1095 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17172] It is appreciated that GAM1095 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1095 target genes. The mRNA of each one of this plurality of GAM1095 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1095 RNA, herein designated GAM RNA, and which when bound by GAM1095 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1095 target proteins.

[17173] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1095 gene, herein designated GAM GENE, on one or more GAM1095 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17174] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1095 correlate with, and may

be deduced from, the identity of the target genes which GAM1095 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17175] Nucleotide sequences of the GAM1095 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1095 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1095 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1095 are further described hereinbelow with reference to Table Table1.

[17176] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1095 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17177] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1096 (GAM1096) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17178] GAM1096 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1096 was detected is described hereinabove with reference to Figs. 2-8.

[17179] GAM1096 gene, herein designated GAM GENE, and GAM1096 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17180] GAM1096 gene, herein designated GAM GENE, encodes a GAM1096 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1096 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1096 precursor RNA is designated SEQ ID:1069, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1069 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[17181] GAM1096 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1096 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17182] An enzyme complex designated DICER COMPLEX, dices the GAM1096 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1096 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1096 RNA is designated SEQ ID:2745, and is provided hereinbelow with reference to the sequence listing part.

[17183] GAM1096 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1096 target RNA, herein designated GAM TARGET RNA. GAM1096 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[17184] GAM1096 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1096 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1096 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1096 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1096 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17185] The complementary binding of GAM1096 RNA, herein

designated GAM RNA, to target binding sites on GAM1096 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1096 target RNA, herein designated GAM TARGET RNA, into GAM1096 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17186] It is appreciated that GAM1096 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1096 target genes. The mRNA of each one of this plurality of GAM1096 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1096 RNA, herein designated GAM RNA, and which when bound by GAM1096 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1096 target proteins.

[17187] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1096 gene, herein designated GAM GENE, on one or more GAM1096 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17188] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1096 correlate with, and may be deduced from, the identity of the target genes which GAM1096 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17189] Nucleotide sequences of the GAM1096 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1096 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1096 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1096 are further described hereinbelow with reference to Table Table1.

[17190] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1096 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17191] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1097 (GAM1097) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17192] GAM1097 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1097 was detected is described hereinabove with reference to Figs. 2-8.

[17193] GAM1097 gene, herein designated GAM GENE, and GAM1097 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17194] GAM1097 gene, herein designated GAM GENE, encodes a GAM1097 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1097 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1097 precursor RNA is designated SEQ ID:1070, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1070 is located at position 3113933 relative to contig NT_030737.5, on chromosome 8.

[17195] GAM1097 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1097 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17196] An enzyme complex designated DICER COMPLEX, dices the GAM1097 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1097 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1097 RNA is designated SEQ ID:2746, and is provided hereinbelow with reference to the sequence listing part.

[17197] GAM1097 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1097 target RNA, herein designated GAM TARGET RNA. GAM1097 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17198] GAM1097 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1097 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1097 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1097 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1097 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17199] The complementary binding of GAM1097 RNA, herein designated GAM RNA, to target binding sites on GAM1097 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1097 target RNA, herein designated GAM TARGET RNA, into GAM1097 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17200] It is appreciated that GAM1097 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1097 target genes. The mRNA of each one of this plurality of GAM1097 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1097 RNA, herein designated GAM RNA, and which when bound by GAM1097 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1097 target proteins.

[17201] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1097 gene, herein designated GAM GENE, on one or more GAM1097 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17202] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1097 correlate with, and may be deduced from, the identity of the target genes which GAM1097 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17203] Nucleotide sequences of the GAM1097 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1097 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1097 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1097 are further described hereinbelow with reference to Table Table1.

[17204] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1097 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17205] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1098 (GAM1098) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17206] GAM1098 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1098 was detected is described hereinabove with reference to Figs. 2-8.

[17207] GAM1098 gene, herein designated GAM GENE, and GAM1098 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17208] GAM1098 gene, herein designated GAM GENE, encodes a GAM1098 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1098 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1098 precursor RNA is designated SEQ ID:1071, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1071 is located at position 4851356 relative to contig NT_022517.13, on chromosome 3.

[17209] GAM1098 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17210] An enzyme complex designated DICER COMPLEX, dices the GAM1098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1098 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1098 RNA is designated SEQ ID:2747, and is provided hereinbelow with reference to the sequence listing part.

[17211] GAM1098 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1098 target RNA, herein designated GAM TARGET RNA. GAM1098 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17212] GAM1098 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1098 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1098 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1098 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1098 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17213] The complementary binding of GAM1098 RNA, herein designated GAM RNA, to target binding sites on GAM1098 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1098 target RNA, herein designated GAM TARGET RNA, into GAM1098 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17214] It is appreciated that GAM1098 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1098 target genes. The mRNA of each one of this plurality of GAM1098 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1098 RNA, herein designated GAM RNA, and which when bound by GAM1098 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1098 target proteins.

[17215] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1098 gene, herein designated GAM GENE, on one or more GAM1098 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17216] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1098 correlate with, and may be deduced from, the identity of the target genes which GAM1098 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17217] Nucleotide sequences of the GAM1098 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1098 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1098 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1098 are further described hereinbelow with reference to Table Table1.

[17218] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1098 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17219] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1099 (GAM1099) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17220] GAM1099 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1099 was detected is described hereinabove with reference to Figs. 2-8.

[17221] GAM1099 gene, herein designated GAM GENE, and GAM1099 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17222] GAM1099 gene, herein designated GAM GENE, encodes a GAM1099 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1099 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1099 precursor RNA is designated SEQ ID:1072, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1072 is located at position 4792981 relative to contig NT_033968.2, on chromosome 7.

[17223] GAM1099 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17224] An enzyme complex designated DICER COMPLEX, dices the GAM1099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1099 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1099 RNA is designated SEQ ID:2748, and is provided hereinbelow with reference to the sequence listing part.

[17225] GAM1099 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1099 target RNA, herein designated GAM TARGET RNA. GAM1099 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17226] GAM1099 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1099 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1099 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1099 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1099 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17227] The complementary binding of GAM1099 RNA, herein designated GAM RNA, to target binding sites on GAM1099 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1099 target RNA, herein designated GAM TARGET RNA, into GAM1099 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17228] It is appreciated that GAM1099 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1099 target genes. The mRNA of each one of this

plurality of GAM1099 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1099 RNA, herein designated GAM RNA, and which when bound by GAM1099 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1099 target proteins.

[17229] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1099 gene, herein designated GAM GENE, on one or more GAM1099 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17230] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1099 correlate with, and may be deduced from, the identity of the target genes which GAM1099 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17231] Nucleotide sequences of the GAM1099 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1099 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1099 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1099 are further described hereinbelow with reference to Table Table1.

[17232] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1099 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17233] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1100 (GAM1100) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[17234] GAM1100 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1100 was detected is described hereinabove with reference to Figs. 2-8.

[17235] GAM1100 gene, herein designated GAM GENE, and GAM1100 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17236] GAM1100 gene, herein designated GAM GENE, encodes a GAM1100 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1100 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1100 precursor RNA is designated SEQ ID:1073, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1073 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[17237] GAM1100 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17238] An enzyme complex designated DICER COMPLEX, dices the GAM1100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1100 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1100 RNA is designated SEQ ID:2749, and is provided hereinbelow with reference to the sequence listing part.

[17239] GAM1100 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1100 target RNA, herein designated GAM TARGET RNA. GAM1100 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17240] GAM1100 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1100 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1100 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1100 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1100 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[17241] The complementary binding of GAM1100 RNA, herein designated GAM RNA, to target binding sites on GAM1100 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1100 target RNA, herein designated GAM TARGET RNA, into GAM1100 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17242] It is appreciated that GAM1100 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1100 target genes. The mRNA of each one of this plurality of GAM1100 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1100 RNA, herein designated GAM RNA, and which when bound by GAM1100 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1100 target proteins.

[17243] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1100 gene, herein designated GAM GENE, on one or

more GAM1100 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17244] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1100 correlate with, and may be deduced from, the identity of the target genes which GAM1100 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17245] Nucleotide sequences of the GAM1100 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1100 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1100 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1100 are further de-

scribed hereinbelow with reference to Table Table1.

[17246] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1100 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17247] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1101 (GAM1101) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17248] GAM1101 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1101 was detected is described hereinabove with reference to Figs. 2-8.

[17249] GAM1101 gene, herein designated GAM GENE, and GAM1101 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17250] GAM1101 gene, herein designated GAM GENE, encodes a GAM1101 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1101 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1101 precursor RNA is designated SEQ ID:1074, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1074 is located at position 677944 relative to contig NT_011176.13, on chromosome 19.

[17251] GAM1101 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17252] An enzyme complex designated DICER COMPLEX, dices the GAM1101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1101 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1101 RNA is designated SEQ ID:2750, and is provided hereinbelow with reference to the sequence listing part.

[17253] GAM1101 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1101 target RNA, herein designated GAM TARGET RNA. GAM1101 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17254] GAM1101 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1101 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1101 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1101 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1101 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17255] The complementary binding of GAM1101 RNA, herein designated GAM RNA, to target binding sites on GAM1101 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1101 target RNA, herein designated GAM TARGET RNA, into GAM1101 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17256] It is appreciated that GAM1101 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1101 target genes. The mRNA of each one of this plurality of GAM1101 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1101 RNA, herein designated GAM RNA, and which when bound by GAM1101 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1101 target proteins.

[17257] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1101 gene, herein designated GAM GENE, on one or more GAM1101 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[17258] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1101 correlate with, and may be deduced from, the identity of the target genes which GAM1101 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17259] Nucleotide sequences of the GAM1101 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1101 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1101 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1101 are further described hereinbelow with reference to Table Table1.

[17260] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1101 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17261] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1102 (GAM1102) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[17262] GAM1102 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1102 was detected is described hereinabove with reference to Figs. 2-8.

[17263] GAM1102 gene, herein designated GAM GENE, and GAM1102 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17264] GAM1102 gene, herein designated GAM GENE, encodes a GAM1102 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1102 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1102 precursor RNA is designated SEQ ID:1075, and is provided hereinbelow with reference to the sequence listing part.

[17265] GAM1102 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17266] An enzyme complex designated DICER COMPLEX, dices the GAM1102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1102 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1102 RNA is designated SEQ ID:2751, and is provided hereinbelow with reference to the sequence listing part.

[17267] GAM1102 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1102 target RNA, herein designated GAM TARGET RNA. GAM1102 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17268] GAM1102 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1102 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1102 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1102 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1102 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17269] The complementary binding of GAM1102 RNA, herein designated GAM RNA, to target binding sites on GAM1102 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1102 target RNA, herein designated GAM TARGET RNA, into GAM1102 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17270] It is appreciated that GAM1102 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1102 target genes. The mRNA of each one of this plurality of GAM1102 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1102 RNA, herein designated GAM RNA, and which when bound by GAM1102 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1102 target proteins.

[17271] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1102 gene, herein designated GAM GENE, on one or more GAM1102 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17272] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1102 correlate with, and may be deduced from, the identity of the target genes which GAM1102 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17273] Nucleotide sequences of the GAM1102 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1102 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1102 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1102 are further described hereinbelow with reference to Table Table1.

[17274] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1102 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17275] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1103 (GAM1103) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17276] GAM1103 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1103 was detected is described hereinabove with reference to Figs. 2-8.

[17277] GAM1103 gene, herein designated GAM GENE, and GAM1103 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17278] GAM1103 gene, herein designated GAM GENE, encodes a GAM1103 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1103 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1103 precursor RNA is designated SEQ ID:1076, and is provided hereinbelow with reference to the sequence listing part.

[17279] GAM1103 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1103 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17280] An enzyme complex designated DICER COMPLEX, dices the GAM1103 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1103 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1103 RNA is designated SEQ ID:2752, and is provided hereinbelow with reference to the sequence listing part.

[17281] GAM1103 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1103 target RNA, herein designated GAM TARGET RNA. GAM1103 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17282] GAM1103 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1103 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1103 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1103 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1103 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17283] The complementary binding of GAM1103 RNA, herein designated GAM RNA, to target binding sites on GAM1103 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1103 target RNA, herein designated GAM TARGET RNA, into GAM1103 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17284] It is appreciated that GAM1103 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1103 target genes. The mRNA of each one of this plurality of GAM1103 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1103 RNA, herein designated GAM RNA, and which when bound by GAM1103 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1103 target proteins.

[17285] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1103 gene, herein designated GAM GENE, on one or more GAM1103 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17286] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1103 correlate with, and may

be deduced from, the identity of the target genes which GAM1103 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17287] Nucleotide sequences of the GAM1103 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1103 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1103 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1103 are further described hereinbelow with reference to Table Table1.

[17288] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1103 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17289] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1104 (GAM1104) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17290] GAM1104 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1104 was detected is described hereinabove with reference to Figs. 2-8.

[17291] GAM1104 gene, herein designated GAM GENE, and GAM1104 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17292] GAM1104 gene, herein designated GAM GENE, encodes a GAM1104 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1104 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1104 precursor RNA is designated SEQ ID:1077, and is provided hereinbelow with reference to the sequence listing part.

[17293] GAM1104 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1104 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17294] An enzyme complex designated DICER COMPLEX, dices the GAM1104 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1104 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1104 RNA is designated SEQ ID:2753, and is provided hereinbelow with reference to the sequence listing part.

[17295] GAM1104 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1104 target RNA, herein designated GAM TARGET RNA. GAM1104 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17296] GAM1104 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1104 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1104 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1104 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1104 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17297] The complementary binding of GAM1104 RNA, herein designated GAM RNA, to target binding sites on GAM1104 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1104 target RNA, herein designated GAM TARGET RNA, into GAM1104 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17298] It is appreciated that GAM1104 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1104 target genes. The mRNA of each one of this plurality of GAM1104 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1104 RNA, herein designated GAM RNA, and which when bound by GAM1104 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1104 target proteins.

[17299] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1104 gene, herein designated GAM GENE, on one or more GAM1104 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17300] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1104 correlate with, and may be deduced from, the identity of the target genes which GAM1104 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17301] Nucleotide sequences of the GAM1104 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1104 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1104 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1104 are further described hereinbelow with reference to Table Table1.

[17302] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1104 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17303] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1105 (GAM1105) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17304] GAM1105 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1105 was detected is described hereinabove with reference to Figs. 2-8.

[17305] GAM1105 gene, herein designated GAM GENE, and GAM1105 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17306] GAM1105 gene, herein designated GAM GENE, encodes a GAM1105 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1105 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1105 precursor RNA is

designated SEQ ID:1078, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1078 is located at position 677944 relative to contig NT_011176.13, on chromosome 19.

[17307] GAM1105 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17308] An enzyme complex designated DICER COMPLEX, dices the GAM1105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1105 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1105 RNA is designated SEQ ID:2754, and is provided hereinbelow with reference to the sequence listing part.

[17309] GAM1105 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1105 target RNA, herein designated GAM TARGET RNA. GAM1105 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17310] GAM1105 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1105 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1105 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1105 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1105 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17311] The complementary binding of GAM1105 RNA, herein designated GAM RNA, to target binding sites on GAM1105 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1105 target RNA, herein designated GAM TARGET RNA, into GAM1105 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17312] It is appreciated that GAM1105 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1105 target genes. The mRNA of each one of this plurality of GAM1105 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1105 RNA,

herein designated GAM RNA, and which when bound by GAM1105 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1105 target proteins.

[17313] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1105 gene, herein designated GAM GENE, on one or more GAM1105 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17314] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1105 correlate with, and may be deduced from, the identity of the target genes which

GAM1105 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17315] Nucleotide sequences of the GAM1105 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1105 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1105 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1105 are further described hereinbelow with reference to Table Table1.

[17316] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1105 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17317] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1106 (GAM1106) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17318] GAM1106 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1106 was detected is described hereinabove with reference to Figs. 2-8.

[17319] GAM1106 gene, herein designated GAM GENE, and GAM1106 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17320] GAM1106 gene, herein designated GAM GENE, encodes a GAM1106 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1106 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1106 precursor RNA is designated SEQ ID:1079, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1079 is located at position 17619158 relative to contig NT_011362.7, on chromosome 20.

[17321] GAM1106 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17322] An enzyme complex designated DICER COMPLEX, dices the GAM1106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1106 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1106 RNA is designated SEQ ID:2755, and is provided hereinbelow with reference to the sequence listing part.

[17323] GAM1106 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1106 target RNA, herein designated GAM TARGET RNA. GAM1106 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17324] GAM1106 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1106 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1106 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1106 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1106 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17325] The complementary binding of GAM1106 RNA, herein designated GAM RNA, to target binding sites on GAM1106

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1106 target RNA, herein designated GAM TARGET RNA, into GAM1106 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17326] It is appreciated that GAM1106 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1106 target genes. The mRNA of each one of this plurality of GAM1106 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1106 RNA, herein designated GAM RNA, and which when bound by GAM1106 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1106 target proteins.

[17327] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1106 gene, herein designated GAM GENE, on one or more GAM1106 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17328] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1106 correlate with, and may be deduced from, the identity of the target genes which GAM1106 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17329] Nucleotide sequences of the GAM1106 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1106 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1106 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1106 are further described hereinbelow with reference to Table Table1.

[17330] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1106 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17331] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1107 (GAM1107) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17332] GAM1107 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1107 was detected is described hereinabove with reference to Figs. 2-8.

[17333] GAM1107 gene, herein designated GAM GENE, and GAM1107 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17334] GAM1107 gene, herein designated GAM GENE, encodes a GAM1107 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1107 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1107 precursor RNA is designated SEQ ID:1080, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1080 is located at position 29446 relative to contig NT_009455.12, on chromosome 12.

[17335] GAM1107 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1107 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17336] An enzyme complex designated DICER COMPLEX, dices the GAM1107 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1107 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1107 RNA is designated SEQ ID:2756, and is provided hereinbelow with reference to the sequence listing part.

[17337] GAM1107 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1107 target RNA, herein designated GAM TARGET RNA. GAM1107 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17338] GAM1107 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1107 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1107 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1107 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1107 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17339] The complementary binding of GAM1107 RNA, herein designated GAM RNA, to target binding sites on GAM1107 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1107 target RNA, herein designated GAM TARGET RNA, into GAM1107 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17340] It is appreciated that GAM1107 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1107 target genes. The mRNA of each one of this plurality of GAM1107 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1107 RNA, herein designated GAM RNA, and which when bound by GAM1107 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1107 target proteins.

[17341] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1107 gene, herein designated GAM GENE, on one or more GAM1107 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17342] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1107 correlate with, and may

be deduced from, the identity of the target genes which GAM1107 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17343] Nucleotide sequences of the GAM1107 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1107 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1107 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1107 are further described hereinbelow with reference to Table Table1.

[17344] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1107 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17345] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1108 (GAM1108) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17346] GAM1108 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1108 was detected is described hereinabove with reference to Figs. 2-8.

[17347] GAM1108 gene, herein designated GAM GENE, and GAM1108 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17348] GAM1108 gene, herein designated GAM GENE, encodes a GAM1108 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1108 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1108 precursor RNA is designated SEQ ID:1081, and is provided hereinbelow with reference to the sequence listing part.

[17349] GAM1108 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17350] An enzyme complex designated DICER COMPLEX, dices the GAM1108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1108 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1108 RNA is designated SEQ ID:2757, and is provided hereinbelow with reference to the sequence listing part.

[17351] GAM1108 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1108 target RNA, herein designated GAM TARGET RNA. GAM1108 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17352] GAM1108 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1108 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1108 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1108 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1108 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17353] The complementary binding of GAM1108 RNA, herein designated GAM RNA, to target binding sites on GAM1108 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1108 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1108 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17354] It is appreciated that GAM1108 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1108 target genes. The mRNA of each one of this plurality of GAM1108 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1108 RNA, herein designated GAM RNA, and which when bound by GAM1108 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1108 target proteins.

[17355] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1108 gene, herein designated GAM GENE, on one or more GAM1108 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17356] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1108 correlate with, and may be deduced from, the identity of the target genes which GAM1108 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17357] Nucleotide sequences of the GAM1108 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1108 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1108 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1108 are further described hereinbelow with reference to Table Table1.

[17358] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1108 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[17359] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1109 (GAM1109) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17360] GAM1109 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1109 was detected is described hereinabove with reference to Figs. 2-8.

[17361] GAM1109 gene, herein designated GAM GENE, and GAM1109 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17362] GAM1109 gene, herein designated GAM GENE, encodes a GAM1109 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1109 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1109 precursor RNA is designated SEQ ID:1082, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1082 is located at position 298684 relative to contig NT_035414.2, on chromosome 17.

[17363] GAM1109 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17364] An enzyme complex designated DICER COMPLEX, dices the GAM1109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1109 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1109 RNA is designated SEQ ID:2758, and is provided hereinbelow with reference to the sequence

listing part.

[17365] GAM1109 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1109 target RNA, herein designated GAM TARGET RNA. GAM1109 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17366] GAM1109 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1109 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1109 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1109 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1109 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17367] The complementary binding of GAM1109 RNA, herein designated GAM RNA, to target binding sites on GAM1109 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1109 target RNA, herein designated GAM TARGET RNA, into GAM1109 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17368] It is appreciated that GAM1109 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1109 target genes. The mRNA of each one of this plurality of GAM1109 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1109 RNA, herein designated GAM RNA, and which when bound by GAM1109 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1109 target proteins.

[17369] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1109 gene, herein designated GAM GENE, on one or more GAM1109 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17370] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1109 correlate with, and may be deduced from, the identity of the target genes which GAM1109 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17371] Nucleotide sequences of the GAM1109 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1109 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1109 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1109 are further described hereinbelow with reference to Table Table1.

[17372] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1109 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17373] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1110 (GAM1110) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17374] GAM1110 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1110 was detected is described hereinabove with reference to Figs. 2-8.

[17375] GAM1110 gene, herein designated GAM GENE, and GAM1110 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17376] GAM1110 gene, herein designated GAM GENE, encodes a GAM1110 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1110 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1110 precursor RNA is designated SEQ ID:1083, and is provided hereinbelow with reference to the sequence listing part.

[17377] GAM1110 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[17378] SEQ ID:100051 detected in mouse EST Accession BB067555.2.

[17379] SEQ ID:100052 detected in mouse EST Accession AW476209.1.

[17380] SEQ ID:100053 detected in mouse EST Accession AA474026.1.

[17381] GAM1110 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17382] An enzyme complex designated DICER COMPLEX, dices the GAM1110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1110 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1110 RNA is designated SEQ ID:2759, and is provided hereinbelow with reference to the sequence listing part.

[17383] GAM1110 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1110 target RNA, herein designated GAM TARGET RNA. GAM1110 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17384] GAM1110 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1110 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1110 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1110 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1110 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17385] The complementary binding of GAM1110 RNA, herein designated GAM RNA, to target binding sites on GAM1110 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1110 target RNA, herein designated GAM TARGET RNA, into GAM1110 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17386] It is appreciated that GAM1110 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1110 target genes. The mRNA of each one of this plurality of GAM1110 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1110 RNA, herein designated GAM RNA, and which when bound by GAM1110 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1110 target proteins.

[17387] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1110 gene, herein designated GAM GENE, on one or more GAM1110 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17388] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1110 correlate with, and may be deduced from, the identity of the target genes which GAM1110 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17389] Nucleotide sequences of the GAM1110 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1110 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1110 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1110 are further described hereinbelow with reference to Table Table1.

[17390] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1110 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17391] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1111 (GAM1111) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17392] GAM1111 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1111 was detected is described hereinabove with reference to Figs. 2-8.

[17393] GAM1111 gene, herein designated GAM GENE, and GAM1111 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[17394] GAM1111 gene, herein designated GAM GENE, encodes a GAM1111 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1111 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1111 precursor RNA is designated SEQ ID:1084, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1084 is located at position 25819173 relative to contig NT_007933.10, on chromosome 7.

[17395] GAM1111 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17396] An enzyme complex designated DICER COMPLEX, dices

the GAM1111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1111 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1111 RNA is designated SEQ ID:2760, and is provided hereinbelow with reference to the sequence listing part.

[17397] GAM1111 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1111 target RNA, herein designated GAM TARGET RNA. GAM1111 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17398] GAM1111 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1111 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1111 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1111 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1111 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17399] The complementary binding of GAM1111 RNA, herein designated GAM RNA, to target binding sites on GAM1111 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1111 target RNA, herein designated GAM TARGET RNA, into GAM1111 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17400] It is appreciated that GAM1111 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1111 target genes. The mRNA of each one of this plurality of GAM1111 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1111 RNA, herein designated GAM RNA, and which when bound by GAM1111 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1111 target proteins.

[17401] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1111 gene, herein designated GAM GENE, on one or more GAM1111 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17402] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1111 correlate with, and may be deduced from, the identity of the target genes which GAM1111 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17403] Nucleotide sequences of the GAM1111 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1111 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1111 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1111 are further described hereinbelow with reference to Table Table1.

[17404] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1111 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17405] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1112 (GAM1112) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17406] GAM1112 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1112 was detected is described hereinabove with reference to Figs. 2-8.

[17407] GAM1112 gene, herein designated GAM GENE, and GAM1112 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17408] GAM1112 gene, herein designated GAM GENE, encodes a GAM1112 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1112 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1112 precursor RNA is designated SEQ ID:1085, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1085 is located at position 8699336 rela-

tive to contig NT_011109.13, on chromosome 19.

[17409] GAM1112 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17410] An enzyme complex designated DICER COMPLEX, dices the GAM1112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1112 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1112 RNA is designated SEQ ID:2761, and is provided hereinbelow with reference to the sequence listing part.

[17411] GAM1112 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1112 target RNA, herein designated GAM TARGET RNA. GAM1112 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17412] GAM1112 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1112 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1112 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1112 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1112 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17413] The complementary binding of GAM1112 RNA, herein designated GAM RNA, to target binding sites on GAM1112 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1112 target RNA, herein designated GAM TARGET RNA, into GAM1112 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17414] It is appreciated that GAM1112 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1112 target genes. The mRNA of each one of this plurality of GAM1112 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1112 RNA, herein designated GAM RNA, and which when bound by GAM1112 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1112

target proteins.

[17415] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1112 gene, herein designated GAM GENE, on one or more GAM1112 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17416] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1112 correlate with, and may be deduced from, the identity of the target genes which GAM1112 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17417] Nucleotide sequences of the GAM1112 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1112 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1112 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1112 are further described hereinbelow with reference to Table Table1.

[17418] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1112 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17419] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1113 (GAM1113) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17420] GAM1113 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1113 was detected is described hereinabove with reference to Figs. 2-8.

[17421] GAM1113 gene, herein designated GAM GENE, and

GAM1113 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17422] GAM1113 gene, herein designated GAM GENE, encodes a GAM1113 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1113 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1113 precursor RNA is designated SEQ ID:1086, and is provided hereinbelow with reference to the sequence listing part.

[17423] GAM1113 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17424] An enzyme complex designated DICER COMPLEX, dices the GAM1113 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1113 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1113 RNA is designated SEQ ID:2762, and is provided hereinbelow with reference to the sequence listing part.

[17425] GAM1113 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1113 target RNA, herein designated GAM TARGET RNA. GAM1113 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17426] GAM1113 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1113 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1113

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1113 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1113 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17427] The complementary binding of GAM1113 RNA, herein designated GAM RNA, to target binding sites on GAM1113 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1113 target RNA, herein designated GAM TARGET RNA, into GAM1113 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[17428] It is appreciated that GAM1113 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1113 target genes. The mRNA of each one of this plurality of GAM1113 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1113 RNA, herein designated GAM RNA, and which when bound by GAM1113 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1113 target proteins.

[17429] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1113 gene, herein designated GAM GENE, on one or more GAM1113 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17430] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1113 correlate with, and may be deduced from, the identity of the target genes which GAM1113 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17431] Nucleotide sequences of the GAM1113 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1113 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1113 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1113 are further described hereinbelow with reference to Table Table1.

[17432] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1113 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17433] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1114 (GAM1114) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17434] GAM1114 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1114 was detected is described hereinabove with reference to Figs. 2-8.

[17435] GAM1114 gene, herein designated GAM GENE, and GAM1114 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17436] GAM1114 gene, herein designated GAM GENE, encodes a GAM1114 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1114 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1114 precursor RNA is designated SEQ ID:1087, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1087 is located at position 4990402 relative to contig NT_005795.13, on chromosome 3.

[17437] GAM1114 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1114 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17438] An enzyme complex designated DICER COMPLEX, dices the GAM1114 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1114 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1114 RNA is designated SEQ ID:2763, and is provided hereinbelow with reference to the sequence listing part.

[17439] GAM1114 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1114 target RNA, herein designated GAM TARGET RNA. GAM1114 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17440] GAM1114 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1114 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1114 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1114 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1114 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17441] The complementary binding of GAM1114 RNA, herein designated GAM RNA, to target binding sites on GAM1114 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1114 target RNA, herein designated GAM TARGET RNA, into GAM1114 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17442] It is appreciated that GAM1114 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1114 target genes. The mRNA of each one of this plurality of GAM1114 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1114 RNA, herein designated GAM RNA, and which when bound by GAM1114 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1114 target proteins.

[17443] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1114 gene, herein designated GAM GENE, on one or more GAM1114 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17444] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1114 correlate with, and may be deduced from, the identity of the target genes which GAM1114 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17445] Nucleotide sequences of the GAM1114 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1114 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1114 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1114 are further described hereinbelow with reference to Table Table1.

[17446] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1114 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17447] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1115 (GAM1115) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17448] GAM1115 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1115 was detected is described hereinabove with reference to Figs. 2-8.

[17449] GAM1115 gene, herein designated GAM GENE, and GAM1115 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[17450] GAM1115 gene, herein designated GAM GENE, encodes a GAM1115 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1115 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1115 precursor RNA is designated SEQ ID:1088, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1088 is located at position 5359482 relative to contig NT_007819.11, on chromosome 7.

[17451] GAM1115 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17452] An enzyme complex designated DICER COMPLEX, dices

the GAM1115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1115 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1115 RNA is designated SEQ ID:2764, and is provided hereinbelow with reference to the sequence listing part.

[17453] GAM1115 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1115 target RNA, herein designated GAM TARGET RNA. GAM1115 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17454] GAM1115 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1115 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1115 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1115 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1115 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17455] The complementary binding of GAM1115 RNA, herein designated GAM RNA, to target binding sites on GAM1115 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1115 target RNA, herein designated GAM TARGET RNA, into GAM1115 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17456] It is appreciated that GAM1115 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1115 target genes. The mRNA of each one of this plurality of GAM1115 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1115 RNA, herein designated GAM RNA, and which when bound by GAM1115 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1115 target proteins.

[17457] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1115 gene, herein designated GAM GENE, on one or more GAM1115 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17458] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1115 correlate with, and may be deduced from, the identity of the target genes which GAM1115 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17459] Nucleotide sequences of the GAM1115 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1115 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1115 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1115 are further described hereinbelow with reference to Table Table1.

[17460] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1115 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17461] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1116 (GAM1116) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17462] GAM1116 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1116 was detected is described hereinabove with reference to Figs. 2-8.

[17463] GAM1116 gene, herein designated GAM GENE, and GAM1116 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17464] GAM1116 gene, herein designated GAM GENE, encodes a GAM1116 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1116 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1116 precursor RNA is designated SEQ ID:1089, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1089 is located at position 5992707 rela-

tive to contig NT_005612.11, on chromosome 3.

[17465] GAM1116 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1116 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17466] An enzyme complex designated DICER COMPLEX, dices the GAM1116 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1116 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1116 RNA is designated SEQ ID:2765, and is provided hereinbelow with reference to the sequence listing part.

[17467] GAM1116 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1116 target RNA, herein designated GAM TARGET RNA. GAM1116 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17468] GAM1116 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1116 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1116 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1116 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1116 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17469] The complementary binding of GAM1116 RNA, herein designated GAM RNA, to target binding sites on GAM1116 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1116 target RNA, herein designated GAM TARGET RNA, into GAM1116 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17470] It is appreciated that GAM1116 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1116 target genes. The mRNA of each one of this plurality of GAM1116 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1116 RNA, herein designated GAM RNA, and which when bound by GAM1116 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1116

target proteins.

[17471] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1116 gene, herein designated GAM GENE, on one or more GAM1116 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17472] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1116 correlate with, and may be deduced from, the identity of the target genes which GAM1116 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17473] Nucleotide sequences of the GAM1116 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1116 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1116 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1116 are further described hereinbelow with reference to Table Table1.

[17474] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1116 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17475] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1117 (GAM1117) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17476] GAM1117 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1117 was detected is described hereinabove with reference to Figs. 2-8.

[17477] GAM1117 gene, herein designated GAM GENE, and

GAM1117 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17478] GAM1117 gene, herein designated GAM GENE, encodes a GAM1117 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1117 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1117 precursor RNA is designated SEQ ID:1090, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1090 is located at position 5362451 relative to contig NT_010498.11, on chromosome 16.

[17479] GAM1117 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1117 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17480] An enzyme complex designated DICER COMPLEX, dices the GAM1117 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1117 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1117 RNA is designated SEQ ID:2766, and is provided hereinbelow with reference to the sequence listing part.

[17481] GAM1117 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1117 target RNA, herein designated GAM TARGET RNA. GAM1117 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17482] GAM1117 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1117 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1117 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1117 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1117 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17483] The complementary binding of GAM1117 RNA, herein designated GAM RNA, to target binding sites on GAM1117 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1117 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1117 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17484] It is appreciated that GAM1117 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1117 target genes. The mRNA of each one of this plurality of GAM1117 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1117 RNA, herein designated GAM RNA, and which when bound by GAM1117 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1117 target proteins.

[17485] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1117 gene, herein designated GAM GENE, on one or more GAM1117 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17486] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1117 correlate with, and may be deduced from, the identity of the target genes which GAM1117 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17487] Nucleotide sequences of the GAM1117 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1117 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1117 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1117 are further described hereinbelow with reference to Table Table1.

[17488] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1117 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[17489] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1118 (GAM1118) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17490] GAM1118 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1118 was detected is described hereinabove with reference to Figs. 2-8.

[17491] GAM1118 gene, herein designated GAM GENE, and GAM1118 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17492] GAM1118 gene, herein designated GAM GENE, encodes a GAM1118 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1118 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1118 precursor RNA is designated SEQ ID:1091, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1091 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[17493] GAM1118 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17494] An enzyme complex designated DICER COMPLEX, dices the GAM1118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1118 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1118 RNA is designated SEQ ID:2767, and is provided hereinbelow with reference to the sequence

listing part.

[17495] GAM1118 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1118 target RNA, herein designated GAM TARGET RNA. GAM1118 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17496] GAM1118 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1118 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1118 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1118 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1118 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17497] The complementary binding of GAM1118 RNA, herein designated GAM RNA, to target binding sites on GAM1118 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1118 target RNA, herein designated GAM TARGET RNA, into GAM1118 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17498] It is appreciated that GAM1118 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1118 target genes. The mRNA of each one of this plurality of GAM1118 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1118 RNA, herein designated GAM RNA, and which when bound by GAM1118 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1118 target proteins.

[17499] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1118 gene, herein designated GAM GENE, on one or more GAM1118 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17500] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1118 correlate with, and may be deduced from, the identity of the target genes which GAM1118 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17501] Nucleotide sequences of the GAM1118 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1118 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1118 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1118 are further described hereinbelow with reference to Table Table1.

[17502] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1118 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17503] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1119 (GAM1119) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17504] GAM1119 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1119 was detected is described hereinabove with reference to Figs. 2-8.

[17505] GAM1119 gene, herein designated GAM GENE, and GAM1119 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17506] GAM1119 gene, herein designated GAM GENE, encodes a GAM1119 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1119 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1119 precursor RNA is designated SEQ ID:1092, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1092 is located at position 2589317 relative to contig NT_011519.9, on chromosome 22.

[17507] GAM1119 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[17508] An enzyme complex designated DICER COMPLEX, dices the GAM1119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1119 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1119 RNA is designated SEQ ID:2768, and is provided hereinbelow with reference to the sequence listing part.

[17509] GAM1119 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1119 target RNA, herein designated GAM TARGET RNA. GAM1119 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17510] GAM1119 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1119 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1119 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1119 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1119 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17511] The complementary binding of GAM1119 RNA, herein designated GAM RNA, to target binding sites on GAM1119 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1119 target RNA, herein designated GAM TARGET RNA, into GAM1119 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17512] It is appreciated that GAM1119 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1119 target genes. The mRNA of each one of this plurality of GAM1119 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1119 RNA, herein designated GAM RNA, and which when bound by GAM1119 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1119 target proteins.

[17513] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1119 gene, herein designated GAM GENE, on one or more GAM1119 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17514] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1119 correlate with, and may be deduced from, the identity of the target genes which GAM1119 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17515] Nucleotide sequences of the GAM1119 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1119 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1119 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1119 are further described hereinbelow with reference to Table Table1.

[17516] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1119 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17517] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1120 (GAM1120) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17518] GAM1120 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1120 was detected is described hereinabove with reference to Figs. 2-8.

[17519] GAM1120 gene, herein designated GAM GENE, and GAM1120 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17520] GAM1120 gene, herein designated GAM GENE, encodes a GAM1120 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1120 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1120 precursor RNA is designated SEQ ID:1093, and is provided hereinbelow with

reference to the sequence listing part.

[17521] GAM1120 has 37 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[17522] SEQ ID:99156 detected in mouse EST Accession BE573540.1.

[17523] SEQ ID:99157 detected in mouse EST Accession BI657157.1.

[17524] SEQ ID:99158 detected in mouse EST Accession AI314714.1.

[17525] SEQ ID:99159 detected in mouse EST Accession BF120559.1.

[17526] SEQ ID:99160 detected in mouse EST Accession AA414773.1.

[17527] SEQ ID:99161 detected in mouse EST Accession BI693070.1.

[17528] SEQ ID:99162 detected in mouse EST Accession BI688321.1.

[17529] SEQ ID:99163 detected in mouse EST Accession BF785462.1.

[17530] SEQ ID:99164 detected in mouse EST Accession

BF454862.1.

[17531] SEQ ID:99165 detected in mouse EST Accession BI156043.1.

[17532] SEQ ID:98224 detected in mouse EST Accession AL024328.1.

[17533] SEQ ID:98225 detected in mouse EST Accession AW681385.1.

[17534] SEQ ID:98226 detected in mouse EST Accession BE860595.1.

[17535] SEQ ID:98227 detected in mouse EST Accession AA589031.1.

[17536] SEQ ID:98228 detected in mouse EST Accession AU016124.1.

[17537] SEQ ID:98229 detected in mouse EST Accession AW988911.1.

[17538] SEQ ID:98230 detected in mouse EST Accession BF016642.1.

[17539] SEQ ID:98231 detected in mouse EST Accession AA120399.1.

[17540] SEQ ID:98232 detected in mouse EST Accession AA692748.1.

[17541] SEQ ID:98233 detected in mouse EST Accession AA589661.1.

[17542] SEQ ID:98234 detected in mouse EST Accession BG083946.1.

[17543] SEQ ID:98235 detected in mouse EST Accession BG078060.1.

[17544] SEQ ID:98236 detected in mouse EST Accession BG802025.1.

[17545] SEQ ID:98237 detected in mouse EST Accession AU018118.1.

[17546] SEQ ID:98238 detected in mouse EST Accession AA646147.1.

[17547] SEQ ID:98239 detected in mouse EST Accession AA122854.1.

[17548] SEQ ID:98240 detected in mouse EST Accession AI573357.1.

[17549] SEQ ID:98241 detected in mouse EST Accession BI660487.1.

[17550] SEQ ID:98242 detected in mouse EST Accession BI158190.1.

[17551] SEQ ID:98243 detected in mouse EST Accession BE951936.1.

[17552] SEQ ID:98244 detected in mouse EST Accession BG071084.1.

[17553] SEQ ID:98245 detected in mouse EST Accession

AA545087.1.

[17554] SEQ ID:98246 detected in mouse EST Accession AA106981.1.

[17555] SEQ ID:98247 detected in mouse EST Accession BG295832.1.

[17556] SEQ ID:98248 detected in mouse EST Accession BI078320.1.

[17557] SEQ ID:98249 detected in mouse EST Accession BG077811.1.

[17558] SEQ ID:98250 detected in mouse EST Accession BI452791.1.

[17559] GAM1120 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1120 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17560] An enzyme complex designated DICER COMPLEX, dices the GAM1120 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1120 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1120 RNA is designated SEQ ID:2769, and is provided hereinbelow with reference to the sequence listing part.

[17561] GAM1120 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1120 target RNA, herein designated GAM TARGET RNA. GAM1120 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17562] GAM1120 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1120 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1120

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1120 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1120 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17563] The complementary binding of GAM1120 RNA, herein designated GAM RNA, to target binding sites on GAM1120 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1120 target RNA, herein designated GAM TARGET RNA, into GAM1120 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[17564] It is appreciated that GAM1120 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1120 target genes. The mRNA of each one of this plurality of GAM1120 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1120 RNA, herein designated GAM RNA, and which when bound by GAM1120 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1120 target proteins.

[17565] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1120 gene, herein designated GAM GENE, on one or more GAM1120 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17566] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1120 correlate with, and may be deduced from, the identity of the target genes which GAM1120 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17567] Nucleotide sequences of the GAM1120 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1120 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1120 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1120 are further described hereinbelow with reference to Table Table1.

[17568] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1120 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17569] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1121 (GAM1121) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17570] GAM1121 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1121 was detected is described hereinabove with reference to Figs. 2-8.

[17571] GAM1121 gene, herein designated GAM GENE, and GAM1121 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17572] GAM1121 gene, herein designated GAM GENE, encodes a GAM1121 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1121 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1121 precursor RNA is designated SEQ ID:1094, and is provided hereinbelow with reference to the sequence listing part.

[17573] GAM1121 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1121 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17574] An enzyme complex designated DICER COMPLEX, dices the GAM1121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1121 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1121 RNA is designated SEQ ID:2770, and is provided hereinbelow with reference to the sequence listing part.

[17575] GAM1121 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1121 target RNA, herein designated GAM TARGET

RNA. GAM1121 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17576] GAM1121 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1121 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1121 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1121 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1121 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17577] The complementary binding of GAM1121 RNA, herein designated GAM RNA, to target binding sites on GAM1121 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1121 target RNA, herein designated GAM TARGET RNA, into GAM1121 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17578] It is appreciated that GAM1121 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1121 target genes. The mRNA of each one of this plurality of GAM1121 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1121 RNA, herein designated GAM RNA, and which when bound by GAM1121 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1121 target proteins.

[17579] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1121 gene, herein designated GAM GENE, on one or more GAM1121 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17580] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1121 correlate with, and may be deduced from, the identity of the target genes which GAM1121 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17581] Nucleotide sequences of the GAM1121 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1121 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1121 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1121 are further described hereinbelow with reference to Table Table1.

[17582] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1121 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17583] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1122 (GAM1122) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17584] GAM1122 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1122 was detected is described hereinabove with reference to Figs. 2-8.

[17585] GAM1122 gene, herein designated GAM GENE, and GAM1122 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17586] GAM1122 gene, herein designated GAM GENE, encodes a

GAM1122 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1122 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1122 precursor RNA is designated SEQ ID:1095, and is provided hereinbelow with reference to the sequence listing part.

[17587] GAM1122 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17588] An enzyme complex designated DICER COMPLEX, dices the GAM1122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1122 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1122 RNA is designated SEQ ID:2771, and is provided hereinbelow with reference to the sequence listing part.

[17589] GAM1122 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1122 target RNA, herein designated GAM TARGET RNA. GAM1122 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17590] GAM1122 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1122 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1122 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1122 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1122 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17591] The complementary binding of GAM1122 RNA, herein designated GAM RNA, to target binding sites on GAM1122 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1122 target RNA, herein designated GAM TARGET RNA, into GAM1122 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17592] It is appreciated that GAM1122 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1122 target genes. The mRNA of each one of this plurality of GAM1122 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1122 RNA, herein designated GAM RNA, and which when bound by GAM1122 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1122 target proteins.

[17593] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1122 gene, herein designated GAM GENE, on one or more GAM1122 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[17594] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1122 correlate with, and may be deduced from, the identity of the target genes which GAM1122 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17595] Nucleotide sequences of the GAM1122 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1122 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1122 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1122 are further described hereinbelow with reference to Table Table1.

[17596] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1122 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17597] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1123 (GAM1123) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[17598] GAM1123 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1123 was detected is described hereinabove with reference to Figs. 2-8.

[17599] GAM1123 gene, herein designated GAM GENE, and GAM1123 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17600] GAM1123 gene, herein designated GAM GENE, encodes a GAM1123 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1123 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1123 precursor RNA is designated SEQ ID:1096, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1096 is located at position 452958 relative to contig NT_005962.13, on chromosome 3.

[17601] GAM1123 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1123 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17602] An enzyme complex designated DICER COMPLEX, dices the GAM1123 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1123 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1123 RNA is designated SEQ ID:2772, and is provided hereinbelow with reference to the sequence listing part.

[17603] GAM1123 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1123 target RNA, herein designated GAM TARGET RNA. GAM1123 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17604] GAM1123 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1123 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1123 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1123 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1123 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17605] The complementary binding of GAM1123 RNA, herein designated GAM RNA, to target binding sites on GAM1123 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1123 target RNA, herein designated GAM TARGET RNA, into GAM1123 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17606] It is appreciated that GAM1123 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1123 target genes. The mRNA of each one of this plurality of GAM1123 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1123 RNA, herein designated GAM RNA, and which when bound by GAM1123 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1123 target proteins.

[17607] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1123 gene, herein designated GAM GENE, on one or more GAM1123 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17608] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1123 correlate with, and may be deduced from, the identity of the target genes which GAM1123 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17609] Nucleotide sequences of the GAM1123 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1123 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1123 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1123 are further described hereinbelow with reference to Table Table1.

[17610] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1123 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17611] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1124 (GAM1124) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17612] GAM1124 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1124 was detected is described hereinabove with reference to Figs. 2-8.

[17613] GAM1124 gene, herein designated GAM GENE, and GAM1124 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17614] GAM1124 gene, herein designated GAM GENE, encodes a GAM1124 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1124 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1124 precursor RNA is designated SEQ ID:1097, and is provided hereinbelow with reference to the sequence listing part.

[17615] GAM1124 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17616] An enzyme complex designated DICER COMPLEX, dices the GAM1124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1124 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1124 RNA is designated SEQ ID:2773, and is provided hereinbelow with reference to the sequence listing part.

[17617] GAM1124 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1124 target RNA, herein designated GAM TARGET RNA. GAM1124 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17618] GAM1124 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1124 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1124 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1124 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1124 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17619] The complementary binding of GAM1124 RNA, herein designated GAM RNA, to target binding sites on GAM1124 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1124 target RNA, herein designated GAM TARGET RNA, into GAM1124 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17620] It is appreciated that GAM1124 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1124 target genes. The mRNA of each one of this

plurality of GAM1124 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1124 RNA, herein designated GAM RNA, and which when bound by GAM1124 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1124 target proteins.

[17621] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1124 gene, herein designated GAM GENE, on one or more GAM1124 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17622] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1124 correlate with, and may be deduced from, the identity of the target genes which GAM1124 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17623] Nucleotide sequences of the GAM1124 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1124 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1124 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1124 are further described hereinbelow with reference to Table Table1.

[17624] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1124 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17625] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1125 (GAM1125) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[17626] GAM1125 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1125 was detected is described hereinabove with reference to Figs. 2-8.

[17627] GAM1125 gene, herein designated GAM GENE, and GAM1125 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17628] GAM1125 gene, herein designated GAM GENE, encodes a GAM1125 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1125 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1125 precursor RNA is designated SEQ ID:1098, and is provided hereinbelow with reference to the sequence listing part.

[17629] GAM1125 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17630] An enzyme complex designated DICER COMPLEX, dices the GAM1125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1125 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1125 RNA is designated SEQ ID:2774, and is provided hereinbelow with reference to the sequence listing part.

[17631] GAM1125 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1125 target RNA, herein designated GAM TARGET RNA. GAM1125 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[17632] GAM1125 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1125 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1125 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1125 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1125 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17633] The complementary binding of GAM1125 RNA, herein

designated GAM RNA, to target binding sites on GAM1125 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1125 target RNA, herein designated GAM TARGET RNA, into GAM1125 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17634] It is appreciated that GAM1125 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1125 target genes. The mRNA of each one of this plurality of GAM1125 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1125 RNA, herein designated GAM RNA, and which when bound by GAM1125 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1125 target proteins.

[17635] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1125 gene, herein designated GAM GENE, on one or more GAM1125 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17636] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1125 correlate with, and may be deduced from, the identity of the target genes which GAM1125 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17637] Nucleotide sequences of the GAM1125 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1125 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1125 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1125 are further described hereinbelow with reference to Table Table1.

[17638] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1125 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17639] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1126 (GAM1126) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17640] GAM1126 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1126 was detected is described hereinabove with reference to Figs. 2-8.

[17641] GAM1126 gene, herein designated GAM GENE, and GAM1126 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17642] GAM1126 gene, herein designated GAM GENE, encodes a GAM1126 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1126 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1126 precursor RNA is designated SEQ ID:1099, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1099 is located at position 6585898 relative to contig NT_033927.3, on chromosome 11.

[17643] GAM1126 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17644] An enzyme complex designated DICER COMPLEX, dices the GAM1126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1126 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1126 RNA is designated SEQ ID:2775, and is provided hereinbelow with reference to the sequence listing part.

[17645] GAM1126 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1126 target RNA, herein designated GAM TARGET RNA. GAM1126 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17646] GAM1126 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1126 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1126 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1126 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1126 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17647] The complementary binding of GAM1126 RNA, herein designated GAM RNA, to target binding sites on GAM1126 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1126 target RNA, herein designated GAM TARGET RNA, into GAM1126 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17648] It is appreciated that GAM1126 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1126 target genes. The mRNA of each one of this plurality of GAM1126 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1126 RNA, herein designated GAM RNA, and which when bound by GAM1126 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1126 target proteins.

[17649] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1126 gene, herein designated GAM GENE, on one or more GAM1126 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17650] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1126 correlate with, and may be deduced from, the identity of the target genes which GAM1126 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17651] Nucleotide sequences of the GAM1126 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1126 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1126 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1126 are further described hereinbelow with reference to Table Table1.

[17652] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1126 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17653] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1127 (GAM1127) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17654] GAM1127 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1127 was detected is described hereinabove with reference to Figs. 2-8.

[17655] GAM1127 gene, herein designated GAM GENE, and GAM1127 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17656] GAM1127 gene, herein designated GAM GENE, encodes a GAM1127 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1127 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1127 precursor RNA is designated SEQ ID:1100, and is provided hereinbelow with reference to the sequence listing part.

[17657] GAM1127 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17658] An enzyme complex designated DICER COMPLEX, dices the GAM1127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1127 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1127 RNA is designated SEQ ID:2776, and is provided hereinbelow with reference to the sequence listing part.

[17659] GAM1127 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1127 target RNA, herein designated GAM TARGET RNA. GAM1127 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17660] GAM1127 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1127 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1127 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1127 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1127 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17661] The complementary binding of GAM1127 RNA, herein designated GAM RNA, to target binding sites on GAM1127

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1127 target RNA, herein designated GAM TARGET RNA, into GAM1127 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17662] It is appreciated that GAM1127 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1127 target genes. The mRNA of each one of this plurality of GAM1127 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1127 RNA, herein designated GAM RNA, and which when bound by GAM1127 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1127 target proteins.

[17663] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1127 gene, herein designated GAM GENE, on one or more GAM1127 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17664] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1127 correlate with, and may be deduced from, the identity of the target genes which GAM1127 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17665] Nucleotide sequences of the GAM1127 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1127 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1127 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1127 are further described hereinbelow with reference to Table Table1.

[17666] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1127 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17667] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1128 (GAM1128) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17668] GAM1128 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1128 was detected is described hereinabove with reference to Figs. 2-8.

[17669] GAM1128 gene, herein designated GAM GENE, and GAM1128 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17670] GAM1128 gene, herein designated GAM GENE, encodes a GAM1128 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1128 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1128 precursor RNA is designated SEQ ID:1101, and is provided hereinbelow with reference to the sequence listing part.

[17671] GAM1128 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17672] An enzyme complex designated DICER COMPLEX, dices the GAM1128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1128 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1128 RNA is designated SEQ ID:2777, and

is provided hereinbelow with reference to the sequence listing part.

[17673] GAM1128 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1128 target RNA, herein designated GAM TARGET RNA. GAM1128 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17674] GAM1128 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1128 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1128 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1128 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1128 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17675] The complementary binding of GAM1128 RNA, herein designated GAM RNA, to target binding sites on GAM1128 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1128 target RNA, herein designated GAM TARGET RNA, into GAM1128 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17676] It is appreciated that GAM1128 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1128 target genes. The mRNA of each one of this plurality of GAM1128 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1128 RNA, herein designated GAM RNA, and which when bound by

GAM1128 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1128 target proteins.

[17677] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1128 gene, herein designated GAM GENE, on one or more GAM1128 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17678] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1128 correlate with, and may be deduced from, the identity of the target genes which GAM1128 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[17679] Nucleotide sequences of the GAM1128 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1128 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1128 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1128 are further described hereinbelow with reference to Table Table1.

[17680] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1128 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17681] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1129 (GAM1129) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17682] GAM1129 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1129 was detected is described hereinabove

with reference to Figs. 2-8.

[17683] GAM1129 gene, herein designated GAM GENE, and GAM1129 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17684] GAM1129 gene, herein designated GAM GENE, encodes a GAM1129 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1129 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1129 precursor RNA is designated SEQ ID:1102, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1102 is located at position 7447448 relative to contig NT_009307.12, on chromosome 11.

[17685] GAM1129 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17686] An enzyme complex designated DICER COMPLEX, dices the GAM1129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1129 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1129 RNA is designated SEQ ID:2778, and is provided hereinbelow with reference to the sequence listing part.

[17687] GAM1129 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1129 target RNA, herein designated GAM TARGET RNA. GAM1129 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17688] GAM1129 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1129 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1129 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1129 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1129 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17689] The complementary binding of GAM1129 RNA, herein designated GAM RNA, to target binding sites on GAM1129 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1129 target RNA, herein designated GAM TARGET RNA, into GAM1129 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17690] It is appreciated that GAM1129 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1129 target genes. The mRNA of each one of this plurality of GAM1129 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1129 RNA, herein designated GAM RNA, and which when bound by GAM1129 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1129 target proteins.

[17691] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1129 gene, herein designated GAM GENE, on one or more GAM1129 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17692] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1129 correlate with, and may be deduced from, the identity of the target genes which GAM1129 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17693] Nucleotide sequences of the GAM1129 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1129 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1129 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1129 are further described hereinbelow with reference to Table Table1.

[17694] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1129 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17695] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1130 (GAM1130) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17696] GAM1130 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1130 was detected is described hereinabove with reference to Figs. 2-8.

[17697] GAM1130 gene, herein designated GAM GENE, and GAM1130 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17698] GAM1130 gene, herein designated GAM GENE, encodes a GAM1130 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1130 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1130 precursor RNA is

designated SEQ ID:1103, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1103 is located at position 2465088 relative to contig NT_008150.12, on chromosome 8.

[17699] GAM1130 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17700] An enzyme complex designated DICER COMPLEX, dices the GAM1130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1130 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1130 RNA is designated SEQ ID:2779, and is provided hereinbelow with reference to the sequence listing part.

[17701] GAM1130 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1130 target RNA, herein designated GAM TARGET RNA. GAM1130 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17702] GAM1130 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1130 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1130 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1130 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1130 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17703] The complementary binding of GAM1130 RNA, herein designated GAM RNA, to target binding sites on GAM1130 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1130 target RNA, herein designated GAM TARGET RNA, into GAM1130 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17704] It is appreciated that GAM1130 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1130 target genes. The mRNA of each one of this plurality of GAM1130 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1130 RNA,

herein designated GAM RNA, and which when bound by GAM1130 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1130 target proteins.

[17705] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1130 gene, herein designated GAM GENE, on one or more GAM1130 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17706] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1130 correlate with, and may be deduced from, the identity of the target genes which

GAM1130 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17707] Nucleotide sequences of the GAM1130 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1130 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1130 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1130 are further described hereinbelow with reference to Table Table1.

[17708] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1130 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17709] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1131 (GAM1131) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17710] GAM1131 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1131 was detected is described hereinabove with reference to Figs. 2-8.

[17711] GAM1131 gene, herein designated GAM GENE, and GAM1131 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17712] GAM1131 gene, herein designated GAM GENE, encodes a GAM1131 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1131 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1131 precursor RNA is designated SEQ ID:1104, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1104 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[17713] GAM1131 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17714] An enzyme complex designated DICER COMPLEX, dices the GAM1131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1131 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1131 RNA is designated SEQ ID:2780, and is provided hereinbelow with reference to the sequence listing part.

[17715] GAM1131 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1131 target RNA, herein designated GAM TARGET RNA. GAM1131 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17716] GAM1131 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1131 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1131 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1131 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1131 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17717] The complementary binding of GAM1131 RNA, herein designated GAM RNA, to target binding sites on GAM1131

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1131 target RNA, herein designated GAM TARGET RNA, into GAM1131 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17718] It is appreciated that GAM1131 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1131 target genes. The mRNA of each one of this plurality of GAM1131 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1131 RNA, herein designated GAM RNA, and which when bound by GAM1131 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1131 target proteins.

[17719] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1131 gene, herein designated GAM GENE, on one or more GAM1131 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17720] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1131 correlate with, and may be deduced from, the identity of the target genes which GAM1131 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17721] Nucleotide sequences of the GAM1131 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1131 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1131 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1131 are further described hereinbelow with reference to Table Table1.

[17722] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1131 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17723] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1132 (GAM1132) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17724] GAM1132 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1132 was detected is described hereinabove with reference to Figs. 2-8.

[17725] GAM1132 gene, herein designated GAM GENE, and GAM1132 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17726] GAM1132 gene, herein designated GAM GENE, encodes a GAM1132 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1132 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1132 precursor RNA is designated SEQ ID:1105, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1105 is located at position 15268055 relative to contig NT_011362.7, on chromosome 20.

[17727] GAM1132 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17728] An enzyme complex designated DICER COMPLEX, dices the GAM1132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1132 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1132 RNA is designated SEQ ID:2781, and is provided hereinbelow with reference to the sequence listing part.

[17729] GAM1132 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1132 target RNA, herein designated GAM TARGET RNA. GAM1132 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17730] GAM1132 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1132 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1132 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1132 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1132 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17731] The complementary binding of GAM1132 RNA, herein designated GAM RNA, to target binding sites on GAM1132 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1132 target RNA, herein designated GAM TARGET RNA, into GAM1132 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17732] It is appreciated that GAM1132 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1132 target genes. The mRNA of each one of this plurality of GAM1132 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1132 RNA, herein designated GAM RNA, and which when bound by GAM1132 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1132 target proteins.

[17733] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1132 gene, herein designated GAM GENE, on one or more GAM1132 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17734] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1132 correlate with, and may

be deduced from, the identity of the target genes which GAM1132 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17735] Nucleotide sequences of the GAM1132 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1132 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1132 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1132 are further described hereinbelow with reference to Table Table1.

[17736] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1132 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17737] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1133 (GAM1133) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17738] GAM1133 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1133 was detected is described hereinabove with reference to Figs. 2-8.

[17739] GAM1133 gene, herein designated GAM GENE, and GAM1133 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17740] GAM1133 gene, herein designated GAM GENE, encodes a GAM1133 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1133 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1133 precursor RNA is designated SEQ ID:1106, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1106 is located at position 25819165 relative to contig NT_007933.10, on chromosome 7.

[17741] GAM1133 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17742] An enzyme complex designated DICER COMPLEX, dices the GAM1133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1133 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1133 RNA is designated SEQ ID:2782, and is provided hereinbelow with reference to the sequence listing part.

[17743] GAM1133 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1133 target RNA, herein designated GAM TARGET RNA. GAM1133 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[17744] GAM1133 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1133 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1133 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1133 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1133 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17745] The complementary binding of GAM1133 RNA, herein

designated GAM RNA, to target binding sites on GAM1133 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1133 target RNA, herein designated GAM TARGET RNA, into GAM1133 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17746] It is appreciated that GAM1133 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1133 target genes. The mRNA of each one of this plurality of GAM1133 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1133 RNA, herein designated GAM RNA, and which when bound by GAM1133 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1133 target proteins.

[17747] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1133 gene, herein designated GAM GENE, on one or more GAM1133 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17748] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1133 correlate with, and may be deduced from, the identity of the target genes which GAM1133 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17749] Nucleotide sequences of the GAM1133 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1133 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1133 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1133 are further described hereinbelow with reference to Table Table1.

[17750] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1133 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17751] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1134 (GAM1134) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17752] GAM1134 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1134 was detected is described hereinabove with reference to Figs. 2-8.

[17753] GAM1134 gene, herein designated GAM GENE, and GAM1134 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17754] GAM1134 gene, herein designated GAM GENE, encodes a GAM1134 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1134 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1134 precursor RNA is designated SEQ ID:1107, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1107 is located at position 4851374 relative to contig NT_022517.13, on chromosome 3.

[17755] GAM1134 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17756] An enzyme complex designated DICER COMPLEX, dices the GAM1134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1134 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1134 RNA is designated SEQ ID:2783, and is provided hereinbelow with reference to the sequence listing part.

[17757] GAM1134 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1134 target RNA, herein designated GAM TARGET RNA. GAM1134 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17758] GAM1134 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1134 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1134 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1134 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1134 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17759] The complementary binding of GAM1134 RNA, herein designated GAM RNA, to target binding sites on GAM1134 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1134 target RNA, herein designated GAM TARGET RNA, into GAM1134 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17760] It is appreciated that GAM1134 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1134 target genes. The mRNA of each one of this plurality of GAM1134 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1134 RNA, herein designated GAM RNA, and which when bound by GAM1134 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1134 target proteins.

[17761] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1134 gene, herein designated GAM GENE, on one or more GAM1134 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17762] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1134 correlate with, and may be deduced from, the identity of the target genes which GAM1134 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17763] Nucleotide sequences of the GAM1134 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1134 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1134 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1134 are further described hereinbelow with reference to Table Table1.

[17764] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1134 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17765] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1135 (GAM1135) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17766] GAM1135 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1135 was detected is described hereinabove with reference to Figs. 2-8.

[17767] GAM1135 gene, herein designated GAM GENE, and GAM1135 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17768] GAM1135 gene, herein designated GAM GENE, encodes a GAM1135 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1135 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1135 precursor RNA is designated SEQ ID:1108, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1108 is located at position 155440 relative to contig NT_030772.7, on chromosome 10.

[17769] GAM1135 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17770] An enzyme complex designated DICER COMPLEX, dices the GAM1135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1135 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1135 RNA is designated SEQ ID:2784, and is provided hereinbelow with reference to the sequence listing part.

[17771] GAM1135 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1135 target RNA, herein designated GAM TARGET RNA. GAM1135 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17772] GAM1135 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1135 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1135 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1135 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1135 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17773] The complementary binding of GAM1135 RNA, herein designated GAM RNA, to target binding sites on GAM1135 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1135 target RNA, herein designated GAM TARGET RNA, into GAM1135 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17774] It is appreciated that GAM1135 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1135 target genes. The mRNA of each one of this plurality of GAM1135 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1135 RNA, herein designated GAM RNA, and which when bound by GAM1135 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1135 target proteins.

[17775] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1135 gene, herein designated GAM GENE, on one or more GAM1135 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17776] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1135 correlate with, and may be deduced from, the identity of the target genes which GAM1135 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17777] Nucleotide sequences of the GAM1135 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1135 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1135 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1135 are further described hereinbelow with reference to Table Table1.

[17778] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1135 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17779] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1136 (GAM1136) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17780] GAM1136 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1136 was detected is described hereinabove with reference to Figs. 2-8.

[17781] GAM1136 gene, herein designated GAM GENE, and GAM1136 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17782] GAM1136 gene, herein designated GAM GENE, encodes a GAM1136 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1136 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1136 precursor RNA is designated SEQ ID:1109, and is provided hereinbelow with reference to the sequence listing part.

[17783] GAM1136 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17784] An enzyme complex designated DICER COMPLEX, dices the GAM1136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1136 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1136 RNA is designated SEQ ID:2785, and is provided hereinbelow with reference to the sequence listing part.

[17785] GAM1136 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1136 target RNA, herein designated GAM TARGET RNA. GAM1136 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17786] GAM1136 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1136 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1136 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1136 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1136 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17787] The complementary binding of GAM1136 RNA, herein designated GAM RNA, to target binding sites on GAM1136 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1136 target RNA, herein designated GAM TARGET RNA, into GAM1136 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17788] It is appreciated that GAM1136 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1136 target genes. The mRNA of each one of this plurality of GAM1136 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1136 RNA, herein designated GAM RNA, and which when bound by GAM1136 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1136 target proteins.

[17789] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1136 gene, herein designated GAM GENE, on one or more GAM1136 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17790] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1136 correlate with, and may

be deduced from, the identity of the target genes which GAM1136 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17791] Nucleotide sequences of the GAM1136 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1136 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1136 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1136 are further described hereinbelow with reference to Table Table1.

[17792] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1136 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17793] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1137 (GAM1137) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17794] GAM1137 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1137 was detected is described hereinabove with reference to Figs. 2-8.

[17795] GAM1137 gene, herein designated GAM GENE, and GAM1137 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17796] GAM1137 gene, herein designated GAM GENE, encodes a GAM1137 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1137 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1137 precursor RNA is designated SEQ ID:1110, and is provided hereinbelow with reference to the sequence listing part.

[17797] GAM1137 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17798] An enzyme complex designated DICER COMPLEX, dices the GAM1137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1137 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1137 RNA is designated SEQ ID:2786, and is provided hereinbelow with reference to the sequence listing part.

[17799] GAM1137 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1137 target RNA, herein designated GAM TARGET RNA. GAM1137 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17800] GAM1137 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1137 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1137 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1137 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1137 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17801] The complementary binding of GAM1137 RNA, herein designated GAM RNA, to target binding sites on GAM1137 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1137 target RNA, herein designated GAM TARGET RNA, into GAM1137 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17802] It is appreciated that GAM1137 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1137 target genes. The mRNA of each one of this plurality of GAM1137 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1137 RNA, herein designated GAM RNA, and which when bound by GAM1137 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1137 target proteins.

[17803] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1137 gene, herein designated GAM GENE, on one or more GAM1137 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17804] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1137 correlate with, and may be deduced from, the identity of the target genes which GAM1137 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17805] Nucleotide sequences of the GAM1137 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1137 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1137 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1137 are further described hereinbelow with reference to Table Table1.

[17806] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1137 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17807] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1138 (GAM1138) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17808] GAM1138 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1138 was detected is described hereinabove with reference to Figs. 2-8.

[17809] GAM1138 gene, herein designated GAM GENE, and GAM1138 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17810] GAM1138 gene, herein designated GAM GENE, encodes a GAM1138 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1138 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1138 precursor RNA is

designated SEQ ID:1111, and is provided hereinbelow with reference to the sequence listing part.

[17811] GAM1138 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17812] An enzyme complex designated DICER COMPLEX, dices the GAM1138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1138 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1138 RNA is designated SEQ ID:2787, and is provided hereinbelow with reference to the sequence

listing part.

[17813] GAM1138 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1138 target RNA, herein designated GAM TARGET RNA. GAM1138 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17814] GAM1138 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1138 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1138 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1138 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1138 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17815] The complementary binding of GAM1138 RNA, herein designated GAM RNA, to target binding sites on GAM1138 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1138 target RNA, herein designated GAM TARGET RNA, into GAM1138 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17816] It is appreciated that GAM1138 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1138 target genes. The mRNA of each one of this plurality of GAM1138 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1138 RNA, herein designated GAM RNA, and which when bound by GAM1138 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1138 target proteins.

[17817] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1138 gene, herein designated GAM GENE, on one or more GAM1138 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17818] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1138 correlate with, and may be deduced from, the identity of the target genes which GAM1138 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17819] Nucleotide sequences of the GAM1138 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1138 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1138 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1138 are further described hereinbelow with reference to Table Table1.

[17820] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1138 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17821] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1139 (GAM1139) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17822] GAM1139 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1139 was detected is described hereinabove with reference to Figs. 2-8.

[17823] GAM1139 gene, herein designated GAM GENE, and GAM1139 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17824] GAM1139 gene, herein designated GAM GENE, encodes a GAM1139 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1139 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1139 precursor RNA is designated SEQ ID:1112, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1112 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[17825] GAM1139 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[17826] An enzyme complex designated DICER COMPLEX, dices the GAM1139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1139 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1139 RNA is designated SEQ ID:2788, and is provided hereinbelow with reference to the sequence listing part.

[17827] GAM1139 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1139 target RNA, herein designated GAM TARGET RNA. GAM1139 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17828] GAM1139 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1139 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1139 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1139 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1139 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17829] The complementary binding of GAM1139 RNA, herein designated GAM RNA, to target binding sites on GAM1139 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1139 target RNA, herein designated GAM TARGET RNA, into GAM1139 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17830] It is appreciated that GAM1139 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1139 target genes. The mRNA of each one of this plurality of GAM1139 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1139 RNA, herein designated GAM RNA, and which when bound by GAM1139 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1139 target proteins.

[17831] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1139 gene, herein designated GAM GENE, on one or more GAM1139 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17832] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1139 correlate with, and may be deduced from, the identity of the target genes which GAM1139 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17833] Nucleotide sequences of the GAM1139 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1139 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1139 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1139 are further described hereinbelow with reference to Table Table1.

[17834] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1139 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17835] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1140 (GAM1140) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17836] GAM1140 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1140 was detected is described hereinabove with reference to Figs. 2-8.

[17837] GAM1140 gene, herein designated GAM GENE, and GAM1140 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17838] GAM1140 gene, herein designated GAM GENE, encodes a GAM1140 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1140 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1140 precursor RNA is designated SEQ ID:1113, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1113 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[17839] GAM1140 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[17840] SEQ ID:100226 detected in mouse EST Accession AA144533.1.

[17841] SEQ ID:100227 detected in mouse EST Accession AA671455.1.

[17842] SEQ ID:100228 detected in mouse EST Accession AW824753.1.

[17843] SEQ ID:100229 detected in mouse EST Accession BE943987.1.

[17844] SEQ ID:100230 detected in mouse EST Accession BE691413.1.

[17845] SEQ ID:100231 detected in mouse EST Accession BE691447.1.

[17846] SEQ ID:100232 detected in mouse EST Accession BG808025.1.

[17847] SEQ ID:100233 detected in mouse EST Accession

BG808010.1.

[17848] SEQ ID:100234 detected in mouse EST Accession BG807850.1.

[17849] SEQ ID:100235 detected in mouse EST Accession BG805970.1.

[17850] SEQ ID:100236 detected in mouse EST Accession BG145596.1.

[17851] SEQ ID:100237 detected in mouse EST Accession BE692802.1.

[17852] SEQ ID:100238 detected in mouse EST Accession AW208601.1.

[17853] SEQ ID:100239 detected in mouse EST Accession BB609859.1.

[17854] SEQ ID:100240 detected in mouse EST Accession BB610842.1.

[17855] GAM1140 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17856] An enzyme complex designated DICER COMPLEX, dices the GAM1140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1140 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1140 RNA is designated SEQ ID:2789, and is provided hereinbelow with reference to the sequence listing part.

[17857] GAM1140 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1140 target RNA, herein designated GAM TARGET RNA. GAM1140 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17858] GAM1140 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1140 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1140 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1140 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1140 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17859] The complementary binding of GAM1140 RNA, herein designated GAM RNA, to target binding sites on GAM1140 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1140 target RNA, herein designated GAM TARGET RNA, into GAM1140 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17860] It is appreciated that GAM1140 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1140 target genes. The mRNA of each one of this plurality of GAM1140 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1140 RNA, herein designated GAM RNA, and which when bound by GAM1140 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1140 target proteins.

[17861] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1140 gene, herein designated GAM GENE, on one or more GAM1140 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17862] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1140 correlate with, and may be deduced from, the identity of the target genes which GAM1140 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17863] Nucleotide sequences of the GAM1140 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1140 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1140 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1140 are further described hereinbelow with reference to Table Table1.

[17864] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1140 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17865] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1141 (GAM1141) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17866] GAM1141 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1141 was detected is described hereinabove with reference to Figs. 2-8.

[17867] GAM1141 gene, herein designated GAM GENE, and GAM1141 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17868] GAM1141 gene, herein designated GAM GENE, encodes a GAM1141 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1141 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1141 precursor RNA is

designated SEQ ID:1114, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1114 is located at position 3579561 relative to contig NT_008476.13, on chromosome 9.

[17869] GAM1141 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17870] An enzyme complex designated DICER COMPLEX, dices the GAM1141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1141 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1141 RNA is designated SEQ ID:2790, and is provided hereinbelow with reference to the sequence listing part.

[17871] GAM1141 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1141 target RNA, herein designated GAM TARGET RNA. GAM1141 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17872] GAM1141 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1141 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1141 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1141 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1141 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17873] The complementary binding of GAM1141 RNA, herein designated GAM RNA, to target binding sites on GAM1141 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1141 target RNA, herein designated GAM TARGET RNA, into GAM1141 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17874] It is appreciated that GAM1141 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1141 target genes. The mRNA of each one of this plurality of GAM1141 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1141 RNA,

herein designated GAM RNA, and which when bound by GAM1141 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1141 target proteins.

[17875] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1141 gene, herein designated GAM GENE, on one or more GAM1141 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17876] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1141 correlate with, and may be deduced from, the identity of the target genes which

GAM1141 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17877] Nucleotide sequences of the GAM1141 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1141 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1141 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1141 are further described hereinbelow with reference to Table Table1.

[17878] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1141 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17879] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1142 (GAM1142) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17880] GAM1142 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1142 was detected is described hereinabove with reference to Figs. 2-8.

[17881] GAM1142 gene, herein designated GAM GENE, and GAM1142 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17882] GAM1142 gene, herein designated GAM GENE, encodes a GAM1142 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1142 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1142 precursor RNA is designated SEQ ID:1115, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1115 is located at position 3674875 relative to contig NT_007914.10, on chromosome 7.

[17883] GAM1142 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17884] An enzyme complex designated DICER COMPLEX, dices the GAM1142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1142 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1142 RNA is designated SEQ ID:2791, and is provided hereinbelow with reference to the sequence listing part.

[17885] GAM1142 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1142 target RNA, herein designated GAM TARGET RNA. GAM1142 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17886] GAM1142 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1142 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1142 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1142 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1142 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17887] The complementary binding of GAM1142 RNA, herein designated GAM RNA, to target binding sites on GAM1142

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1142 target RNA, herein designated GAM TARGET RNA, into GAM1142 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17888] It is appreciated that GAM1142 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1142 target genes. The mRNA of each one of this plurality of GAM1142 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1142 RNA, herein designated GAM RNA, and which when bound by GAM1142 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1142 target proteins.

[17889] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1142 gene, herein designated GAM GENE, on one or more GAM1142 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17890] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1142 correlate with, and may be deduced from, the identity of the target genes which GAM1142 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17891] Nucleotide sequences of the GAM1142 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1142 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1142 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1142 are further described hereinbelow with reference to Table Table1.

[17892] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1142 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17893] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1143 (GAM1143) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17894] GAM1143 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1143 was detected is described hereinabove with reference to Figs. 2-8.

[17895] GAM1143 gene, herein designated GAM GENE, and GAM1143 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17896] GAM1143 gene, herein designated GAM GENE, encodes a GAM1143 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1143 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1143 precursor RNA is designated SEQ ID:1116, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1116 is located at position 2281488 relative to contig NT_033905.3, on chromosome 18.

[17897] GAM1143 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17898] An enzyme complex designated DICER COMPLEX, dices the GAM1143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1143 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1143 RNA is designated SEQ ID:2792, and is provided hereinbelow with reference to the sequence listing part.

[17899] GAM1143 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1143 target RNA, herein designated GAM TARGET RNA. GAM1143 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17900] GAM1143 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1143 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1143 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1143 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1143 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17901] The complementary binding of GAM1143 RNA, herein designated GAM RNA, to target binding sites on GAM1143 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1143 target RNA, herein designated GAM TARGET RNA, into GAM1143 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17902] It is appreciated that GAM1143 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1143 target genes. The mRNA of each one of this plurality of GAM1143 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1143 RNA, herein designated GAM RNA, and which when bound by GAM1143 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1143 target proteins.

[17903] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1143 gene, herein designated GAM GENE, on one or more GAM1143 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17904] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1143 correlate with, and may

be deduced from, the identity of the target genes which GAM1143 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17905] Nucleotide sequences of the GAM1143 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1143 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1143 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1143 are further described hereinbelow with reference to Table Table1.

[17906] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1143 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17907] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1144 (GAM1144) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17908] GAM1144 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1144 was detected is described hereinabove with reference to Figs. 2-8.

[17909] GAM1144 gene, herein designated GAM GENE, and GAM1144 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17910] GAM1144 gene, herein designated GAM GENE, encodes a GAM1144 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1144 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1144 precursor RNA is designated SEQ ID:1117, and is provided hereinbelow with reference to the sequence listing part.

[17911] GAM1144 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17912] An enzyme complex designated DICER COMPLEX, dices the GAM1144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1144 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1144 RNA is designated SEQ ID:2793, and is provided hereinbelow with reference to the sequence listing part.

[17913] GAM1144 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1144 target RNA, herein designated GAM TARGET RNA. GAM1144 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17914] GAM1144 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1144 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1144 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1144 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1144 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17915] The complementary binding of GAM1144 RNA, herein designated GAM RNA, to target binding sites on GAM1144 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1144 target RNA, herein designated GAM TARGET RNA, into GAM1144 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17916] It is appreciated that GAM1144 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1144 target genes. The mRNA of each one of this plurality of GAM1144 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1144 RNA, herein designated GAM RNA, and which when bound by GAM1144 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1144 target proteins.

[17917] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1144 gene, herein designated GAM GENE, on one or more GAM1144 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17918] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1144 correlate with, and may be deduced from, the identity of the target genes which GAM1144 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17919] Nucleotide sequences of the GAM1144 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1144 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1144 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1144 are further described hereinbelow with reference to Table Table1.

[17920] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1144 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17921] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1145 (GAM1145) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17922] GAM1145 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1145 was detected is described hereinabove with reference to Figs. 2-8.

[17923] GAM1145 gene, herein designated GAM GENE, and GAM1145 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17924] GAM1145 gene, herein designated GAM GENE, encodes a GAM1145 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1145 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1145 precursor RNA is

designated SEQ ID:1118, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1118 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[17925] GAM1145 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17926] An enzyme complex designated DICER COMPLEX, dices the GAM1145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1145 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1145 RNA is designated SEQ ID:2794, and is provided hereinbelow with reference to the sequence listing part.

[17927] GAM1145 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1145 target RNA, herein designated GAM TARGET RNA. GAM1145 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17928] GAM1145 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1145 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1145 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1145 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1145 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17929] The complementary binding of GAM1145 RNA, herein designated GAM RNA, to target binding sites on GAM1145 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1145 target RNA, herein designated GAM TARGET RNA, into GAM1145 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17930] It is appreciated that GAM1145 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1145 target genes. The mRNA of each one of this plurality of GAM1145 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1145 RNA,

herein designated GAM RNA, and which when bound by GAM1145 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1145 target proteins.

[17931] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1145 gene, herein designated GAM GENE, on one or more GAM1145 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17932] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1145 correlate with, and may be deduced from, the identity of the target genes which

GAM1145 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17933] Nucleotide sequences of the GAM1145 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1145 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1145 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1145 are further described hereinbelow with reference to Table Table1.

[17934] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1145 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17935] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1146 (GAM1146) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17936] GAM1146 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1146 was detected is described hereinabove with reference to Figs. 2-8.

[17937] GAM1146 gene, herein designated GAM GENE, and GAM1146 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17938] GAM1146 gene, herein designated GAM GENE, encodes a GAM1146 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1146 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1146 precursor RNA is designated SEQ ID:1119, and is provided hereinbelow with reference to the sequence listing part.

[17939] GAM1146 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[17940] An enzyme complex designated DICER COMPLEX, dices the GAM1146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1146 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1146 RNA is designated SEQ ID:2795, and is provided hereinbelow with reference to the sequence listing part.

[17941] GAM1146 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1146 target RNA, herein designated GAM TARGET RNA. GAM1146 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17942] GAM1146 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1146 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1146 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1146 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1146 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17943] The complementary binding of GAM1146 RNA, herein designated GAM RNA, to target binding sites on GAM1146 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1146 target RNA, herein designated GAM TARGET RNA, into GAM1146 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17944] It is appreciated that GAM1146 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1146 target genes. The mRNA of each one of this plurality of GAM1146 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1146 RNA, herein designated GAM RNA, and which when bound by GAM1146 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1146 target proteins.

[17945] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1146 gene, herein designated GAM GENE, on one or more GAM1146 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17946] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1146 correlate with, and may be deduced from, the identity of the target genes which GAM1146 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17947] Nucleotide sequences of the GAM1146 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1146 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1146 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1146 are further described hereinbelow with reference to Table Table1.

[17948] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1146 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17949] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1147 (GAM1147) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17950] GAM1147 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1147 was detected is described hereinabove with reference to Figs. 2-8.

[17951] GAM1147 gene, herein designated GAM GENE, and GAM1147 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17952] GAM1147 gene, herein designated GAM GENE, encodes a GAM1147 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1147 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1147 precursor RNA is designated SEQ ID:1120, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1120 is located at position 1014810 relative to contig NT_004671.13, on chromosome 1.

[17953] GAM1147 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17954] An enzyme complex designated DICER COMPLEX, dices the GAM1147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1147 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1147 RNA is designated SEQ ID:2796, and

is provided hereinbelow with reference to the sequence listing part.

[17955] GAM1147 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1147 target RNA, herein designated GAM TARGET RNA. GAM1147 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17956] GAM1147 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1147 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1147 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1147 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1147 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17957] The complementary binding of GAM1147 RNA, herein designated GAM RNA, to target binding sites on GAM1147 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1147 target RNA, herein designated GAM TARGET RNA, into GAM1147 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17958] It is appreciated that GAM1147 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1147 target genes. The mRNA of each one of this plurality of GAM1147 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1147 RNA, herein designated GAM RNA, and which when bound by

GAM1147 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1147 target proteins.

[17959] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1147 gene, herein designated GAM GENE, on one or more GAM1147 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17960] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1147 correlate with, and may be deduced from, the identity of the target genes which GAM1147 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[17961] Nucleotide sequences of the GAM1147 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1147 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1147 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1147 are further described hereinbelow with reference to Table Table1.

[17962] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1147 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17963] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1148 (GAM1148) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17964] GAM1148 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1148 was detected is described hereinabove

with reference to Figs. 2-8.

[17965] GAM1148 gene, herein designated GAM GENE, and GAM1148 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17966] GAM1148 gene, herein designated GAM GENE, encodes a GAM1148 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1148 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1148 precursor RNA is designated SEQ ID:1121, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1121 is located at position 498211 relative to contig NT_004852.13, on chromosome 1.

[17967] GAM1148 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17968] An enzyme complex designated DICER COMPLEX, dices the GAM1148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1148 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1148 RNA is designated SEQ ID:2797, and is provided hereinbelow with reference to the sequence listing part.

[17969] GAM1148 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1148 target RNA, herein designated GAM TARGET RNA. GAM1148 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17970] GAM1148 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1148 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1148 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1148 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1148 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17971] The complementary binding of GAM1148 RNA, herein designated GAM RNA, to target binding sites on GAM1148 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1148 target RNA, herein designated GAM TARGET RNA, into GAM1148 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17972] It is appreciated that GAM1148 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1148 target genes. The mRNA of each one of this plurality of GAM1148 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1148 RNA, herein designated GAM RNA, and which when bound by GAM1148 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1148 target proteins.

[17973] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1148 gene, herein designated GAM GENE, on one or more GAM1148 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17974] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1148 correlate with, and may be deduced from, the identity of the target genes which GAM1148 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17975] Nucleotide sequences of the GAM1148 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1148 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1148 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1148 are further described hereinbelow with reference to Table Table1.

[17976] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1148 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17977] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1149 (GAM1149) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17978] GAM1149 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1149 was detected is described hereinabove with reference to Figs. 2-8.

[17979] GAM1149 gene, herein designated GAM GENE, and GAM1149 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17980] GAM1149 gene, herein designated GAM GENE, encodes a GAM1149 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1149 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1149 precursor RNA is

designated SEQ ID:1122, and is provided hereinbelow with reference to the sequence listing part.

[17981] GAM1149 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17982] An enzyme complex designated DICER COMPLEX, dices the GAM1149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1149 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1149 RNA is designated SEQ ID:2798, and is provided hereinbelow with reference to the sequence

listing part.

[17983] GAM1149 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1149 target RNA, herein designated GAM TARGET RNA. GAM1149 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17984] GAM1149 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1149 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1149 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1149 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1149 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17985] The complementary binding of GAM1149 RNA, herein designated GAM RNA, to target binding sites on GAM1149 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1149 target RNA, herein designated GAM TARGET RNA, into GAM1149 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[17986] It is appreciated that GAM1149 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1149 target genes. The mRNA of each one of this plurality of GAM1149 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1149 RNA, herein designated GAM RNA, and which when bound by GAM1149 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1149 target proteins.

[17987] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1149 gene, herein designated GAM GENE, on one or more GAM1149 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[17988] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1149 correlate with, and may be deduced from, the identity of the target genes which GAM1149 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[17989] Nucleotide sequences of the GAM1149 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1149 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1149 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1149 are further described hereinbelow with reference to Table Table1.

[17990] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1149 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[17991] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1150 (GAM1150) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[17992] GAM1150 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1150 was detected is described hereinabove with reference to Figs. 2-8.

[17993] GAM1150 gene, herein designated GAM GENE, and GAM1150 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[17994] GAM1150 gene, herein designated GAM GENE, encodes a GAM1150 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1150 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1150 precursor RNA is designated SEQ ID:1123, and is provided hereinbelow with reference to the sequence listing part.

[17995] GAM1150 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[17996] An enzyme complex designated DICER COMPLEX, dices

the GAM1150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1150 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1150 RNA is designated SEQ ID:2799, and is provided hereinbelow with reference to the sequence listing part.

[17997] GAM1150 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1150 target RNA, herein designated GAM TARGET RNA. GAM1150 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[17998] GAM1150 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1150 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1150 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1150 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1150 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[17999] The complementary binding of GAM1150 RNA, herein designated GAM RNA, to target binding sites on GAM1150 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1150 target RNA, herein designated GAM TARGET RNA, into GAM1150 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18000] It is appreciated that GAM1150 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1150 target genes. The mRNA of each one of this plurality of GAM1150 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1150 RNA, herein designated GAM RNA, and which when bound by GAM1150 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1150 target proteins.

[18001] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1150 gene, herein designated GAM GENE, on one or more GAM1150 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18002] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1150 correlate with, and may be deduced from, the identity of the target genes which GAM1150 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18003] Nucleotide sequences of the GAM1150 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1150 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1150 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1150 are further described hereinbelow with reference to Table Table1.

[18004] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1150 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18005] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1151 (GAM1151) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18006] GAM1151 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1151 was detected is described hereinabove with reference to Figs. 2-8.

[18007] GAM1151 gene, herein designated GAM GENE, and GAM1151 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18008] GAM1151 gene, herein designated GAM GENE, encodes a GAM1151 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1151 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1151 precursor RNA is designated SEQ ID:1124, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1124 is located at position 1364370 rela-

tive to contig NT_035014.2, on chromosome 9.

[18009] GAM1151 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18010] An enzyme complex designated DICER COMPLEX, dices the GAM1151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1151 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1151 RNA is designated SEQ ID:2800, and is provided hereinbelow with reference to the sequence listing part.

[18011] GAM1151 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1151 target RNA, herein designated GAM TARGET RNA. GAM1151 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18012] GAM1151 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1151 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1151 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1151 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1151 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18013] The complementary binding of GAM1151 RNA, herein designated GAM RNA, to target binding sites on GAM1151 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1151 target RNA, herein designated GAM TARGET RNA, into GAM1151 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18014] It is appreciated that GAM1151 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1151 target genes. The mRNA of each one of this plurality of GAM1151 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1151 RNA, herein designated GAM RNA, and which when bound by GAM1151 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1151

target proteins.

[18015] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1151 gene, herein designated GAM GENE, on one or more GAM1151 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18016] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1151 correlate with, and may be deduced from, the identity of the target genes which GAM1151 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18017] Nucleotide sequences of the GAM1151 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1151 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1151 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1151 are further described hereinbelow with reference to Table Table1.

[18018] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1151 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18019] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1152 (GAM1152) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18020] GAM1152 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1152 was detected is described hereinabove with reference to Figs. 2-8.

[18021] GAM1152 gene, herein designated GAM GENE, and

GAM1152 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18022] GAM1152 gene, herein designated GAM GENE, encodes a GAM1152 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1152 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1152 precursor RNA is designated SEQ ID:1125, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1125 is located at position 1605760 relative to contig NT_009799.11, on chromosome 13.

[18023] GAM1152 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18024] An enzyme complex designated DICER COMPLEX, dices the GAM1152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1152 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1152 RNA is designated SEQ ID:2801, and is provided hereinbelow with reference to the sequence listing part.

[18025] GAM1152 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1152 target RNA, herein designated GAM TARGET RNA. GAM1152 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18026] GAM1152 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1152 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1152 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1152 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1152 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18027] The complementary binding of GAM1152 RNA, herein designated GAM RNA, to target binding sites on GAM1152 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1152 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1152 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18028] It is appreciated that GAM1152 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1152 target genes. The mRNA of each one of this plurality of GAM1152 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1152 RNA, herein designated GAM RNA, and which when bound by GAM1152 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1152 target proteins.

[18029] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1152 gene, herein designated GAM GENE, on one or more GAM1152 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18030] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1152 correlate with, and may be deduced from, the identity of the target genes which GAM1152 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18031] Nucleotide sequences of the GAM1152 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1152 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1152 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1152 are further described hereinbelow with reference to Table Table1.

[18032] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1152 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[18033] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1153 (GAM1153) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18034] GAM1153 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1153 was detected is described hereinabove with reference to Figs. 2-8.

[18035] GAM1153 gene, herein designated GAM GENE, and GAM1153 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18036] GAM1153 gene, herein designated GAM GENE, encodes a GAM1153 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1153 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1153 precursor RNA is designated SEQ ID:1126, and is provided hereinbelow with reference to the sequence listing part.

[18037] GAM1153 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18038] An enzyme complex designated DICER COMPLEX, dices the GAM1153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1153 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1153 RNA is designated SEQ ID:2802, and is provided hereinbelow with reference to the sequence listing part.

[18039] GAM1153 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1153 target RNA, herein designated GAM TARGET RNA. GAM1153 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18040] GAM1153 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1153 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1153 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1153 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1153 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18041] The complementary binding of GAM1153 RNA, herein designated GAM RNA, to target binding sites on GAM1153 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1153 target RNA, herein designated GAM TARGET RNA, into GAM1153 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18042] It is appreciated that GAM1153 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1153 target genes. The mRNA of each one of this plurality of GAM1153 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1153 RNA, herein designated GAM RNA, and which when bound by GAM1153 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1153 target proteins.

[18043] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1153 gene, herein designated GAM GENE, on one or more GAM1153 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18044] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1153 correlate with, and may be deduced from, the identity of the target genes which GAM1153 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18045] Nucleotide sequences of the GAM1153 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1153 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1153 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1153 are further described hereinbelow with reference to Table Table1.

[18046] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1153 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18047] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1154 (GAM1154) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18048] GAM1154 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1154 was detected is described hereinabove with reference to Figs. 2-8.

[18049] GAM1154 gene, herein designated GAM GENE, and GAM1154 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[18050] GAM1154 gene, herein designated GAM GENE, encodes a GAM1154 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1154 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1154 precursor RNA is designated SEQ ID:1127, and is provided hereinbelow with reference to the sequence listing part.

[18051] GAM1154 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18052] An enzyme complex designated DICER COMPLEX, dices the GAM1154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1154 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1154 RNA is designated SEQ ID:2803, and is provided hereinbelow with reference to the sequence listing part.

[18053] GAM1154 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1154 target RNA, herein designated GAM TARGET RNA. GAM1154 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18054] GAM1154 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1154 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1154 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1154 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1154 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18055] The complementary binding of GAM1154 RNA, herein designated GAM RNA, to target binding sites on GAM1154 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1154 target RNA, herein designated GAM TARGET RNA, into GAM1154 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18056] It is appreciated that GAM1154 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1154 target genes. The mRNA of each one of this plurality of GAM1154 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1154 RNA, herein designated GAM RNA, and which when bound by GAM1154 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1154 target proteins.

[18057] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1154 gene, herein designated GAM GENE, on one or more GAM1154 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18058] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1154 correlate with, and may be deduced from, the identity of the target genes which GAM1154 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18059] Nucleotide sequences of the GAM1154 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1154 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1154 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1154 are further described hereinbelow with reference to Table Table1.

[18060] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1154 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18061] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1155 (GAM1155) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18062] GAM1155 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1155 was detected is described hereinabove with reference to Figs. 2-8.

[18063] GAM1155 gene, herein designated GAM GENE, and GAM1155 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18064] GAM1155 gene, herein designated GAM GENE, encodes a GAM1155 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1155 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1155 precursor RNA is designated SEQ ID:1128, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1128 is located at position 2071050 relative to contig NT_008183.13, on chromosome 8.

[18065] GAM1155 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18066] An enzyme complex designated DICER COMPLEX, dices the GAM1155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1155 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1155 RNA is designated SEQ ID:2804, and is provided hereinbelow with reference to the sequence listing part.

[18067] GAM1155 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1155 target RNA, herein designated GAM TARGET RNA. GAM1155 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18068] GAM1155 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1155 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1155 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1155 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1155 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18069] The complementary binding of GAM1155 RNA, herein designated GAM RNA, to target binding sites on GAM1155 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1155 target RNA, herein designated GAM TARGET RNA, into GAM1155 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18070] It is appreciated that GAM1155 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1155 target genes. The mRNA of each one of this plurality of GAM1155 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1155 RNA, herein designated GAM RNA, and which when bound by GAM1155 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1155 target proteins.

[18071] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1155 gene, herein designated GAM GENE, on one or more GAM1155 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18072] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1155 correlate with, and may be deduced from, the identity of the target genes which GAM1155 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18073] Nucleotide sequences of the GAM1155 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1155 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1155 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1155 are further described hereinbelow with reference to Table Table1.

[18074] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1155 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18075] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1156 (GAM1156) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18076] GAM1156 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1156 was detected is described hereinabove with reference to Figs. 2-8.

[18077] GAM1156 gene, herein designated GAM GENE, and GAM1156 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18078] GAM1156 gene, herein designated GAM GENE, encodes a GAM1156 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1156 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1156 precursor RNA is designated SEQ ID:1129, and is provided hereinbelow with reference to the sequence listing part.

[18079] GAM1156 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18080] An enzyme complex designated DICER COMPLEX, dices the GAM1156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1156 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1156 RNA is designated SEQ ID:2805, and is provided hereinbelow with reference to the sequence listing part.

[18081] GAM1156 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1156 target RNA, herein designated GAM TARGET RNA. GAM1156 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18082] GAM1156 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1156 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1156 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1156 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1156 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18083] The complementary binding of GAM1156 RNA, herein designated GAM RNA, to target binding sites on GAM1156 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1156 target RNA, herein designated GAM TARGET RNA, into GAM1156 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18084] It is appreciated that GAM1156 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1156 target genes. The mRNA of each one of this plurality of GAM1156 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1156 RNA, herein designated GAM RNA, and which when bound by GAM1156 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1156 target proteins.

[18085] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1156 gene, herein designated GAM GENE, on one or more GAM1156 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18086] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1156 correlate with, and may be deduced from, the identity of the target genes which GAM1156 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18087] Nucleotide sequences of the GAM1156 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1156 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1156 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1156 are further described hereinbelow with reference to Table Table1.

[18088] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1156 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18089] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1157 (GAM1157) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18090] GAM1157 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1157 was detected is described hereinabove with reference to Figs. 2-8.

[18091] GAM1157 gene, herein designated GAM GENE, and GAM1157 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18092] GAM1157 gene, herein designated GAM GENE, encodes a GAM1157 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1157 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1157 precursor RNA is designated SEQ ID:1130, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1130 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[18093] GAM1157 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1157 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18094] An enzyme complex designated DICER COMPLEX, dices the GAM1157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1157 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1157 RNA is designated SEQ ID:2806, and is provided hereinbelow with reference to the sequence listing part.

[18095] GAM1157 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1157 target RNA, herein designated GAM TARGET

RNA. GAM1157 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18096] GAM1157 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1157 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1157 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1157 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1157 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18097] The complementary binding of GAM1157 RNA, herein designated GAM RNA, to target binding sites on GAM1157 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1157 target RNA, herein designated GAM TARGET RNA, into GAM1157 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18098] It is appreciated that GAM1157 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1157 target genes. The mRNA of each one of this plurality of GAM1157 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1157 RNA, herein designated GAM RNA, and which when bound by GAM1157 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1157 target proteins.

[18099] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1157 gene, herein designated GAM GENE, on one or more GAM1157 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18100] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1157 correlate with, and may be deduced from, the identity of the target genes which GAM1157 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18101] Nucleotide sequences of the GAM1157 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1157 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1157 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1157 are further described hereinbelow with reference to Table Table1.

[18102] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1157 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18103] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1158 (GAM1158) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18104] GAM1158 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1158 was detected is described hereinabove with reference to Figs. 2-8.

[18105] GAM1158 gene, herein designated GAM GENE, and GAM1158 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18106] GAM1158 gene, herein designated GAM GENE, encodes a

GAM1158 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1158 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1158 precursor RNA is designated SEQ ID:1131, and is provided hereinbelow with reference to the sequence listing part.

[18107] GAM1158 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18108] An enzyme complex designated DICER COMPLEX, dices the GAM1158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1158 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1158 RNA is designated SEQ ID:2807, and is provided hereinbelow with reference to the sequence listing part.

[18109] GAM1158 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1158 target RNA, herein designated GAM TARGET RNA. GAM1158 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18110] GAM1158 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1158 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1158 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1158 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1158 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18111] The complementary binding of GAM1158 RNA, herein designated GAM RNA, to target binding sites on GAM1158 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1158 target RNA, herein designated GAM TARGET RNA, into GAM1158 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18112] It is appreciated that GAM1158 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1158 target genes. The mRNA of each one of this plurality of GAM1158 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1158 RNA, herein designated GAM RNA, and which when bound by GAM1158 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1158 target proteins.

[18113] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1158 gene, herein designated GAM GENE, on one or more GAM1158 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[18114] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1158 correlate with, and may be deduced from, the identity of the target genes which GAM1158 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18115] Nucleotide sequences of the GAM1158 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1158 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1158 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1158 are further described hereinbelow with reference to Table Table1.

[18116] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1158 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18117] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1159 (GAM1159) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[18118] GAM1159 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1159 was detected is described hereinabove with reference to Figs. 2-8.

[18119] GAM1159 gene, herein designated GAM GENE, and GAM1159 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18120] GAM1159 gene, herein designated GAM GENE, encodes a GAM1159 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1159 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1159 precursor RNA is designated SEQ ID:1132, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1132 is located at position 18710504 relative to contig NT_011512.7, on chromosome 21.

[18121] GAM1159 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1159 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18122] An enzyme complex designated DICER COMPLEX, dices the GAM1159 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1159 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1159 RNA is designated SEQ ID:2808, and is provided hereinbelow with reference to the sequence listing part.

[18123] GAM1159 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1159 target RNA, herein designated GAM TARGET RNA. GAM1159 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18124] GAM1159 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1159 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1159 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1159 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1159 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18125] The complementary binding of GAM1159 RNA, herein designated GAM RNA, to target binding sites on GAM1159 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1159 target RNA, herein designated GAM TARGET RNA, into GAM1159 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18126] It is appreciated that GAM1159 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1159 target genes. The mRNA of each one of this plurality of GAM1159 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1159 RNA, herein designated GAM RNA, and which when bound by GAM1159 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1159 target proteins.

[18127] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1159 gene, herein designated GAM GENE, on one or more GAM1159 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18128] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1159 correlate with, and may be deduced from, the identity of the target genes which GAM1159 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18129] Nucleotide sequences of the GAM1159 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1159 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1159 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1159 are further described hereinbelow with reference to Table Table1.

[18130] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1159 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18131] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1160 (GAM1160) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18132] GAM1160 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1160 was detected is described hereinabove with reference to Figs. 2-8.

[18133] GAM1160 gene, herein designated GAM GENE, and GAM1160 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18134] GAM1160 gene, herein designated GAM GENE, encodes a GAM1160 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1160 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1160 precursor RNA is designated SEQ ID:1133, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1133 is located at position 9083217 relative to contig NT_007592.11, on chromosome 6.

[18135] GAM1160 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18136] An enzyme complex designated DICER COMPLEX, dices the GAM1160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1160 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1160 RNA is designated SEQ ID:2809, and is provided hereinbelow with reference to the sequence listing part.

[18137] GAM1160 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1160 target RNA, herein designated GAM TARGET RNA. GAM1160 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18138] GAM1160 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1160 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1160 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1160 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1160 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18139] The complementary binding of GAM1160 RNA, herein designated GAM RNA, to target binding sites on GAM1160 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1160 target RNA, herein designated GAM TARGET RNA, into GAM1160 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18140] It is appreciated that GAM1160 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1160 target genes. The mRNA of each one of this plurality of GAM1160 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1160 RNA, herein designated GAM RNA, and which when bound by GAM1160 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1160 target proteins.

[18141] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1160 gene, herein designated GAM GENE, on one or more GAM1160 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18142] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1160 correlate with, and may be deduced from, the identity of the target genes which GAM1160 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18143] Nucleotide sequences of the GAM1160 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1160 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1160 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1160 are further described hereinbelow with reference to Table Table1.

[18144] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1160 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18145] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1161 (GAM1161) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18146] GAM1161 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1161 was detected is described hereinabove with reference to Figs. 2-8.

[18147] GAM1161 gene, herein designated GAM GENE, and GAM1161 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18148] GAM1161 gene, herein designated GAM GENE, encodes a GAM1161 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1161 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1161 precursor RNA is designated SEQ ID:1134, and is provided hereinbelow with reference to the sequence listing part.

[18149] GAM1161 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18150] An enzyme complex designated DICER COMPLEX, dices the GAM1161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1161 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1161 RNA is designated SEQ ID:2810, and is provided hereinbelow with reference to the sequence listing part.

[18151] GAM1161 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1161 target RNA, herein designated GAM TARGET RNA. GAM1161 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18152] GAM1161 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1161 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1161 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1161 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1161 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[18153] The complementary binding of GAM1161 RNA, herein designated GAM RNA, to target binding sites on GAM1161 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1161 target RNA, herein designated GAM TARGET RNA, into GAM1161 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18154] It is appreciated that GAM1161 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1161 target genes. The mRNA of each one of this plurality of GAM1161 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1161 RNA, herein designated GAM RNA, and which when bound by GAM1161 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1161 target proteins.

[18155] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1161 gene, herein designated GAM GENE, on one or

more GAM1161 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18156] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1161 correlate with, and may be deduced from, the identity of the target genes which GAM1161 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18157] Nucleotide sequences of the GAM1161 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1161 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1161 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1161 are further de-

scribed hereinbelow with reference to Table Table1.

[18158] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1161 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18159] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1162 (GAM1162) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18160] GAM1162 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1162 was detected is described hereinabove with reference to Figs. 2-8.

[18161] GAM1162 gene, herein designated GAM GENE, and GAM1162 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18162] GAM1162 gene, herein designated GAM GENE, encodes a GAM1162 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1162 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1162 precursor RNA is designated SEQ ID:1135, and is provided hereinbelow with reference to the sequence listing part.

[18163] GAM1162 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18164] An enzyme complex designated DICER COMPLEX, dices the GAM1162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1162 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1162 RNA is designated SEQ ID:2811, and is provided hereinbelow with reference to the sequence listing part.

[18165] GAM1162 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1162 target RNA, herein designated GAM TARGET RNA. GAM1162 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18166] GAM1162 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1162 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1162 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1162 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1162 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18167] The complementary binding of GAM1162 RNA, herein designated GAM RNA, to target binding sites on GAM1162 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1162 target RNA, herein designated GAM TARGET RNA, into GAM1162 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18168] It is appreciated that GAM1162 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1162 target genes. The mRNA of each one of this plurality of GAM1162 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1162 RNA, herein designated GAM RNA, and which when bound by GAM1162 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1162 target proteins.

[18169] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1162 gene, herein designated GAM GENE, on one or more GAM1162 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18170] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1162 correlate with, and may be deduced from, the identity of the target genes which GAM1162 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18171] Nucleotide sequences of the GAM1162 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1162 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1162 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1162 are further described hereinbelow with reference to Table Table1.

[18172] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1162 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18173] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1163 (GAM1163) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18174] GAM1163 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1163 was detected is described hereinabove with reference to Figs. 2-8.

[18175] GAM1163 gene, herein designated GAM GENE, and GAM1163 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18176] GAM1163 gene, herein designated GAM GENE, encodes a GAM1163 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1163 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1163 precursor RNA is designated SEQ ID:1136, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1136 is located at position 1471877 relative to contig NT_027140.5, on chromosome 13.

[18177] GAM1163 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18178] An enzyme complex designated DICER COMPLEX, dices the GAM1163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1163 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1163 RNA is designated SEQ ID:2812, and is provided hereinbelow with reference to the sequence listing part.

[18179] GAM1163 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1163 target RNA, herein designated GAM TARGET RNA. GAM1163 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18180] GAM1163 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1163 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1163 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1163 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1163 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18181] The complementary binding of GAM1163 RNA, herein designated GAM RNA, to target binding sites on GAM1163 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1163 target RNA, herein designated GAM TARGET RNA, into GAM1163 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18182] It is appreciated that GAM1163 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1163 target genes. The mRNA of each one of this plurality of GAM1163 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1163 RNA, herein designated GAM RNA, and which when bound by GAM1163 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1163 target proteins.

[18183] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1163 gene, herein designated GAM GENE, on one or more GAM1163 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18184] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1163 correlate with, and may be deduced from, the identity of the target genes which GAM1163 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18185] Nucleotide sequences of the GAM1163 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1163 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1163 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1163 are further described hereinbelow with reference to Table Table1.

[18186] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1163 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18187] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1164 (GAM1164) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18188] GAM1164 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1164 was detected is described hereinabove with reference to Figs. 2-8.

[18189] GAM1164 gene, herein designated GAM GENE, and GAM1164 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18190] GAM1164 gene, herein designated GAM GENE, encodes a GAM1164 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1164 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1164 precursor RNA is designated SEQ ID:1137, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1137 is located at position 2111206 relative to contig NT_034410.2, on chromosome 1.

[18191] GAM1164 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18192] An enzyme complex designated DICER COMPLEX, dices the GAM1164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1164 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1164 RNA is designated SEQ ID:2813, and is provided hereinbelow with reference to the sequence listing part.

[18193] GAM1164 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1164 target RNA, herein designated GAM TARGET RNA. GAM1164 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18194] GAM1164 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1164 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1164 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1164 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1164 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18195] The complementary binding of GAM1164 RNA, herein designated GAM RNA, to target binding sites on GAM1164 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1164 target RNA, herein designated GAM TARGET RNA, into GAM1164 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18196] It is appreciated that GAM1164 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1164 target genes. The mRNA of each one of this

plurality of GAM1164 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1164 RNA, herein designated GAM RNA, and which when bound by GAM1164 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1164 target proteins.

[18197] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1164 gene, herein designated GAM GENE, on one or more GAM1164 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18198] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1164 correlate with, and may be deduced from, the identity of the target genes which GAM1164 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18199] Nucleotide sequences of the GAM1164 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1164 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1164 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1164 are further described hereinbelow with reference to Table Table1.

[18200] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1164 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18201] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1165 (GAM1165) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[18202] GAM1165 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1165 was detected is described hereinabove with reference to Figs. 2-8.

[18203] GAM1165 gene, herein designated GAM GENE, and GAM1165 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18204] GAM1165 gene, herein designated GAM GENE, encodes a GAM1165 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1165 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1165 precursor RNA is designated SEQ ID:1138, and is provided hereinbelow with reference to the sequence listing part.

[18205] GAM1165 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18206] An enzyme complex designated DICER COMPLEX, dices the GAM1165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1165 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1165 RNA is designated SEQ ID:2814, and is provided hereinbelow with reference to the sequence listing part.

[18207] GAM1165 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1165 target RNA, herein designated GAM TARGET RNA. GAM1165 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[18208] GAM1165 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1165 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1165 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1165 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1165 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18209] The complementary binding of GAM1165 RNA, herein

designated GAM RNA, to target binding sites on GAM1165 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1165 target RNA, herein designated GAM TARGET RNA, into GAM1165 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18210] It is appreciated that GAM1165 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1165 target genes. The mRNA of each one of this plurality of GAM1165 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1165 RNA, herein designated GAM RNA, and which when bound by GAM1165 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1165 target proteins.

[18211] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1165 gene, herein designated GAM GENE, on one or more GAM1165 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18212] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1165 correlate with, and may be deduced from, the identity of the target genes which GAM1165 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18213] Nucleotide sequences of the GAM1165 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1165 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1165 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1165 are further described hereinbelow with reference to Table Table1.

[18214] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1165 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18215] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1166 (GAM1166) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18216] GAM1166 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1166 was detected is described hereinabove with reference to Figs. 2-8.

[18217] GAM1166 gene, herein designated GAM GENE, and GAM1166 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18218] GAM1166 gene, herein designated GAM GENE, encodes a GAM1166 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1166 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1166 precursor RNA is designated SEQ ID:1139, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1139 is located at position 20390664 relative to contig NT_024524.11, on chromosome 13.

[18219] GAM1166 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18220] An enzyme complex designated DICER COMPLEX, dices the GAM1166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1166 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1166 RNA is designated SEQ ID:2815, and is provided hereinbelow with reference to the sequence listing part.

[18221] GAM1166 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1166 target RNA, herein designated GAM TARGET RNA. GAM1166 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18222] GAM1166 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1166 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1166 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1166 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1166 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18223] The complementary binding of GAM1166 RNA, herein designated GAM RNA, to target binding sites on GAM1166 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1166 target RNA, herein designated GAM TARGET RNA, into GAM1166 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18224] It is appreciated that GAM1166 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1166 target genes. The mRNA of each one of this plurality of GAM1166 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1166 RNA, herein designated GAM RNA, and which when bound by GAM1166 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1166 target proteins.

[18225] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1166 gene, herein designated GAM GENE, on one or more GAM1166 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18226] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1166 correlate with, and may be deduced from, the identity of the target genes which GAM1166 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18227] Nucleotide sequences of the GAM1166 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1166 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1166 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1166 are further described hereinbelow with reference to Table Table1.

[18228] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1166 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18229] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1167 (GAM1167) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18230] GAM1167 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1167 was detected is described hereinabove with reference to Figs. 2-8.

[18231] GAM1167 gene, herein designated GAM GENE, and GAM1167 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18232] GAM1167 gene, herein designated GAM GENE, encodes a GAM1167 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1167 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1167 precursor RNA is designated SEQ ID:1140, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1140 is located at position 404102 relative to contig NT_011530.10, on chromosome X.

[18233] GAM1167 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:97977, which mouse homolog is detected in mouse EST accession BB355006.2.

[18234] GAM1167 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18235] An enzyme complex designated DICER COMPLEX, dices the GAM1167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1167 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1167 RNA is designated SEQ ID:2816, and is provided hereinbelow with reference to the sequence listing part.

[18236] GAM1167 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1167 target RNA, herein designated GAM TARGET RNA. GAM1167 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18237] GAM1167 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1167 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1167 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1167 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1167 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18238] The complementary binding of GAM1167 RNA, herein designated GAM RNA, to target binding sites on GAM1167 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1167 target RNA, herein designated GAM TARGET RNA, into GAM1167 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18239] It is appreciated that GAM1167 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1167 target genes. The mRNA of each one of this plurality of GAM1167 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1167 RNA, herein designated GAM RNA, and which when bound by GAM1167 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1167 target proteins.

[18240] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1167 gene, herein designated GAM GENE, on one or more GAM1167 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18241] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1167 correlate with, and may be deduced from, the identity of the target genes which GAM1167 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18242] Nucleotide sequences of the GAM1167 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1167 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1167 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1167 are further described hereinbelow with reference to Table Table1.

[18243] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1167 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18244] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1168 (GAM1168) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18245] GAM1168 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1168 was detected is described hereinabove with reference to Figs. 2-8.

[18246] GAM1168 gene, herein designated GAM GENE, and GAM1168 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[18247] GAM1168 gene, herein designated GAM GENE, encodes a GAM1168 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1168 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1168 precursor RNA is designated SEQ ID:1141, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1141 is located at position 1235095 relative to contig NT_009526.11, on chromosome 12.

[18248] GAM1168 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[18249] SEQ ID:100023 detected in mouse EST Accession AI326210.1.

[18250] SEQ ID:98954 detected in mouse EST Accession BI965972.1.

[18251] SEQ ID:98955 detected in mouse EST Accession BI965652.1.

[18252] GAM1168 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18253] An enzyme complex designated DICER COMPLEX, dices the GAM1168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1168 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1168 RNA is designated SEQ ID:2817, and is provided hereinbelow with reference to the sequence listing part.

[18254] GAM1168 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1168 target RNA, herein designated GAM TARGET RNA. GAM1168 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18255] GAM1168 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1168 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1168 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1168 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1168 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18256] The complementary binding of GAM1168 RNA, herein designated GAM RNA, to target binding sites on GAM1168 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1168 target RNA, herein designated GAM TARGET RNA, into GAM1168 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18257] It is appreciated that GAM1168 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1168 target genes. The mRNA of each one of this plurality of GAM1168 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1168 RNA, herein designated GAM RNA, and which when bound by GAM1168 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1168 target proteins.

[18258] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1168 gene, herein designated GAM GENE, on one or more GAM1168 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18259] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1168 correlate with, and may be deduced from, the identity of the target genes which GAM1168 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18260] Nucleotide sequences of the GAM1168 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1168 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1168 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1168 are further described hereinbelow with reference to Table Table1.

[18261] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1168 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18262] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1169 (GAM1169) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18263] GAM1169 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1169 was detected is described hereinabove with reference to Figs. 2-8.

[18264] GAM1169 gene, herein designated GAM GENE, and GAM1169 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[18265] GAM1169 gene, herein designated GAM GENE, encodes a GAM1169 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1169 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1169 precursor RNA is designated SEQ ID:1142, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1142 is located at position 174359 relative to contig NT_007819.11, on chromosome 7.

[18266] GAM1169 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18267] An enzyme complex designated DICER COMPLEX, dices

the GAM1169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1169 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1169 RNA is designated SEQ ID:2818, and is provided hereinbelow with reference to the sequence listing part.

[18268] GAM1169 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1169 target RNA, herein designated GAM TARGET RNA. GAM1169 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18269] GAM1169 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1169 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1169 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1169 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1169 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18270] The complementary binding of GAM1169 RNA, herein designated GAM RNA, to target binding sites on GAM1169 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1169 target RNA, herein designated GAM TARGET RNA, into GAM1169 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18271] It is appreciated that GAM1169 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1169 target genes. The mRNA of each one of this plurality of GAM1169 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1169 RNA, herein designated GAM RNA, and which when bound by GAM1169 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1169 target proteins.

[18272] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1169 gene, herein designated GAM GENE, on one or more GAM1169 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18273] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1169 correlate with, and may be deduced from, the identity of the target genes which GAM1169 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18274] Nucleotide sequences of the GAM1169 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1169 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1169 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1169 are further described hereinbelow with reference to Table Table1.

[18275] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1169 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18276] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1170 (GAM1170) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18277] GAM1170 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1170 was detected is described hereinabove with reference to Figs. 2-8.

[18278] GAM1170 gene, herein designated GAM GENE, and GAM1170 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18279] GAM1170 gene, herein designated GAM GENE, encodes a GAM1170 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1170 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1170 precursor RNA is designated SEQ ID:1143, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1143 is located at position 1654434 rela-

tive to contig NT_005986.13, on chromosome 3.

[18280] GAM1170 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18281] An enzyme complex designated DICER COMPLEX, dices the GAM1170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1170 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1170 RNA is designated SEQ ID:2819, and is provided hereinbelow with reference to the sequence listing part.

[18282] GAM1170 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1170 target RNA, herein designated GAM TARGET RNA. GAM1170 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18283] GAM1170 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1170 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1170 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1170 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1170 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18284] The complementary binding of GAM1170 RNA, herein designated GAM RNA, to target binding sites on GAM1170 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1170 target RNA, herein designated GAM TARGET RNA, into GAM1170 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18285] It is appreciated that GAM1170 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1170 target genes. The mRNA of each one of this plurality of GAM1170 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1170 RNA, herein designated GAM RNA, and which when bound by GAM1170 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1170

target proteins.

[18286] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1170 gene, herein designated GAM GENE, on one or more GAM1170 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18287] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1170 correlate with, and may be deduced from, the identity of the target genes which GAM1170 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18288] Nucleotide sequences of the GAM1170 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1170 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1170 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1170 are further described hereinbelow with reference to Table Table1.

[18289] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1170 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18290] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1171 (GAM1171) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18291] GAM1171 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1171 was detected is described hereinabove with reference to Figs. 2-8.

[18292] GAM1171 gene, herein designated GAM GENE, and

GAM1171 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18293] GAM1171 gene, herein designated GAM GENE, encodes a GAM1171 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1171 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1171 precursor RNA is designated SEQ ID:1144, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1144 is located at position 1654434 relative to contig NT_005986.13, on chromosome 3.

[18294] GAM1171 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18295] An enzyme complex designated DICER COMPLEX, dices the GAM1171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1171 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1171 RNA is designated SEQ ID:2820, and is provided hereinbelow with reference to the sequence listing part.

[18296] GAM1171 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1171 target RNA, herein designated GAM TARGET RNA. GAM1171 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18297] GAM1171 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1171 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1171 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1171 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1171 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18298] The complementary binding of GAM1171 RNA, herein designated GAM RNA, to target binding sites on GAM1171 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1171 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1171 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18299] It is appreciated that GAM1171 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1171 target genes. The mRNA of each one of this plurality of GAM1171 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1171 RNA, herein designated GAM RNA, and which when bound by GAM1171 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1171 target proteins.

[18300] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1171 gene, herein designated GAM GENE, on one or more GAM1171 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18301] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1171 correlate with, and may be deduced from, the identity of the target genes which GAM1171 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18302] Nucleotide sequences of the GAM1171 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1171 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1171 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1171 are further described hereinbelow with reference to Table Table1.

[18303] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1171 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[18304] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1172 (GAM1172) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18305] GAM1172 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1172 was detected is described hereinabove with reference to Figs. 2-8.

[18306] GAM1172 gene, herein designated GAM GENE, and GAM1172 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18307] GAM1172 gene, herein designated GAM GENE, encodes a GAM1172 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1172 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1172 precursor RNA is designated SEQ ID:1145, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1145 is located at position 2556957 relative to contig NT_011196.11, on chromosome 19.

[18308] GAM1172 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18309] An enzyme complex designated DICER COMPLEX, dices the GAM1172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1172 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1172 RNA is designated SEQ ID:2821, and is provided hereinbelow with reference to the sequence

listing part.

[18310] GAM1172 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1172 target RNA, herein designated GAM TARGET RNA. GAM1172 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18311] GAM1172 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1172 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1172 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1172 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1172 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18312] The complementary binding of GAM1172 RNA, herein designated GAM RNA, to target binding sites on GAM1172 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1172 target RNA, herein designated GAM TARGET RNA, into GAM1172 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18313] It is appreciated that GAM1172 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1172 target genes. The mRNA of each one of this plurality of GAM1172 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1172 RNA, herein designated GAM RNA, and which when bound by GAM1172 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1172 target proteins.

[18314] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1172 gene, herein designated GAM GENE, on one or more GAM1172 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18315] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1172 correlate with, and may be deduced from, the identity of the target genes which GAM1172 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18316] Nucleotide sequences of the GAM1172 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1172 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1172 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1172 are further described hereinbelow with reference to Table Table1.

[18317] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1172 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18318] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1173 (GAM1173) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18319] GAM1173 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1173 was detected is described hereinabove with reference to Figs. 2-8.

[18320] GAM1173 gene, herein designated GAM GENE, and GAM1173 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18321] GAM1173 gene, herein designated GAM GENE, encodes a GAM1173 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1173 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1173 precursor RNA is designated SEQ ID:1146, and is provided hereinbelow with reference to the sequence listing part.

[18322] GAM1173 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18323] An enzyme complex designated DICER COMPLEX, dices

the GAM1173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1173 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1173 RNA is designated SEQ ID:2822, and is provided hereinbelow with reference to the sequence listing part.

[18324] GAM1173 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1173 target RNA, herein designated GAM TARGET RNA. GAM1173 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18325] GAM1173 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1173 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1173 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1173 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1173 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18326] The complementary binding of GAM1173 RNA, herein designated GAM RNA, to target binding sites on GAM1173 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1173 target RNA, herein designated GAM TARGET RNA, into GAM1173 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18327] It is appreciated that GAM1173 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1173 target genes. The mRNA of each one of this plurality of GAM1173 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1173 RNA, herein designated GAM RNA, and which when bound by GAM1173 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1173 target proteins.

[18328] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1173 gene, herein designated GAM GENE, on one or more GAM1173 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18329] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1173 correlate with, and may be deduced from, the identity of the target genes which GAM1173 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18330] Nucleotide sequences of the GAM1173 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1173 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1173 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1173 are further described hereinbelow with reference to Table Table1.

[18331] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1173 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18332] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1174 (GAM1174) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18333] GAM1174 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1174 was detected is described hereinabove with reference to Figs. 2-8.

[18334] GAM1174 gene, herein designated GAM GENE, and GAM1174 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18335] GAM1174 gene, herein designated GAM GENE, encodes a GAM1174 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1174 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1174 precursor RNA is designated SEQ ID:1147, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1147 is located at position 365849 relative

to contig NT_010799.11, on chromosome 17.

[18336] GAM1174 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[18337] SEQ ID:99289 detected in mouse EST Accession AA144533.1.

[18338] SEQ ID:99290 detected in mouse EST Accession AA671455.1.

[18339] SEQ ID:99291 detected in mouse EST Accession BE691413.1.

[18340] SEQ ID:99292 detected in mouse EST Accession BE691447.1.

[18341] SEQ ID:99293 detected in mouse EST Accession BG145596.1.

[18342] SEQ ID:99294 detected in mouse EST Accession BE692802.1.

[18343] SEQ ID:99312 detected in mouse EST Accession AW208601.1.

[18344] SEQ ID:99313 detected in mouse EST Accession BB609859.1.

[18345] SEQ ID:99314 detected in mouse EST Accession

AW824753.1.

[18346] SEQ ID:99315 detected in mouse EST Accession BE943987.1.

[18347] SEQ ID:99316 detected in mouse EST Accession BG808025.1.

[18348] SEQ ID:99317 detected in mouse EST Accession BG808010.1.

[18349] SEQ ID:99318 detected in mouse EST Accession BG807850.1.

[18350] SEQ ID:99319 detected in mouse EST Accession BG805970.1.

[18351] SEQ ID:99320 detected in mouse EST Accession BB610842.1.

[18352] GAM1174 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18353] An enzyme complex designated DICER COMPLEX, dices the GAM1174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1174 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1174 RNA is designated SEQ ID:2823, and is provided hereinbelow with reference to the sequence listing part.

[18354] GAM1174 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1174 target RNA, herein designated GAM TARGET RNA. GAM1174 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18355] GAM1174 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1174 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1174 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1174 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1174 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18356] The complementary binding of GAM1174 RNA, herein designated GAM RNA, to target binding sites on GAM1174 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1174 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1174 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18357] It is appreciated that GAM1174 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1174 target genes. The mRNA of each one of this plurality of GAM1174 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1174 RNA, herein designated GAM RNA, and which when bound by GAM1174 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1174 target proteins.

[18358] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1174 gene, herein designated GAM GENE, on one or more GAM1174 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18359] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1174 correlate with, and may be deduced from, the identity of the target genes which GAM1174 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18360] Nucleotide sequences of the GAM1174 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1174 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1174 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1174 are further described hereinbelow with reference to Table Table1.

[18361] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1174 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[18362] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1175 (GAM1175) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18363] GAM1175 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1175 was detected is described hereinabove with reference to Figs. 2-8.

[18364] GAM1175 gene, herein designated GAM GENE, and GAM1175 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18365] GAM1175 gene, herein designated GAM GENE, encodes a GAM1175 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1175 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1175 precursor RNA is designated SEQ ID:1148, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1148 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[18366] GAM1175 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18367] An enzyme complex designated DICER COMPLEX, dices the GAM1175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1175 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1175 RNA is designated SEQ ID:2824, and is provided hereinbelow with reference to the sequence

listing part.

[18368] GAM1175 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1175 target RNA, herein designated GAM TARGET RNA. GAM1175 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18369] GAM1175 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1175 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1175 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1175 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1175 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18370] The complementary binding of GAM1175 RNA, herein designated GAM RNA, to target binding sites on GAM1175

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1175 target RNA, herein designated GAM TARGET RNA, into GAM1175 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18371] It is appreciated that GAM1175 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1175 target genes. The mRNA of each one of this plurality of GAM1175 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1175 RNA, herein designated GAM RNA, and which when bound by GAM1175 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1175 target proteins.

[18372] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1175 gene, herein designated GAM GENE, on one or more GAM1175 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18373] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1175 correlate with, and may be deduced from, the identity of the target genes which GAM1175 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18374] Nucleotide sequences of the GAM1175 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1175 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1175 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1175 are further described hereinbelow with reference to Table Table1.

[18375] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1175 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18376] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1176 (GAM1176) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18377] GAM1176 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1176 was detected is described hereinabove with reference to Figs. 2-8.

[18378] GAM1176 gene, herein designated GAM GENE, and GAM1176 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18379] GAM1176 gene, herein designated GAM GENE, encodes a GAM1176 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1176 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1176 precursor RNA is designated SEQ ID:1149, and is provided hereinbelow with reference to the sequence listing part.

[18380] GAM1176 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18381] An enzyme complex designated DICER COMPLEX, dices the GAM1176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1176 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1176 RNA is designated SEQ ID:2825, and

is provided hereinbelow with reference to the sequence listing part.

[18382] GAM1176 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1176 target RNA, herein designated GAM TARGET RNA. GAM1176 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18383] GAM1176 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1176 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1176 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1176 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1176 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18384] The complementary binding of GAM1176 RNA, herein designated GAM RNA, to target binding sites on GAM1176 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1176 target RNA, herein designated GAM TARGET RNA, into GAM1176 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18385] It is appreciated that GAM1176 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1176 target genes. The mRNA of each one of this plurality of GAM1176 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1176 RNA, herein designated GAM RNA, and which when bound by

GAM1176 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1176 target proteins.

[18386] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1176 gene, herein designated GAM GENE, on one or more GAM1176 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18387] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1176 correlate with, and may be deduced from, the identity of the target genes which GAM1176 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[18388] Nucleotide sequences of the GAM1176 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1176 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1176 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1176 are further described hereinbelow with reference to Table Table1.

[18389] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1176 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18390] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1177 (GAM1177) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18391] GAM1177 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1177 was detected is described hereinabove

with reference to Figs. 2-8.

[18392] GAM1177 gene, herein designated GAM GENE, and GAM1177 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18393] GAM1177 gene, herein designated GAM GENE, encodes a GAM1177 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1177 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1177 precursor RNA is designated SEQ ID:1150, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1150 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[18394] GAM1177 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18395] An enzyme complex designated DICER COMPLEX, dices the GAM1177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1177 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1177 RNA is designated SEQ ID:2826, and is provided hereinbelow with reference to the sequence listing part.

[18396] GAM1177 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1177 target RNA, herein designated GAM TARGET RNA. GAM1177 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18397] GAM1177 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1177 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1177 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1177 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1177 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18398] The complementary binding of GAM1177 RNA, herein designated GAM RNA, to target binding sites on GAM1177 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1177 target RNA, herein designated GAM TARGET RNA, into GAM1177 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18399] It is appreciated that GAM1177 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1177 target genes. The mRNA of each one of this plurality of GAM1177 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1177 RNA, herein designated GAM RNA, and which when bound by GAM1177 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1177 target proteins.

[18400] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1177 gene, herein designated GAM GENE, on one or more GAM1177 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18401] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1177 correlate with, and may be deduced from, the identity of the target genes which GAM1177 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18402] Nucleotide sequences of the GAM1177 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1177 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1177 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1177 are further described hereinbelow with reference to Table Table1.

[18403] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1177 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18404] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1178 (GAM1178) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18405] GAM1178 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1178 was detected is described hereinabove with reference to Figs. 2-8.

[18406] GAM1178 gene, herein designated GAM GENE, and GAM1178 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18407] GAM1178 gene, herein designated GAM GENE, encodes a GAM1178 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1178 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1178 precursor RNA is

designated SEQ ID:1151, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1151 is located at position 464436 relative to contig NT_010692.9, on chromosome 17.

[18408] GAM1178 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[18409] SEQ ID:98201 detected in mouse EST Accession AA068787.1.

[18410] SEQ ID:98202 detected in mouse EST Accession BE625629.1.

[18411] SEQ ID:98203 detected in mouse EST Accession BI792530.1.

[18412] SEQ ID:98204 detected in mouse EST Accession BE380224.1.

[18413] SEQ ID:98205 detected in mouse EST Accession BE309708.1.

[18414] SEQ ID:98206 detected in mouse EST Accession BI100916.1.

[18415] SEQ ID:98208 detected in mouse EST Accession AA823029.1.

[18416] SEQ ID:98209 detected in mouse EST Accession BG296866.1.

[18417] GAM1178 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18418] An enzyme complex designated DICER COMPLEX, dices the GAM1178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1178 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 97%) nucleotide sequence of GAM1178 RNA is designated SEQ ID:2827, and is provided hereinbelow with reference to the sequence

listing part.

[18419] GAM1178 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1178 target RNA, herein designated GAM TARGET RNA. GAM1178 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18420] GAM1178 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1178 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1178 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1178 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1178 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18421] The complementary binding of GAM1178 RNA, herein designated GAM RNA, to target binding sites on GAM1178 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1178 target RNA, herein designated GAM TARGET RNA, into GAM1178 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18422] It is appreciated that GAM1178 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1178 target genes. The mRNA of each one of this plurality of GAM1178 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1178 RNA, herein designated GAM RNA, and which when bound by GAM1178 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1178 target proteins.

[18423] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1178 gene, herein designated GAM GENE, on one or more GAM1178 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18424] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1178 correlate with, and may be deduced from, the identity of the target genes which GAM1178 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18425] Nucleotide sequences of the GAM1178 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1178 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1178 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1178 are further described hereinbelow with reference to Table Table1.

[18426] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1178 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18427] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1179 (GAM1179) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18428] GAM1179 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1179 was detected is described hereinabove with reference to Figs. 2-8.

[18429] GAM1179 gene, herein designated GAM GENE, and GAM1179 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18430] GAM1179 gene, herein designated GAM GENE, encodes a GAM1179 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1179 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1179 precursor RNA is designated SEQ ID:1152, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1152 is located at position 524765 relative to contig NT_035456.2, on chromosome 17.

[18431] GAM1179 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[18432] An enzyme complex designated DICER COMPLEX, dices the GAM1179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1179 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1179 RNA is designated SEQ ID:2828, and is provided hereinbelow with reference to the sequence listing part.

[18433] GAM1179 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1179 target RNA, herein designated GAM TARGET RNA. GAM1179 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18434] GAM1179 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1179 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1179 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1179 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1179 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18435] The complementary binding of GAM1179 RNA, herein designated GAM RNA, to target binding sites on GAM1179 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1179 target RNA, herein designated GAM TARGET RNA, into GAM1179 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18436] It is appreciated that GAM1179 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1179 target genes. The mRNA of each one of this plurality of GAM1179 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1179 RNA, herein designated GAM RNA, and which when bound by GAM1179 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1179 target proteins.

[18437] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1179 gene, herein designated GAM GENE, on one or more GAM1179 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18438] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1179 correlate with, and may be deduced from, the identity of the target genes which GAM1179 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18439] Nucleotide sequences of the GAM1179 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1179 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1179 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1179 are further described hereinbelow with reference to Table Table1.

[18440] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1179 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18441] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1180 (GAM1180) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18442] GAM1180 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1180 was detected is described hereinabove with reference to Figs. 2-8.

[18443] GAM1180 gene, herein designated GAM GENE, and GAM1180 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18444] GAM1180 gene, herein designated GAM GENE, encodes a GAM1180 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1180 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1180 precursor RNA is designated SEQ ID:1153, and is provided hereinbelow with

reference to the sequence listing part.

[18445] GAM1180 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18446] An enzyme complex designated DICER COMPLEX, dices the GAM1180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1180 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1180 RNA is designated SEQ ID:2829, and is provided hereinbelow with reference to the sequence listing part.

[18447] GAM1180 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1180 target RNA, herein designated GAM TARGET RNA. GAM1180 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18448] GAM1180 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1180 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1180 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1180 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1180 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18449] The complementary binding of GAM1180 RNA, herein designated GAM RNA, to target binding sites on GAM1180 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1180 target RNA, herein designated GAM TARGET RNA, into GAM1180 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18450] It is appreciated that GAM1180 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1180 target genes. The mRNA of each one of this plurality of GAM1180 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1180 RNA, herein designated GAM RNA, and which when bound by GAM1180 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1180

target proteins.

[18451] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1180 gene, herein designated GAM GENE, on one or more GAM1180 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18452] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1180 correlate with, and may be deduced from, the identity of the target genes which GAM1180 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18453] Nucleotide sequences of the GAM1180 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1180 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1180 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1180 are further described hereinbelow with reference to Table Table1.

[18454] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1180 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18455] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1181 (GAM1181) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18456] GAM1181 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1181 was detected is described hereinabove with reference to Figs. 2-8.

[18457] GAM1181 gene, herein designated GAM GENE, and

GAM1181 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18458] GAM1181 gene, herein designated GAM GENE, encodes a GAM1181 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1181 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1181 precursor RNA is designated SEQ ID:1154, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1154 is located at position 579693 relative to contig NT_023451.11, on chromosome 6.

[18459] GAM1181 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18460] An enzyme complex designated DICER COMPLEX, dices the GAM1181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1181 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1181 RNA is designated SEQ ID:2830, and is provided hereinbelow with reference to the sequence listing part.

[18461] GAM1181 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1181 target RNA, herein designated GAM TARGET RNA. GAM1181 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18462] GAM1181 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1181 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1181 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1181 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1181 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18463] The complementary binding of GAM1181 RNA, herein designated GAM RNA, to target binding sites on GAM1181 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1181 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1181 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18464] It is appreciated that GAM1181 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1181 target genes. The mRNA of each one of this plurality of GAM1181 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1181 RNA, herein designated GAM RNA, and which when bound by GAM1181 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1181 target proteins.

[18465] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1181 gene, herein designated GAM GENE, on one or more GAM1181 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18466] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1181 correlate with, and may be deduced from, the identity of the target genes which GAM1181 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18467] Nucleotide sequences of the GAM1181 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1181 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1181 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1181 are further described hereinbelow with reference to Table Table1.

[18468] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1181 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[18469] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1182 (GAM1182) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18470] GAM1182 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1182 was detected is described hereinabove with reference to Figs. 2-8.

[18471] GAM1182 gene, herein designated GAM GENE, and GAM1182 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18472] GAM1182 gene, herein designated GAM GENE, encodes a GAM1182 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1182 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1182 precursor RNA is designated SEQ ID:1155, and is provided hereinbelow with reference to the sequence listing part.

[18473] GAM1182 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18474] An enzyme complex designated DICER COMPLEX, dices the GAM1182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1182 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1182 RNA is designated SEQ ID:2831, and is provided hereinbelow with reference to the sequence listing part.

[18475] GAM1182 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1182 target RNA, herein designated GAM TARGET RNA. GAM1182 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18476] GAM1182 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1182 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1182 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1182 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1182 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18477] The complementary binding of GAM1182 RNA, herein designated GAM RNA, to target binding sites on GAM1182 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1182 target RNA, herein designated GAM TARGET RNA, into GAM1182 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18478] It is appreciated that GAM1182 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1182 target genes. The mRNA of each one of this plurality of GAM1182 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1182 RNA, herein designated GAM RNA, and which when bound by GAM1182 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1182 target proteins.

[18479] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1182 gene, herein designated GAM GENE, on one or more GAM1182 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18480] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1182 correlate with, and may be deduced from, the identity of the target genes which GAM1182 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18481] Nucleotide sequences of the GAM1182 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1182 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1182 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1182 are further described hereinbelow with reference to Table Table1.

[18482] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1182 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18483] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1183 (GAM1183) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18484] GAM1183 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1183 was detected is described hereinabove with reference to Figs. 2-8.

[18485] GAM1183 gene, herein designated GAM GENE, and GAM1183 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[18486] GAM1183 gene, herein designated GAM GENE, encodes a GAM1183 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1183 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1183 precursor RNA is designated SEQ ID:1156, and is provided hereinbelow with reference to the sequence listing part.

[18487] GAM1183 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18488] An enzyme complex designated DICER COMPLEX, dices the GAM1183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1183 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1183 RNA is designated SEQ ID:2832, and is provided hereinbelow with reference to the sequence listing part.

[18489] GAM1183 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1183 target RNA, herein designated GAM TARGET RNA. GAM1183 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18490] GAM1183 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1183 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1183 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1183 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1183 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18491] The complementary binding of GAM1183 RNA, herein designated GAM RNA, to target binding sites on GAM1183 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1183 target RNA, herein designated GAM TARGET RNA, into GAM1183 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18492] It is appreciated that GAM1183 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1183 target genes. The mRNA of each one of this plurality of GAM1183 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1183 RNA, herein designated GAM RNA, and which when bound by GAM1183 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1183 target proteins.

[18493] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1183 gene, herein designated GAM GENE, on one or more GAM1183 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18494] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1183 correlate with, and may be deduced from, the identity of the target genes which GAM1183 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18495] Nucleotide sequences of the GAM1183 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1183 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1183 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1183 are further described hereinbelow with reference to Table Table1.

[18496] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1183 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18497] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1184 (GAM1184) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18498] GAM1184 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1184 was detected is described hereinabove with reference to Figs. 2-8.

[18499] GAM1184 gene, herein designated GAM GENE, and GAM1184 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18500] GAM1184 gene, herein designated GAM GENE, encodes a GAM1184 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1184 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1184 precursor RNA is designated SEQ ID:1157, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1157 is located at position 840738 relative to contig NT_011530.10, on chromosome X.

[18501] GAM1184 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18502] An enzyme complex designated DICER COMPLEX, dices the GAM1184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1184 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1184 RNA is designated SEQ ID:2833, and is provided hereinbelow with reference to the sequence listing part.

[18503] GAM1184 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1184 target RNA, herein designated GAM TARGET RNA. GAM1184 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18504] GAM1184 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1184 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1184 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1184 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1184 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18505] The complementary binding of GAM1184 RNA, herein designated GAM RNA, to target binding sites on GAM1184 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1184 target RNA, herein designated GAM TARGET RNA, into GAM1184 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18506] It is appreciated that GAM1184 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1184 target genes. The mRNA of each one of this plurality of GAM1184 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1184 RNA, herein designated GAM RNA, and which when bound by GAM1184 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1184 target proteins.

[18507] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1184 gene, herein designated GAM GENE, on one or more GAM1184 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18508] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1184 correlate with, and may be deduced from, the identity of the target genes which GAM1184 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18509] Nucleotide sequences of the GAM1184 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1184 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1184 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1184 are further described hereinbelow with reference to Table Table1.

[18510] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1184 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18511] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1185 (GAM1185) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18512] GAM1185 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1185 was detected is described hereinabove with reference to Figs. 2-8.

[18513] GAM1185 gene, herein designated GAM GENE, and GAM1185 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18514] GAM1185 gene, herein designated GAM GENE, encodes a GAM1185 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1185 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1185 precursor RNA is designated SEQ ID:1158, and is provided hereinbelow with reference to the sequence listing part.

[18515] GAM1185 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18516] An enzyme complex designated DICER COMPLEX, dices the GAM1185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1185 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1185 RNA is designated SEQ ID:2834, and is provided hereinbelow with reference to the sequence listing part.

[18517] GAM1185 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1185 target RNA, herein designated GAM TARGET RNA. GAM1185 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18518] GAM1185 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1185 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1185 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1185 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1185 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18519] The complementary binding of GAM1185 RNA, herein designated GAM RNA, to target binding sites on GAM1185 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1185 target RNA, herein designated GAM TARGET RNA, into GAM1185 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18520] It is appreciated that GAM1185 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1185 target genes. The mRNA of each one of this plurality of GAM1185 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1185 RNA, herein designated GAM RNA, and which when bound by GAM1185 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1185 target proteins.

[18521] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1185 gene, herein designated GAM GENE, on one or more GAM1185 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18522] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1185 correlate with, and may be deduced from, the identity of the target genes which GAM1185 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18523] Nucleotide sequences of the GAM1185 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1185 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1185 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1185 are further described hereinbelow with reference to Table Table1.

[18524] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1185 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18525] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1186 (GAM1186) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18526] GAM1186 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1186 was detected is described hereinabove with reference to Figs. 2-8.

[18527] GAM1186 gene, herein designated GAM GENE, and GAM1186 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18528] GAM1186 gene, herein designated GAM GENE, encodes a GAM1186 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1186 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1186 precursor RNA is designated SEQ ID:1159, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1159 is located at position 3779424 relative to contig NT_011255.11, on chromosome 19.

[18529] GAM1186 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1186 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18530] An enzyme complex designated DICER COMPLEX, dices the GAM1186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1186 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1186 RNA is designated SEQ ID:2835, and is provided hereinbelow with reference to the sequence listing part.

[18531] GAM1186 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1186 target RNA, herein designated GAM TARGET

RNA. GAM1186 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18532] GAM1186 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1186 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1186 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1186 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1186 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18533] The complementary binding of GAM1186 RNA, herein designated GAM RNA, to target binding sites on GAM1186 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1186 target RNA, herein designated GAM TARGET RNA, into GAM1186 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18534] It is appreciated that GAM1186 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1186 target genes. The mRNA of each one of this plurality of GAM1186 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1186 RNA, herein designated GAM RNA, and which when bound by GAM1186 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1186 target proteins.

[18535] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1186 gene, herein designated GAM GENE, on one or more GAM1186 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18536] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1186 correlate with, and may be deduced from, the identity of the target genes which GAM1186 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18537] Nucleotide sequences of the GAM1186 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1186 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1186 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1186 are further described hereinbelow with reference to Table Table1.

[18538] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1186 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18539] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1187 (GAM1187) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18540] GAM1187 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1187 was detected is described hereinabove with reference to Figs. 2-8.

[18541] GAM1187 gene, herein designated GAM GENE, and GAM1187 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18542] GAM1187 gene, herein designated GAM GENE, encodes a

GAM1187 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1187 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1187 precursor RNA is designated SEQ ID:1160, and is provided hereinbelow with reference to the sequence listing part.

[18543] GAM1187 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18544] An enzyme complex designated DICER COMPLEX, dices the GAM1187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1187 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1187 RNA is designated SEQ ID:2836, and is provided hereinbelow with reference to the sequence listing part.

[18545] GAM1187 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1187 target RNA, herein designated GAM TARGET RNA. GAM1187 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18546] GAM1187 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1187 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1187 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1187 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1187 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18547] The complementary binding of GAM1187 RNA, herein designated GAM RNA, to target binding sites on GAM1187 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1187 target RNA, herein designated GAM TARGET RNA, into GAM1187 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18548] It is appreciated that GAM1187 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1187 target genes. The mRNA of each one of this plurality of GAM1187 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1187 RNA, herein designated GAM RNA, and which when bound by GAM1187 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1187 target proteins.

[18549] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1187 gene, herein designated GAM GENE, on one or more GAM1187 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[18550] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1187 correlate with, and may be deduced from, the identity of the target genes which GAM1187 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18551] Nucleotide sequences of the GAM1187 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1187 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1187 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1187 are further described hereinbelow with reference to Table Table1.

[18552] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1187 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18553] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1188 (GAM1188) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[18554] GAM1188 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1188 was detected is described hereinabove with reference to Figs. 2-8.

[18555] GAM1188 gene, herein designated GAM GENE, and GAM1188 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18556] GAM1188 gene, herein designated GAM GENE, encodes a GAM1188 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1188 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1188 precursor RNA is designated SEQ ID:1161, and is provided hereinbelow with reference to the sequence listing part.

[18557] GAM1188 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18558] An enzyme complex designated DICER COMPLEX, dices the GAM1188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1188 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1188 RNA is designated SEQ ID:2837, and is provided hereinbelow with reference to the sequence listing part.

[18559] GAM1188 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1188 target RNA, herein designated GAM TARGET RNA. GAM1188 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18560] GAM1188 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1188 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1188 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1188 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1188 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18561] The complementary binding of GAM1188 RNA, herein designated GAM RNA, to target binding sites on GAM1188 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1188 target RNA, herein designated GAM TARGET RNA, into GAM1188 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18562] It is appreciated that GAM1188 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1188 target genes. The mRNA of each one of this plurality of GAM1188 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1188 RNA, herein designated GAM RNA, and which when bound by GAM1188 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1188 target proteins.

[18563] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1188 gene, herein designated GAM GENE, on one or more GAM1188 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18564] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1188 correlate with, and may be deduced from, the identity of the target genes which GAM1188 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18565] Nucleotide sequences of the GAM1188 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1188 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1188 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1188 are further described hereinbelow with reference to Table Table1.

[18566] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1188 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18567] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1189 (GAM1189) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18568] GAM1189 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1189 was detected is described hereinabove with reference to Figs. 2-8.

[18569] GAM1189 gene, herein designated GAM GENE, and GAM1189 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18570] GAM1189 gene, herein designated GAM GENE, encodes a GAM1189 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1189 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1189 precursor RNA is designated SEQ ID:1162, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1162 is located at position 4941128 relative to contig NT_004668.13, on chromosome 1.

[18571] GAM1189 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18572] An enzyme complex designated DICER COMPLEX, dices the GAM1189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1189 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1189 RNA is designated SEQ ID:2838, and is provided hereinbelow with reference to the sequence listing part.

[18573] GAM1189 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1189 target RNA, herein designated GAM TARGET RNA. GAM1189 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18574] GAM1189 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1189 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1189 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1189 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1189 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18575] The complementary binding of GAM1189 RNA, herein designated GAM RNA, to target binding sites on GAM1189 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1189 target RNA, herein designated GAM TARGET RNA, into GAM1189 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18576] It is appreciated that GAM1189 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1189 target genes. The mRNA of each one of this

plurality of GAM1189 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1189 RNA, herein designated GAM RNA, and which when bound by GAM1189 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1189 target proteins.

[18577] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1189 gene, herein designated GAM GENE, on one or more GAM1189 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18578] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1189 correlate with, and may be deduced from, the identity of the target genes which GAM1189 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18579] Nucleotide sequences of the GAM1189 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1189 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1189 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1189 are further described hereinbelow with reference to Table Table1.

[18580] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1189 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18581] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1190 (GAM1190) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[18582] GAM1190 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1190 was detected is described hereinabove with reference to Figs. 2-8.

[18583] GAM1190 gene, herein designated GAM GENE, and GAM1190 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18584] GAM1190 gene, herein designated GAM GENE, encodes a GAM1190 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1190 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1190 precursor RNA is designated SEQ ID:1163, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1163 is located at position 7591718 relative to contig NT_033927.3, on chromosome 11.

[18585] GAM1190 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18586] An enzyme complex designated DICER COMPLEX, dices the GAM1190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1190 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1190 RNA is designated SEQ ID:2839, and is provided hereinbelow with reference to the sequence listing part.

[18587] GAM1190 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1190 target RNA, herein designated GAM TARGET RNA. GAM1190 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18588] GAM1190 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1190 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1190 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1190 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1190 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[18589] The complementary binding of GAM1190 RNA, herein designated GAM RNA, to target binding sites on GAM1190 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1190 target RNA, herein designated GAM TARGET RNA, into GAM1190 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18590] It is appreciated that GAM1190 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1190 target genes. The mRNA of each one of this plurality of GAM1190 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1190 RNA, herein designated GAM RNA, and which when bound by GAM1190 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1190 target proteins.

[18591] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1190 gene, herein designated GAM GENE, on one or

more GAM1190 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18592] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1190 correlate with, and may be deduced from, the identity of the target genes which GAM1190 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18593] Nucleotide sequences of the GAM1190 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1190 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1190 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1190 are further de-

scribed hereinbelow with reference to Table Table1.

[18594] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1190 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18595] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1191 (GAM1191) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18596] GAM1191 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1191 was detected is described hereinabove with reference to Figs. 2-8.

[18597] GAM1191 gene, herein designated GAM GENE, and GAM1191 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18598] GAM1191 gene, herein designated GAM GENE, encodes a GAM1191 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1191 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1191 precursor RNA is designated SEQ ID:1164, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1164 is located at position 1235063 relative to contig NT_009526.11, on chromosome 12.

[18599] GAM1191 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[18600] SEQ ID:98422 detected in mouse EST Accession AI326210.1.

[18601] SEQ ID:98423 detected in mouse EST Accession BI965652.1.

[18602] SEQ ID:98693 detected in mouse EST Accession BI965972.1.

[18603] GAM1191 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18604] An enzyme complex designated DICER COMPLEX, dices the GAM1191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1191 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1191 RNA is designated SEQ ID:2840, and is provided hereinbelow with reference to the sequence listing part.

[18605] GAM1191 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1191 target RNA, herein designated GAM TARGET RNA. GAM1191 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18606] GAM1191 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1191 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1191 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1191 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1191 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[18607] The complementary binding of GAM1191 RNA, herein designated GAM RNA, to target binding sites on GAM1191 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1191 target RNA, herein designated GAM TARGET RNA, into GAM1191 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18608] It is appreciated that GAM1191 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1191 target genes. The mRNA of each one of this plurality of GAM1191 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1191 RNA, herein designated GAM RNA, and which when bound by GAM1191 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1191 target proteins.

[18609] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1191 gene, herein designated GAM GENE, on one or

more GAM1191 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18610] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1191 correlate with, and may be deduced from, the identity of the target genes which GAM1191 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18611] Nucleotide sequences of the GAM1191 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1191 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1191 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1191 are further de-

scribed hereinbelow with reference to Table Table1.

[18612] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1191 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18613] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1192 (GAM1192) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18614] GAM1192 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1192 was detected is described hereinabove with reference to Figs. 2-8.

[18615] GAM1192 gene, herein designated GAM GENE, and GAM1192 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18616] GAM1192 gene, herein designated GAM GENE, encodes a GAM1192 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1192 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1192 precursor RNA is designated SEQ ID:1165, and is provided hereinbelow with reference to the sequence listing part.

[18617] GAM1192 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18618] An enzyme complex designated DICER COMPLEX, dices the GAM1192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1192 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1192 RNA is designated SEQ ID:2841, and is provided hereinbelow with reference to the sequence listing part.

[18619] GAM1192 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1192 target RNA, herein designated GAM TARGET RNA. GAM1192 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18620] GAM1192 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1192 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1192 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1192 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1192 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18621] The complementary binding of GAM1192 RNA, herein designated GAM RNA, to target binding sites on GAM1192 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1192 target RNA, herein designated GAM TARGET RNA, into GAM1192 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18622] It is appreciated that GAM1192 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1192 target genes. The mRNA of each one of this plurality of GAM1192 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1192 RNA, herein designated GAM RNA, and which when bound by GAM1192 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1192 target proteins.

[18623] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1192 gene, herein designated GAM GENE, on one or more GAM1192 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18624] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1192 correlate with, and may be deduced from, the identity of the target genes which GAM1192 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18625] Nucleotide sequences of the GAM1192 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1192 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1192 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1192 are further described hereinbelow with reference to Table Table1.

[18626] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1192 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18627] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1193 (GAM1193) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18628] GAM1193 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1193 was detected is described hereinabove with reference to Figs. 2-8.

[18629] GAM1193 gene, herein designated GAM GENE, and GAM1193 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18630] GAM1193 gene, herein designated GAM GENE, encodes a GAM1193 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1193 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1193 precursor RNA is designated SEQ ID:1166, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1166 is located at position 6591313 relative to contig NT_011109.13, on chromosome 19.

[18631] GAM1193 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18632] An enzyme complex designated DICER COMPLEX, dices the GAM1193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1193 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1193 RNA is designated SEQ ID:2842, and is provided hereinbelow with reference to the sequence listing part.

[18633] GAM1193 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1193 target RNA, herein designated GAM TARGET RNA. GAM1193 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18634] GAM1193 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1193 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1193 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1193 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1193 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18635] The complementary binding of GAM1193 RNA, herein designated GAM RNA, to target binding sites on GAM1193 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1193 target RNA, herein designated GAM TARGET RNA, into GAM1193 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18636] It is appreciated that GAM1193 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1193 target genes. The mRNA of each one of this plurality of GAM1193 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1193 RNA, herein designated GAM RNA, and which when bound by GAM1193 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1193 target proteins.

[18637] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1193 gene, herein designated GAM GENE, on one or more GAM1193 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18638] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1193 correlate with, and may be deduced from, the identity of the target genes which GAM1193 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18639] Nucleotide sequences of the GAM1193 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1193 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1193 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1193 are further described hereinbelow with reference to Table Table1.

[18640] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1193 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18641] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1194 (GAM1194) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18642] GAM1194 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1194 was detected is described hereinabove with reference to Figs. 2-8.

[18643] GAM1194 gene, herein designated GAM GENE, and GAM1194 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18644] GAM1194 gene, herein designated GAM GENE, encodes a GAM1194 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1194 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1194 precursor RNA is designated SEQ ID:1167, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1167 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[18645] GAM1194 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18646] An enzyme complex designated DICER COMPLEX, dices the GAM1194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1194 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1194 RNA is designated SEQ ID:2843, and is provided hereinbelow with reference to the sequence listing part.

[18647] GAM1194 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1194 target RNA, herein designated GAM TARGET RNA. GAM1194 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18648] GAM1194 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1194 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1194 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1194 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1194 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18649] The complementary binding of GAM1194 RNA, herein designated GAM RNA, to target binding sites on GAM1194 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1194 target RNA, herein designated GAM TARGET RNA, into GAM1194 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18650] It is appreciated that GAM1194 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1194 target genes. The mRNA of each one of this

plurality of GAM1194 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1194 RNA, herein designated GAM RNA, and which when bound by GAM1194 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1194 target proteins.

[18651] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1194 gene, herein designated GAM GENE, on one or more GAM1194 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18652] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1194 correlate with, and may be deduced from, the identity of the target genes which GAM1194 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18653] Nucleotide sequences of the GAM1194 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1194 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1194 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1194 are further described hereinbelow with reference to Table Table1.

[18654] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1194 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18655] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1195 (GAM1195) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[18656] GAM1195 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1195 was detected is described hereinabove with reference to Figs. 2-8.

[18657] GAM1195 gene, herein designated GAM GENE, and GAM1195 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18658] GAM1195 gene, herein designated GAM GENE, encodes a GAM1195 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1195 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1195 precursor RNA is designated SEQ ID:1168, and is provided hereinbelow with reference to the sequence listing part.

[18659] GAM1195 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18660] An enzyme complex designated DICER COMPLEX, dices the GAM1195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1195 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1195 RNA is designated SEQ ID:2844, and is provided hereinbelow with reference to the sequence listing part.

[18661] GAM1195 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1195 target RNA, herein designated GAM TARGET RNA. GAM1195 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[18662] GAM1195 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1195 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1195 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1195 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1195 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18663] The complementary binding of GAM1195 RNA, herein

designated GAM RNA, to target binding sites on GAM1195 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1195 target RNA, herein designated GAM TARGET RNA, into GAM1195 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18664] It is appreciated that GAM1195 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1195 target genes. The mRNA of each one of this plurality of GAM1195 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1195 RNA, herein designated GAM RNA, and which when bound by GAM1195 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1195 target proteins.

[18665] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1195 gene, herein designated GAM GENE, on one or more GAM1195 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18666] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1195 correlate with, and may be deduced from, the identity of the target genes which GAM1195 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18667] Nucleotide sequences of the GAM1195 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1195 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1195 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1195 are further described hereinbelow with reference to Table Table1.

[18668] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1195 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18669] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1196 (GAM1196) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18670] GAM1196 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1196 was detected is described hereinabove with reference to Figs. 2-8.

[18671] GAM1196 gene, herein designated GAM GENE, and GAM1196 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18672] GAM1196 gene, herein designated GAM GENE, encodes a GAM1196 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1196 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1196 precursor RNA is designated SEQ ID:1169, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1169 is located at position 317521 relative to contig NT_005526.12, on chromosome 3.

[18673] GAM1196 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18674] An enzyme complex designated DICER COMPLEX, dices the GAM1196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1196 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1196 RNA is designated SEQ ID:2845, and is provided hereinbelow with reference to the sequence listing part.

[18675] GAM1196 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1196 target RNA, herein designated GAM TARGET RNA. GAM1196 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18676] GAM1196 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1196 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1196 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1196 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1196 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18677] The complementary binding of GAM1196 RNA, herein designated GAM RNA, to target binding sites on GAM1196 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1196 target RNA, herein designated GAM TARGET RNA, into GAM1196 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18678] It is appreciated that GAM1196 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1196 target genes. The mRNA of each one of this plurality of GAM1196 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1196 RNA, herein designated GAM RNA, and which when bound by GAM1196 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1196 target proteins.

[18679] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1196 gene, herein designated GAM GENE, on one or more GAM1196 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18680] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1196 correlate with, and may be deduced from, the identity of the target genes which GAM1196 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18681] Nucleotide sequences of the GAM1196 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1196 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1196 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1196 are further described hereinbelow with reference to Table Table1.

[18682] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1196 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18683] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1197 (GAM1197) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18684] GAM1197 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1197 was detected is described hereinabove with reference to Figs. 2-8.

[18685] GAM1197 gene, herein designated GAM GENE, and GAM1197 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18686] GAM1197 gene, herein designated GAM GENE, encodes a GAM1197 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1197 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1197 precursor RNA is designated SEQ ID:1170, and is provided hereinbelow with reference to the sequence listing part.

[18687] GAM1197 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18688] An enzyme complex designated DICER COMPLEX, dices the GAM1197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1197 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1197 RNA is designated SEQ ID:2846, and is provided hereinbelow with reference to the sequence listing part.

[18689] GAM1197 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1197 target RNA, herein designated GAM TARGET RNA. GAM1197 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18690] GAM1197 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1197 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1197 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1197 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1197 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18691] The complementary binding of GAM1197 RNA, herein designated GAM RNA, to target binding sites on GAM1197

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1197 target RNA, herein designated GAM TARGET RNA, into GAM1197 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18692] It is appreciated that GAM1197 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1197 target genes. The mRNA of each one of this plurality of GAM1197 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1197 RNA, herein designated GAM RNA, and which when bound by GAM1197 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1197 target proteins.

[18693] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1197 gene, herein designated GAM GENE, on one or more GAM1197 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18694] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1197 correlate with, and may be deduced from, the identity of the target genes which GAM1197 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18695] Nucleotide sequences of the GAM1197 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1197 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1197 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1197 are further described hereinbelow with reference to Table Table1.

[18696] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1197 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18697] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1198 (GAM1198) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18698] GAM1198 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1198 was detected is described hereinabove with reference to Figs. 2-8.

[18699] GAM1198 gene, herein designated GAM GENE, and GAM1198 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18700] GAM1198 gene, herein designated GAM GENE, encodes a GAM1198 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1198 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1198 precursor RNA is designated SEQ ID:1171, and is provided hereinbelow with reference to the sequence listing part.

[18701] GAM1198 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18702] An enzyme complex designated DICER COMPLEX, dices the GAM1198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1198 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1198 RNA is designated SEQ ID:2847, and

is provided hereinbelow with reference to the sequence listing part.

[18703] GAM1198 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1198 target RNA, herein designated GAM TARGET RNA. GAM1198 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18704] GAM1198 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1198 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1198 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1198 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1198 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18705] The complementary binding of GAM1198 RNA, herein designated GAM RNA, to target binding sites on GAM1198 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1198 target RNA, herein designated GAM TARGET RNA, into GAM1198 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18706] It is appreciated that GAM1198 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1198 target genes. The mRNA of each one of this plurality of GAM1198 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1198 RNA, herein designated GAM RNA, and which when bound by

GAM1198 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1198 target proteins.

[18707] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1198 gene, herein designated GAM GENE, on one or more GAM1198 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18708] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1198 correlate with, and may be deduced from, the identity of the target genes which GAM1198 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[18709] Nucleotide sequences of the GAM1198 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1198 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1198 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1198 are further described hereinbelow with reference to Table Table1.

[18710] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1198 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18711] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1199 (GAM1199) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18712] GAM1199 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1199 was detected is described hereinabove

with reference to Figs. 2-8.

[18713] GAM1199 gene, herein designated GAM GENE, and GAM1199 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18714] GAM1199 gene, herein designated GAM GENE, encodes a GAM1199 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1199 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1199 precursor RNA is designated SEQ ID:1172, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1172 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[18715] GAM1199 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18716] An enzyme complex designated DICER COMPLEX, dices the GAM1199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1199 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1199 RNA is designated SEQ ID:2848, and is provided hereinbelow with reference to the sequence listing part.

[18717] GAM1199 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1199 target RNA, herein designated GAM TARGET RNA. GAM1199 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18718] GAM1199 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1199 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1199 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1199 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1199 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18719] The complementary binding of GAM1199 RNA, herein designated GAM RNA, to target binding sites on GAM1199 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1199 target RNA, herein designated GAM TARGET RNA, into GAM1199 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18720] It is appreciated that GAM1199 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1199 target genes. The mRNA of each one of this plurality of GAM1199 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1199 RNA, herein designated GAM RNA, and which when bound by GAM1199 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1199 target proteins.

[18721] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1199 gene, herein designated GAM GENE, on one or more GAM1199 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18722] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1199 correlate with, and may be deduced from, the identity of the target genes which GAM1199 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18723] Nucleotide sequences of the GAM1199 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1199 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1199 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1199 are further described hereinbelow with reference to Table Table1.

[18724] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1199 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18725] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1200 (GAM1200) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18726] GAM1200 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1200 was detected is described hereinabove with reference to Figs. 2-8.

[18727] GAM1200 gene, herein designated GAM GENE, and GAM1200 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18728] GAM1200 gene, herein designated GAM GENE, encodes a GAM1200 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1200 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1200 precursor RNA is

designated SEQ ID:1173, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1173 is located at position 5430243 relative to contig NT_024115.13, on chromosome 10.

[18729] GAM1200 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18730] An enzyme complex designated DICER COMPLEX, dices the GAM1200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1200 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1200 RNA is designated SEQ ID:2849, and is provided hereinbelow with reference to the sequence listing part.

[18731] GAM1200 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1200 target RNA, herein designated GAM TARGET RNA. GAM1200 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18732] GAM1200 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1200 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1200 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1200 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1200 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18733] The complementary binding of GAM1200 RNA, herein designated GAM RNA, to target binding sites on GAM1200 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1200 target RNA, herein designated GAM TARGET RNA, into GAM1200 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18734] It is appreciated that GAM1200 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1200 target genes. The mRNA of each one of this plurality of GAM1200 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1200 RNA,

herein designated GAM RNA, and which when bound by GAM1200 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1200 target proteins.

[18735] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1200 gene, herein designated GAM GENE, on one or more GAM1200 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18736] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1200 correlate with, and may be deduced from, the identity of the target genes which

GAM1200 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18737] Nucleotide sequences of the GAM1200 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1200 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1200 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1200 are further described hereinbelow with reference to Table Table1.

[18738] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1200 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18739] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1201 (GAM1201) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18740] GAM1201 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1201 was detected is described hereinabove with reference to Figs. 2-8.

[18741] GAM1201 gene, herein designated GAM GENE, and GAM1201 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18742] GAM1201 gene, herein designated GAM GENE, encodes a GAM1201 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1201 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1201 precursor RNA is designated SEQ ID:1174, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1174 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[18743] GAM1201 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18744] An enzyme complex designated DICER COMPLEX, dices the GAM1201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1201 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1201 RNA is designated SEQ ID:2850, and is provided hereinbelow with reference to the sequence listing part.

[18745] GAM1201 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1201 target RNA, herein designated GAM TARGET RNA. GAM1201 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18746] GAM1201 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1201 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1201 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1201 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1201 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18747] The complementary binding of GAM1201 RNA, herein designated GAM RNA, to target binding sites on GAM1201

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1201 target RNA, herein designated GAM TARGET RNA, into GAM1201 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18748] It is appreciated that GAM1201 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1201 target genes. The mRNA of each one of this plurality of GAM1201 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1201 RNA, herein designated GAM RNA, and which when bound by GAM1201 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1201 target proteins.

[18749] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1201 gene, herein designated GAM GENE, on one or more GAM1201 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18750] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1201 correlate with, and may be deduced from, the identity of the target genes which GAM1201 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18751] Nucleotide sequences of the GAM1201 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1201 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1201 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1201 are further described hereinbelow with reference to Table Table1.

[18752] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1201 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18753] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1202 (GAM1202) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18754] GAM1202 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1202 was detected is described hereinabove with reference to Figs. 2-8.

[18755] GAM1202 gene, herein designated GAM GENE, and GAM1202 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18756] GAM1202 gene, herein designated GAM GENE, encodes a GAM1202 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1202 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1202 precursor RNA is designated SEQ ID:1175, and is provided hereinbelow with reference to the sequence listing part.

[18757] GAM1202 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[18758] SEQ ID:99204 detected in mouse EST Accession BI453661.1.

[18759] SEQ ID:99205 detected in mouse EST Accession AA184326.1.

[18760] SEQ ID:99206 detected in mouse EST Accession AI060752.1.

[18761] SEQ ID:99207 detected in mouse EST Accession AA546767.1.

[18762] SEQ ID:98086 detected in mouse EST Accession AL022643.1.

[18763] SEQ ID:98087 detected in mouse EST Accession BF452099.1.

[18764] SEQ ID:98088 detected in mouse EST Accession BE531895.1.

[18765] GAM1202 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18766] An enzyme complex designated DICER COMPLEX, dices the GAM1202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1202 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1202 RNA is designated SEQ ID:2851, and is provided hereinbelow with reference to the sequence listing part.

[18767] GAM1202 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1202 target RNA, herein designated GAM TARGET RNA. GAM1202 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18768] GAM1202 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1202 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1202 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1202 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1202 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18769] The complementary binding of GAM1202 RNA, herein designated GAM RNA, to target binding sites on GAM1202 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1202 target RNA, herein designated GAM TARGET RNA, into GAM1202 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18770] It is appreciated that GAM1202 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1202 target genes. The mRNA of each one of this plurality of GAM1202 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1202 RNA, herein designated GAM RNA, and which when bound by GAM1202 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1202 target proteins.

[18771] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1202 gene, herein designated GAM GENE, on one or more GAM1202 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18772] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1202 correlate with, and may be deduced from, the identity of the target genes which GAM1202 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18773] Nucleotide sequences of the GAM1202 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1202 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1202 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1202 are further described hereinbelow with reference to Table Table1.

[18774] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1202 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18775] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1203 (GAM1203) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18776] GAM1203 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1203 was detected is described hereinabove with reference to Figs. 2-8.

[18777] GAM1203 gene, herein designated GAM GENE, and GAM1203 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18778] GAM1203 gene, herein designated GAM GENE, encodes a GAM1203 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1203 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1203 precursor RNA is designated SEQ ID:1176, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1176 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[18779] GAM1203 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18780] An enzyme complex designated DICER COMPLEX, dices the GAM1203 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1203 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1203 RNA is designated SEQ ID:2852, and is provided hereinbelow with reference to the sequence listing part.

[18781] GAM1203 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1203 target RNA, herein designated GAM TARGET RNA. GAM1203 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18782] GAM1203 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1203 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1203

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1203 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1203 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18783] The complementary binding of GAM1203 RNA, herein designated GAM RNA, to target binding sites on GAM1203 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1203 target RNA, herein designated GAM TARGET RNA, into GAM1203 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[18784] It is appreciated that GAM1203 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1203 target genes. The mRNA of each one of this plurality of GAM1203 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1203 RNA, herein designated GAM RNA, and which when bound by GAM1203 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1203 target proteins.

[18785] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1203 gene, herein designated GAM GENE, on one or more GAM1203 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18786] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1203 correlate with, and may be deduced from, the identity of the target genes which GAM1203 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18787] Nucleotide sequences of the GAM1203 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1203 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1203 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1203 are further described hereinbelow with reference to Table Table1.

[18788] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1203 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18789] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1204 (GAM1204) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18790] GAM1204 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1204 was detected is described hereinabove with reference to Figs. 2-8.

[18791] GAM1204 gene, herein designated GAM GENE, and GAM1204 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18792] GAM1204 gene, herein designated GAM GENE, encodes a GAM1204 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1204 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1204 precursor RNA is designated SEQ ID:1177, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1177 is located at position 25856588 relative to contig NT_005403.11, on chromosome 2.

[18793] GAM1204 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18794] An enzyme complex designated DICER COMPLEX, dices the GAM1204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1204 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1204 RNA is designated SEQ ID:2853, and is provided hereinbelow with reference to the sequence listing part.

[18795] GAM1204 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1204 target RNA, herein designated GAM TARGET RNA. GAM1204 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18796] GAM1204 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1204 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1204 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1204 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1204 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18797] The complementary binding of GAM1204 RNA, herein designated GAM RNA, to target binding sites on GAM1204 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1204 target RNA, herein designated GAM TARGET RNA, into GAM1204 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18798] It is appreciated that GAM1204 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1204 target genes. The mRNA of each one of this plurality of GAM1204 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1204 RNA, herein designated GAM RNA, and which when bound by GAM1204 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1204 target proteins.

[18799] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1204 gene, herein designated GAM GENE, on one or more GAM1204 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18800] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1204 correlate with, and may be deduced from, the identity of the target genes which GAM1204 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18801] Nucleotide sequences of the GAM1204 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1204 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1204 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1204 are further described hereinbelow with reference to Table Table1.

[18802] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1204 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18803] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1205 (GAM1205) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18804] GAM1205 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1205 was detected is described hereinabove with reference to Figs. 2-8.

[18805] GAM1205 gene, herein designated GAM GENE, and GAM1205 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[18806] GAM1205 gene, herein designated GAM GENE, encodes a GAM1205 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1205 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1205 precursor RNA is designated SEQ ID:1178, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1178 is located at position 2349689 relative to contig NT_021907.13, on chromosome 1.

[18807] GAM1205 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18808] An enzyme complex designated DICER COMPLEX, dices

the GAM1205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1205 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1205 RNA is designated SEQ ID:2854, and is provided hereinbelow with reference to the sequence listing part.

[18809] GAM1205 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1205 target RNA, herein designated GAM TARGET RNA. GAM1205 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18810] GAM1205 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1205 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1205 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1205 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1205 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18811] The complementary binding of GAM1205 RNA, herein designated GAM RNA, to target binding sites on GAM1205 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1205 target RNA, herein designated GAM TARGET RNA, into GAM1205 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18812] It is appreciated that GAM1205 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1205 target genes. The mRNA of each one of this plurality of GAM1205 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1205 RNA, herein designated GAM RNA, and which when bound by GAM1205 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1205 target proteins.

[18813] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1205 gene, herein designated GAM GENE, on one or more GAM1205 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18814] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1205 correlate with, and may be deduced from, the identity of the target genes which GAM1205 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18815] Nucleotide sequences of the GAM1205 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1205 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1205 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1205 are further described hereinbelow with reference to Table Table1.

[18816] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1205 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18817] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1206 (GAM1206) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18818] GAM1206 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1206 was detected is described hereinabove with reference to Figs. 2-8.

[18819] GAM1206 gene, herein designated GAM GENE, and GAM1206 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18820] GAM1206 gene, herein designated GAM GENE, encodes a GAM1206 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1206 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1206 precursor RNA is designated SEQ ID:1179, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1179 is located at position 1426091 rela-

tive to contig NT_033241.3, on chromosome 11.

[18821] GAM1206 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18822] An enzyme complex designated DICER COMPLEX, dices the GAM1206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1206 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1206 RNA is designated SEQ ID:2855, and is provided hereinbelow with reference to the sequence listing part.

[18823] GAM1206 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1206 target RNA, herein designated GAM TARGET RNA. GAM1206 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18824] GAM1206 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1206 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1206 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1206 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1206 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18825] The complementary binding of GAM1206 RNA, herein designated GAM RNA, to target binding sites on GAM1206 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1206 target RNA, herein designated GAM TARGET RNA, into GAM1206 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18826] It is appreciated that GAM1206 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1206 target genes. The mRNA of each one of this plurality of GAM1206 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1206 RNA, herein designated GAM RNA, and which when bound by GAM1206 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1206

target proteins.

[18827] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1206 gene, herein designated GAM GENE, on one or more GAM1206 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18828] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1206 correlate with, and may be deduced from, the identity of the target genes which GAM1206 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18829] Nucleotide sequences of the GAM1206 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1206 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1206 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1206 are further described hereinbelow with reference to Table Table1.

[18830] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1206 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18831] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1207 (GAM1207) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18832] GAM1207 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1207 was detected is described hereinabove with reference to Figs. 2-8.

[18833] GAM1207 gene, herein designated GAM GENE, and

GAM1207 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18834] GAM1207 gene, herein designated GAM GENE, encodes a GAM1207 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1207 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1207 precursor RNA is designated SEQ ID:1180, and is provided hereinbelow with reference to the sequence listing part.

[18835] GAM1207 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18836] An enzyme complex designated DICER COMPLEX, dices the GAM1207 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1207 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1207 RNA is designated SEQ ID:2856, and is provided hereinbelow with reference to the sequence listing part.

[18837] GAM1207 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1207 target RNA, herein designated GAM TARGET RNA. GAM1207 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18838] GAM1207 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1207 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1207

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1207 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1207 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18839] The complementary binding of GAM1207 RNA, herein designated GAM RNA, to target binding sites on GAM1207 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1207 target RNA, herein designated GAM TARGET RNA, into GAM1207 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[18840] It is appreciated that GAM1207 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1207 target genes. The mRNA of each one of this plurality of GAM1207 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1207 RNA, herein designated GAM RNA, and which when bound by GAM1207 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1207 target proteins.

[18841] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1207 gene, herein designated GAM GENE, on one or more GAM1207 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18842] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1207 correlate with, and may be deduced from, the identity of the target genes which GAM1207 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18843] Nucleotide sequences of the GAM1207 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1207 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1207 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1207 are further described hereinbelow with reference to Table Table1.

[18844] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1207 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18845] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1208 (GAM1208) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18846] GAM1208 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1208 was detected is described hereinabove with reference to Figs. 2-8.

[18847] GAM1208 gene, herein designated GAM GENE, and GAM1208 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18848] GAM1208 gene, herein designated GAM GENE, encodes a GAM1208 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1208 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1208 precursor RNA is designated SEQ ID:1181, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1181 is located at position 896767 relative to contig NT_010274.13, on chromosome 15.

[18849] GAM1208 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18850] An enzyme complex designated DICER COMPLEX, dices the GAM1208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1208 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1208 RNA is designated SEQ ID:2857, and is provided hereinbelow with reference to the sequence listing part.

[18851] GAM1208 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1208 target RNA, herein designated GAM TARGET RNA. GAM1208 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18852] GAM1208 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1208 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1208 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1208 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1208 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18853] The complementary binding of GAM1208 RNA, herein designated GAM RNA, to target binding sites on GAM1208 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1208 target RNA, herein designated GAM TARGET RNA, into GAM1208 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18854] It is appreciated that GAM1208 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1208 target genes. The mRNA of each one of this plurality of GAM1208 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1208 RNA, herein designated GAM RNA, and which when bound by GAM1208 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1208 target proteins.

[18855] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1208 gene, herein designated GAM GENE, on one or more GAM1208 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18856] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1208 correlate with, and may be deduced from, the identity of the target genes which GAM1208 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18857] Nucleotide sequences of the GAM1208 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1208 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1208 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1208 are further described hereinbelow with reference to Table Table1.

[18858] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1208 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18859] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1209 (GAM1209) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18860] GAM1209 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1209 was detected is described hereinabove with reference to Figs. 2-8.

[18861] GAM1209 gene, herein designated GAM GENE, and GAM1209 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[18862] GAM1209 gene, herein designated GAM GENE, encodes a GAM1209 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1209 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1209 precursor RNA is designated SEQ ID:1182, and is provided hereinbelow with reference to the sequence listing part.

[18863] GAM1209 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18864] An enzyme complex designated DICER COMPLEX, dices the GAM1209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1209 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1209 RNA is designated SEQ ID:2858, and is provided hereinbelow with reference to the sequence listing part.

[18865] GAM1209 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1209 target RNA, herein designated GAM TARGET RNA. GAM1209 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18866] GAM1209 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1209 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1209 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1209 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1209 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18867] The complementary binding of GAM1209 RNA, herein designated GAM RNA, to target binding sites on GAM1209 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1209 target RNA, herein designated GAM TARGET RNA, into GAM1209 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18868] It is appreciated that GAM1209 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1209 target genes. The mRNA of each one of this plurality of GAM1209 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1209 RNA, herein designated GAM RNA, and which when bound by GAM1209 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1209 target proteins.

[18869] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1209 gene, herein designated GAM GENE, on one or more GAM1209 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18870] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1209 correlate with, and may be deduced from, the identity of the target genes which GAM1209 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18871] Nucleotide sequences of the GAM1209 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1209 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1209 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1209 are further described hereinbelow with reference to Table Table1.

[18872] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1209 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18873] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1210 (GAM1210) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18874] GAM1210 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1210 was detected is described hereinabove with reference to Figs. 2-8.

[18875] GAM1210 gene, herein designated GAM GENE, and GAM1210 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18876] GAM1210 gene, herein designated GAM GENE, encodes a GAM1210 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1210 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1210 precursor RNA is designated SEQ ID:1183, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1183 is located at position 1135927 relative to contig NT_029289.7, on chromosome 5.

[18877] GAM1210 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18878] An enzyme complex designated DICER COMPLEX, dices the GAM1210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1210 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1210 RNA is designated SEQ ID:2859, and is provided hereinbelow with reference to the sequence listing part.

[18879] GAM1210 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1210 target RNA, herein designated GAM TARGET RNA. GAM1210 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18880] GAM1210 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1210 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1210 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1210 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1210 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18881] The complementary binding of GAM1210 RNA, herein designated GAM RNA, to target binding sites on GAM1210 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1210 target RNA, herein designated GAM TARGET RNA, into GAM1210 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18882] It is appreciated that GAM1210 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1210 target genes. The mRNA of each one of this plurality of GAM1210 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1210 RNA, herein designated GAM RNA, and which when bound by GAM1210 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1210 target proteins.

[18883] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1210 gene, herein designated GAM GENE, on one or more GAM1210 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18884] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1210 correlate with, and may be deduced from, the identity of the target genes which GAM1210 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18885] Nucleotide sequences of the GAM1210 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1210 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1210 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1210 are further described hereinbelow with reference to Table Table1.

[18886] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1210 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18887] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1211 (GAM1211) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18888] GAM1211 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1211 was detected is described hereinabove with reference to Figs. 2-8.

[18889] GAM1211 gene, herein designated GAM GENE, and GAM1211 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18890] GAM1211 gene, herein designated GAM GENE, encodes a GAM1211 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1211 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1211 precursor RNA is designated SEQ ID:1184, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1184 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[18891] GAM1211 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18892] An enzyme complex designated DICER COMPLEX, dices the GAM1211 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1211 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1211 RNA is designated SEQ ID:2860, and is provided hereinbelow with reference to the sequence listing part.

[18893] GAM1211 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1211 target RNA, herein designated GAM TARGET RNA. GAM1211 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18894] GAM1211 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1211 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1211

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1211 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1211 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18895] The complementary binding of GAM1211 RNA, herein designated GAM RNA, to target binding sites on GAM1211 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1211 target RNA, herein designated GAM TARGET RNA, into GAM1211 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[18896] It is appreciated that GAM1211 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1211 target genes. The mRNA of each one of this plurality of GAM1211 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1211 RNA, herein designated GAM RNA, and which when bound by GAM1211 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1211 target proteins.

[18897] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1211 gene, herein designated GAM GENE, on one or more GAM1211 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18898] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1211 correlate with, and may be deduced from, the identity of the target genes which GAM1211 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18899] Nucleotide sequences of the GAM1211 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1211 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1211 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1211 are further described hereinbelow with reference to Table Table1.

[18900] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1211 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18901] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1212 (GAM1212) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18902] GAM1212 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1212 was detected is described hereinabove with reference to Figs. 2-8.

[18903] GAM1212 gene, herein designated GAM GENE, and GAM1212 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18904] GAM1212 gene, herein designated GAM GENE, encodes a GAM1212 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1212 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1212 precursor RNA is designated SEQ ID:1185, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1185 is located at position 3434852 relative to contig NT_009714.13, on chromosome 12.

[18905] GAM1212 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99214, which mouse homolog is detected in mouse EST accession BG288438.1.

[18906] GAM1212 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18907] An enzyme complex designated DICER COMPLEX, dices the GAM1212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1212 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1212 RNA is designated SEQ ID:2861, and is provided hereinbelow with reference to the sequence listing part.

[18908] GAM1212 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1212 target RNA, herein designated GAM TARGET RNA. GAM1212 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18909] GAM1212 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1212 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1212 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1212 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1212 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18910] The complementary binding of GAM1212 RNA, herein designated GAM RNA, to target binding sites on GAM1212 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1212 target RNA, herein designated GAM TARGET RNA, into GAM1212 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18911] It is appreciated that GAM1212 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1212 target genes. The mRNA of each one of this plurality of GAM1212 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1212 RNA, herein designated GAM RNA, and which when bound by GAM1212 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1212 target proteins.

[18912] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1212 gene, herein designated GAM GENE, on one or more GAM1212 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18913] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1212 correlate with, and may

be deduced from, the identity of the target genes which GAM1212 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18914] Nucleotide sequences of the GAM1212 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1212 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1212 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1212 are further described hereinbelow with reference to Table Table1.

[18915] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1212 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18916] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1213 (GAM1213) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18917] GAM1213 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1213 was detected is described hereinabove with reference to Figs. 2-8.

[18918] GAM1213 gene, herein designated GAM GENE, and GAM1213 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18919] GAM1213 gene, herein designated GAM GENE, encodes a GAM1213 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1213 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1213 precursor RNA is designated SEQ ID:1186, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1186 is located at position 19858317 relative to contig NT_011387.8, on chromosome 20.

[18920] GAM1213 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18921] An enzyme complex designated DICER COMPLEX, dices the GAM1213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1213 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1213 RNA is designated SEQ ID:2862, and is provided hereinbelow with reference to the sequence listing part.

[18922] GAM1213 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1213 target RNA, herein designated GAM TARGET RNA. GAM1213 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[18923] GAM1213 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1213 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1213 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1213 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1213 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18924] The complementary binding of GAM1213 RNA, herein

designated GAM RNA, to target binding sites on GAM1213 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1213 target RNA, herein designated GAM TARGET RNA, into GAM1213 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18925] It is appreciated that GAM1213 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1213 target genes. The mRNA of each one of this plurality of GAM1213 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1213 RNA, herein designated GAM RNA, and which when bound by GAM1213 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1213 target proteins.

[18926] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1213 gene, herein designated GAM GENE, on one or more GAM1213 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18927] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1213 correlate with, and may be deduced from, the identity of the target genes which GAM1213 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18928] Nucleotide sequences of the GAM1213 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1213 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1213 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1213 are further described hereinbelow with reference to Table Table1.

[18929] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1213 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18930] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1214 (GAM1214) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18931] GAM1214 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1214 was detected is described hereinabove with reference to Figs. 2-8.

[18932] GAM1214 gene, herein designated GAM GENE, and GAM1214 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18933] GAM1214 gene, herein designated GAM GENE, encodes a GAM1214 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1214 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1214 precursor RNA is designated SEQ ID:1187, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1187 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[18934] GAM1214 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18935] An enzyme complex designated DICER COMPLEX, dices the GAM1214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1214 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1214 RNA is designated SEQ ID:2863, and is provided hereinbelow with reference to the sequence listing part.

[18936] GAM1214 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1214 target RNA, herein designated GAM TARGET RNA. GAM1214 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18937] GAM1214 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1214 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1214 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1214 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1214 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18938] The complementary binding of GAM1214 RNA, herein designated GAM RNA, to target binding sites on GAM1214 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1214 target RNA, herein designated GAM TARGET RNA, into GAM1214 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18939] It is appreciated that GAM1214 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1214 target genes. The mRNA of each one of this plurality of GAM1214 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1214 RNA, herein designated GAM RNA, and which when bound by GAM1214 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1214 target proteins.

[18940] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1214 gene, herein designated GAM GENE, on one or more GAM1214 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18941] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1214 correlate with, and may be deduced from, the identity of the target genes which GAM1214 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18942] Nucleotide sequences of the GAM1214 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1214 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1214 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1214 are further described hereinbelow with reference to Table Table1.

[18943] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1214 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18944] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1215 (GAM1215) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18945] GAM1215 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1215 was detected is described hereinabove with reference to Figs. 2-8.

[18946] GAM1215 gene, herein designated GAM GENE, and GAM1215 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18947] GAM1215 gene, herein designated GAM GENE, encodes a GAM1215 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1215 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1215 precursor RNA is designated SEQ ID:1188, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1188 is located at position 4851366 relative to contig NT_022517.13, on chromosome 3.

[18948] GAM1215 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18949] An enzyme complex designated DICER COMPLEX, dices the GAM1215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1215 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1215 RNA is designated SEQ ID:2864, and is provided hereinbelow with reference to the sequence listing part.

[18950] GAM1215 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1215 target RNA, herein designated GAM TARGET RNA. GAM1215 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18951] GAM1215 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1215 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1215 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1215 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1215 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18952] The complementary binding of GAM1215 RNA, herein designated GAM RNA, to target binding sites on GAM1215 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1215 target RNA, herein designated GAM TARGET RNA, into GAM1215 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18953] It is appreciated that GAM1215 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1215 target genes. The mRNA of each one of this plurality of GAM1215 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1215 RNA, herein designated GAM RNA, and which when bound by GAM1215 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1215 target proteins.

[18954] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1215 gene, herein designated GAM GENE, on one or more GAM1215 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18955] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1215 correlate with, and may be deduced from, the identity of the target genes which GAM1215 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18956] Nucleotide sequences of the GAM1215 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1215 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1215 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1215 are further described hereinbelow with reference to Table Table1.

[18957] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1215 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18958] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1216 (GAM1216) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18959] GAM1216 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1216 was detected is described hereinabove with reference to Figs. 2-8.

[18960] GAM1216 gene, herein designated GAM GENE, and GAM1216 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18961] GAM1216 gene, herein designated GAM GENE, encodes a GAM1216 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1216 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1216 precursor RNA is designated SEQ ID:1189, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1189 is located at position 12548632 relative to contig NT_017568.11, on chromosome 9.

[18962] GAM1216 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18963] An enzyme complex designated DICER COMPLEX, dices the GAM1216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1216 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1216 RNA is designated SEQ ID:2865, and is provided hereinbelow with reference to the sequence listing part.

[18964] GAM1216 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1216 target RNA, herein designated GAM TARGET RNA. GAM1216 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18965] GAM1216 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1216 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1216 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1216 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1216 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18966] The complementary binding of GAM1216 RNA, herein designated GAM RNA, to target binding sites on GAM1216 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1216 target RNA, herein designated GAM TARGET RNA, into GAM1216 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18967] It is appreciated that GAM1216 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1216 target genes. The mRNA of each one of this

plurality of GAM1216 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1216 RNA, herein designated GAM RNA, and which when bound by GAM1216 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1216 target proteins.

[18968] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1216 gene, herein designated GAM GENE, on one or more GAM1216 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18969] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1216 correlate with, and may be deduced from, the identity of the target genes which GAM1216 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18970] Nucleotide sequences of the GAM1216 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1216 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1216 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1216 are further described hereinbelow with reference to Table Table1.

[18971] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1216 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18972] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1217 (GAM1217) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[18973] GAM1217 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1217 was detected is described hereinabove with reference to Figs. 2-8.

[18974] GAM1217 gene, herein designated GAM GENE, and GAM1217 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18975] GAM1217 gene, herein designated GAM GENE, encodes a GAM1217 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1217 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1217 precursor RNA is designated SEQ ID:1190, and is provided hereinbelow with reference to the sequence listing part.

[18976] GAM1217 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18977] An enzyme complex designated DICER COMPLEX, dices the GAM1217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1217 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1217 RNA is designated SEQ ID:2866, and is provided hereinbelow with reference to the sequence listing part.

[18978] GAM1217 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1217 target RNA, herein designated GAM TARGET RNA. GAM1217 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[18979] GAM1217 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1217 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1217 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1217 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1217 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18980] The complementary binding of GAM1217 RNA, herein

designated GAM RNA, to target binding sites on GAM1217 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1217 target RNA, herein designated GAM TARGET RNA, into GAM1217 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18981] It is appreciated that GAM1217 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1217 target genes. The mRNA of each one of this plurality of GAM1217 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1217 RNA, herein designated GAM RNA, and which when bound by GAM1217 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1217 target proteins.

[18982] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1217 gene, herein designated GAM GENE, on one or more GAM1217 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18983] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1217 correlate with, and may be deduced from, the identity of the target genes which GAM1217 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18984] Nucleotide sequences of the GAM1217 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1217 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1217 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1217 are further described hereinbelow with reference to Table Table1.

[18985] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1217 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[18986] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1218 (GAM1218) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[18987] GAM1218 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1218 was detected is described hereinabove with reference to Figs. 2-8.

[18988] GAM1218 gene, herein designated GAM GENE, and GAM1218 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[18989] GAM1218 gene, herein designated GAM GENE, encodes a GAM1218 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1218 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1218 precursor RNA is designated SEQ ID:1191, and is provided hereinbelow with reference to the sequence listing part.

[18990] GAM1218 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[18991] An enzyme complex designated DICER COMPLEX, dices the GAM1218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1218 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1218 RNA is designated SEQ ID:2867, and is provided hereinbelow with reference to the sequence listing part.

[18992] GAM1218 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1218 target RNA, herein designated GAM TARGET RNA. GAM1218 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[18993] GAM1218 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1218 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1218 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1218 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1218 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[18994] The complementary binding of GAM1218 RNA, herein designated GAM RNA, to target binding sites on GAM1218 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1218 target RNA, herein designated GAM TARGET RNA, into GAM1218 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[18995] It is appreciated that GAM1218 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1218 target genes. The mRNA of each one of this plurality of GAM1218 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1218 RNA,

herein designated GAM RNA, and which when bound by GAM1218 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1218 target proteins.

[18996] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1218 gene, herein designated GAM GENE, on one or more GAM1218 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[18997] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1218 correlate with, and may be deduced from, the identity of the target genes which

GAM1218 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[18998] Nucleotide sequences of the GAM1218 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1218 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1218 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1218 are further described hereinbelow with reference to Table Table1.

[18999] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1218 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19000] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1219 (GAM1219) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19001] GAM1219 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1219 was detected is described hereinabove with reference to Figs. 2-8.

[19002] GAM1219 gene, herein designated GAM GENE, and GAM1219 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19003] GAM1219 gene, herein designated GAM GENE, encodes a GAM1219 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1219 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1219 precursor RNA is designated SEQ ID:1192, and is provided hereinbelow with reference to the sequence listing part.

[19004] GAM1219 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[19005] An enzyme complex designated DICER COMPLEX, dices the GAM1219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1219 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1219 RNA is designated SEQ ID:2868, and is provided hereinbelow with reference to the sequence listing part.

[19006] GAM1219 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1219 target RNA, herein designated GAM TARGET RNA. GAM1219 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19007] GAM1219 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1219 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1219 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1219 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1219 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19008] The complementary binding of GAM1219 RNA, herein designated GAM RNA, to target binding sites on GAM1219 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1219 target RNA, herein designated GAM TARGET RNA, into GAM1219 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19009] It is appreciated that GAM1219 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1219 target genes. The mRNA of each one of this plurality of GAM1219 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1219 RNA, herein designated GAM RNA, and which when bound by GAM1219 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1219 target proteins.

[19010] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1219 gene, herein designated GAM GENE, on one or more GAM1219 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19011] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1219 correlate with, and may be deduced from, the identity of the target genes which GAM1219 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19012] Nucleotide sequences of the GAM1219 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1219 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1219 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1219 are further described hereinbelow with reference to Table Table1.

[19013] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1219 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19014] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1220 (GAM1220) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19015] GAM1220 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1220 was detected is described hereinabove with reference to Figs. 2-8.

[19016] GAM1220 gene, herein designated GAM GENE, and GAM1220 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19017] GAM1220 gene, herein designated GAM GENE, encodes a GAM1220 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1220 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1220 precursor RNA is designated SEQ ID:1193, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1193 is located at position 4851355 relative to contig NT_022517.13, on chromosome 3.

[19018] GAM1220 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19019] An enzyme complex designated DICER COMPLEX, dices the GAM1220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1220 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1220 RNA is designated SEQ ID:2869, and

is provided hereinbelow with reference to the sequence listing part.

[19020] GAM1220 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1220 target RNA, herein designated GAM TARGET RNA. GAM1220 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19021] GAM1220 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1220 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1220 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1220 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1220 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19022] The complementary binding of GAM1220 RNA, herein designated GAM RNA, to target binding sites on GAM1220 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1220 target RNA, herein designated GAM TARGET RNA, into GAM1220 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19023] It is appreciated that GAM1220 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1220 target genes. The mRNA of each one of this plurality of GAM1220 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1220 RNA, herein designated GAM RNA, and which when bound by

GAM1220 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1220 target proteins.

[19024] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1220 gene, herein designated GAM GENE, on one or more GAM1220 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19025] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1220 correlate with, and may be deduced from, the identity of the target genes which GAM1220 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[19026] Nucleotide sequences of the GAM1220 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1220 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1220 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1220 are further described hereinbelow with reference to Table Table1.

[19027] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1220 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19028] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1221 (GAM1221) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19029] GAM1221 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1221 was detected is described hereinabove

with reference to Figs. 2-8.

[19030] GAM1221 gene, herein designated GAM GENE, and GAM1221 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19031] GAM1221 gene, herein designated GAM GENE, encodes a GAM1221 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1221 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1221 precursor RNA is designated SEQ ID:1194, and is provided hereinbelow with reference to the sequence listing part.

[19032] GAM1221 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98072, which mouse homolog is detected in mouse EST accession BI713945.1.

[19033] GAM1221 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19034] An enzyme complex designated DICER COMPLEX, dices the GAM1221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1221 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1221 RNA is designated SEQ ID:2870, and is provided hereinbelow with reference to the sequence listing part.

[19035] GAM1221 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1221 target RNA, herein designated GAM TARGET RNA. GAM1221 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19036] GAM1221 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1221 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1221 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1221 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1221 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19037] The complementary binding of GAM1221 RNA, herein designated GAM RNA, to target binding sites on GAM1221 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1221 target RNA, herein designated GAM TARGET RNA, into GAM1221 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19038] It is appreciated that GAM1221 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1221 target genes. The mRNA of each one of this plurality of GAM1221 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1221 RNA, herein designated GAM RNA, and which when bound by GAM1221 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1221 target proteins.

[19039] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1221 gene, herein designated GAM GENE, on one or more GAM1221 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19040] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1221 correlate with, and may be deduced from, the identity of the target genes which GAM1221 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19041] Nucleotide sequences of the GAM1221 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1221 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1221 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1221 are further described hereinbelow with reference to Table Table1.

[19042] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1221 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19043] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1222 (GAM1222) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19044] GAM1222 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1222 was detected is described hereinabove with reference to Figs. 2-8.

[19045] GAM1222 gene, herein designated GAM GENE, and GAM1222 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19046] GAM1222 gene, herein designated GAM GENE, encodes a GAM1222 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1222 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1222 precursor RNA is designated SEQ ID:1195, and is provided hereinbelow with reference to the sequence listing part.

[19047] GAM1222 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19048] An enzyme complex designated DICER COMPLEX, dices the GAM1222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1222 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1222 RNA is designated SEQ ID:2871, and is provided hereinbelow with reference to the sequence listing part.

[19049] GAM1222 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1222 target RNA, herein designated GAM TARGET RNA. GAM1222 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19050] GAM1222 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1222 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1222 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1222 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1222 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19051] The complementary binding of GAM1222 RNA, herein designated GAM RNA, to target binding sites on GAM1222 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1222 target RNA, herein designated GAM TARGET RNA, into GAM1222 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19052] It is appreciated that GAM1222 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1222 target genes. The mRNA of each one of this plurality of GAM1222 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1222 RNA, herein designated GAM RNA, and which when bound by GAM1222 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1222 target proteins.

[19053] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1222 gene, herein designated GAM GENE, on one or more GAM1222 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19054] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1222 correlate with, and may

be deduced from, the identity of the target genes which GAM1222 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19055] Nucleotide sequences of the GAM1222 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1222 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1222 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1222 are further described hereinbelow with reference to Table Table1.

[19056] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1222 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19057] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1223 (GAM1223) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19058] GAM1223 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1223 was detected is described hereinabove with reference to Figs. 2-8.

[19059] GAM1223 gene, herein designated GAM GENE, and GAM1223 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19060] GAM1223 gene, herein designated GAM GENE, encodes a GAM1223 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1223 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1223 precursor RNA is designated SEQ ID:1196, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1196 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[19061] GAM1223 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19062] An enzyme complex designated DICER COMPLEX, dices the GAM1223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1223 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1223 RNA is designated SEQ ID:2872, and is provided hereinbelow with reference to the sequence listing part.

[19063] GAM1223 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1223 target RNA, herein designated GAM TARGET RNA. GAM1223 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[19064] GAM1223 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1223 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1223 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1223 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1223 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19065] The complementary binding of GAM1223 RNA, herein

designated GAM RNA, to target binding sites on GAM1223 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1223 target RNA, herein designated GAM TARGET RNA, into GAM1223 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19066] It is appreciated that GAM1223 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1223 target genes. The mRNA of each one of this plurality of GAM1223 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1223 RNA, herein designated GAM RNA, and which when bound by GAM1223 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1223 target proteins.

[19067] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1223 gene, herein designated GAM GENE, on one or more GAM1223 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19068] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1223 correlate with, and may be deduced from, the identity of the target genes which GAM1223 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19069] Nucleotide sequences of the GAM1223 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1223 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1223 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1223 are further described hereinbelow with reference to Table Table1.

[19070] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1223 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19071] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1224 (GAM1224) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19072] GAM1224 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1224 was detected is described hereinabove with reference to Figs. 2-8.

[19073] GAM1224 gene, herein designated GAM GENE, and GAM1224 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19074] GAM1224 gene, herein designated GAM GENE, encodes a GAM1224 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1224 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1224 precursor RNA is designated SEQ ID:1197, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1197 is located at position 2037056 relative to contig NT_021907.13, on chromosome 1.

[19075] GAM1224 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19076] An enzyme complex designated DICER COMPLEX, dices the GAM1224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1224 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1224 RNA is designated SEQ ID:2873, and is provided hereinbelow with reference to the sequence listing part.

[19077] GAM1224 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1224 target RNA, herein designated GAM TARGET RNA. GAM1224 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19078] GAM1224 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1224 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1224 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1224 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1224 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19079] The complementary binding of GAM1224 RNA, herein designated GAM RNA, to target binding sites on GAM1224 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1224 target RNA, herein designated GAM TARGET RNA, into GAM1224 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19080] It is appreciated that GAM1224 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1224 target genes. The mRNA of each one of this plurality of GAM1224 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1224 RNA, herein designated GAM RNA, and which when bound by GAM1224 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1224 target proteins.

[19081] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1224 gene, herein designated GAM GENE, on one or more GAM1224 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19082] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1224 correlate with, and may be deduced from, the identity of the target genes which GAM1224 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19083] Nucleotide sequences of the GAM1224 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1224 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1224 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1224 are further described hereinbelow with reference to Table Table1.

[19084] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1224 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19085] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1225 (GAM1225) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19086] GAM1225 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1225 was detected is described hereinabove with reference to Figs. 2-8.

[19087] GAM1225 gene, herein designated GAM GENE, and GAM1225 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19088] GAM1225 gene, herein designated GAM GENE, encodes a GAM1225 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1225 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1225 precursor RNA is designated SEQ ID:1198, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1198 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[19089] GAM1225 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19090] An enzyme complex designated DICER COMPLEX, dices the GAM1225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1225 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1225 RNA is designated SEQ ID:2874, and is provided hereinbelow with reference to the sequence listing part.

[19091] GAM1225 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1225 target RNA, herein designated GAM TARGET RNA. GAM1225 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19092] GAM1225 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1225 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1225 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1225 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1225 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19093] The complementary binding of GAM1225 RNA, herein designated GAM RNA, to target binding sites on GAM1225 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1225 target RNA, herein designated GAM TARGET RNA, into GAM1225 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19094] It is appreciated that GAM1225 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1225 target genes. The mRNA of each one of this plurality of GAM1225 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1225 RNA, herein designated GAM RNA, and which when bound by GAM1225 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1225 target proteins.

[19095] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1225 gene, herein designated GAM GENE, on one or more GAM1225 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19096] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1225 correlate with, and may be deduced from, the identity of the target genes which GAM1225 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19097] Nucleotide sequences of the GAM1225 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1225 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1225 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1225 are further described hereinbelow with reference to Table Table1.

[19098] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1225 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19099] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1226 (GAM1226) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19100] GAM1226 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1226 was detected is described hereinabove with reference to Figs. 2-8.

[19101] GAM1226 gene, herein designated GAM GENE, and GAM1226 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19102] GAM1226 gene, herein designated GAM GENE, encodes a GAM1226 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1226 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1226 precursor RNA is designated SEQ ID:1199, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1199 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[19103] GAM1226 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19104] An enzyme complex designated DICER COMPLEX, dices the GAM1226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1226 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1226 RNA is designated SEQ ID:2875, and is provided hereinbelow with reference to the sequence listing part.

[19105] GAM1226 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1226 target RNA, herein designated GAM TARGET RNA. GAM1226 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19106] GAM1226 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1226 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1226 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1226 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1226 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19107] The complementary binding of GAM1226 RNA, herein designated GAM RNA, to target binding sites on GAM1226 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1226 target RNA, herein designated GAM TARGET RNA, into GAM1226 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19108] It is appreciated that GAM1226 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1226 target genes. The mRNA of each one of this

plurality of GAM1226 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1226 RNA, herein designated GAM RNA, and which when bound by GAM1226 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1226 target proteins.

[19109] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1226 gene, herein designated GAM GENE, on one or more GAM1226 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19110] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1226 correlate with, and may be deduced from, the identity of the target genes which GAM1226 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19111] Nucleotide sequences of the GAM1226 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1226 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1226 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1226 are further described hereinbelow with reference to Table Table1.

[19112] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1226 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19113] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1227 (GAM1227) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[19114] GAM1227 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1227 was detected is described hereinabove with reference to Figs. 2-8.

[19115] GAM1227 gene, herein designated GAM GENE, and GAM1227 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19116] GAM1227 gene, herein designated GAM GENE, encodes a GAM1227 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1227 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1227 precursor RNA is designated SEQ ID:1200, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1200 is located at position 7850412 relative to contig NT_007299.11, on chromosome 6.

[19117] GAM1227 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19118] An enzyme complex designated DICER COMPLEX, dices the GAM1227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1227 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1227 RNA is designated SEQ ID:2876, and is provided hereinbelow with reference to the sequence listing part.

[19119] GAM1227 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1227 target RNA, herein designated GAM TARGET RNA. GAM1227 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19120] GAM1227 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1227 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1227 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1227 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1227 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[19121] The complementary binding of GAM1227 RNA, herein designated GAM RNA, to target binding sites on GAM1227 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1227 target RNA, herein designated GAM TARGET RNA, into GAM1227 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19122] It is appreciated that GAM1227 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1227 target genes. The mRNA of each one of this plurality of GAM1227 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1227 RNA, herein designated GAM RNA, and which when bound by GAM1227 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1227 target proteins.

[19123] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1227 gene, herein designated GAM GENE, on one or

more GAM1227 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19124] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1227 correlate with, and may be deduced from, the identity of the target genes which GAM1227 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19125] Nucleotide sequences of the GAM1227 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1227 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1227 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1227 are further de-

scribed hereinbelow with reference to Table Table1.

[19126] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1227 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19127]

[19128] Fig. 8 further provides a conceptual description of a novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1228 (GAM1228) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19129] GAM1228 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1228 was detected is described hereinabove with reference to Figs. 2-8.

[19130] GAM1228 gene, herein designated GAM GENE, and GAM1228 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19131] GAM1228 gene, herein designated GAM GENE, encodes a GAM1228 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1228 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1228 precursor RNA is designated SEQ ID:1201, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1201 is located at position 2840909 relative to contig NT_004734.13, on chromosome 1.

[19132] GAM1228 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19133] An enzyme complex designated DICER COMPLEX, dices the GAM1228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1228 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1228 RNA is designated SEQ ID:2877, and is provided hereinbelow with reference to the sequence listing part.

[19134] GAM1228 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1228 target RNA, herein designated GAM TARGET RNA. GAM1228 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19135] GAM1228 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1228 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1228 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1228 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1228 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19136] The complementary binding of GAM1228 RNA, herein designated GAM RNA, to target binding sites on GAM1228 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1228 target RNA, herein designated GAM TARGET RNA, into GAM1228 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19137] It is appreciated that GAM1228 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1228 target genes. The mRNA of each one of this plurality of GAM1228 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1228 RNA, herein designated GAM RNA, and which when bound by GAM1228 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1228 target proteins.

[19138] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1228 gene, herein designated GAM GENE, on one or more GAM1228 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19139] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1228 correlate with, and may be deduced from, the identity of the target genes which GAM1228 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19140] Nucleotide sequences of the GAM1228 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1228 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1228 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1228 are further described hereinbelow with reference to Table Table1.

[19141] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1228 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19142] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1229 (GAM1229) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19143] GAM1229 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1229 was detected is described hereinabove with reference to Figs. 2-8.

[19144] GAM1229 gene, herein designated GAM GENE, and GAM1229 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19145] GAM1229 gene, herein designated GAM GENE, encodes a GAM1229 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1229 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1229 precursor RNA is designated SEQ ID:1202, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1202 is located at position 312769 relative to contig NT_024683.9, on chromosome 15.

[19146] GAM1229 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1229 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19147] An enzyme complex designated DICER COMPLEX, dices the GAM1229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1229 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1229 RNA is designated SEQ ID:2878, and is provided hereinbelow with reference to the sequence listing part.

[19148] GAM1229 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1229 target RNA, herein designated GAM TARGET

RNA. GAM1229 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19149] GAM1229 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1229 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1229 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1229 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1229 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19150] The complementary binding of GAM1229 RNA, herein designated GAM RNA, to target binding sites on GAM1229 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1229 target RNA, herein designated GAM TARGET RNA, into GAM1229 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19151] It is appreciated that GAM1229 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1229 target genes. The mRNA of each one of this plurality of GAM1229 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1229 RNA, herein designated GAM RNA, and which when bound by GAM1229 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1229 target proteins.

[19152] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1229 gene, herein designated GAM GENE, on one or more GAM1229 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19153] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1229 correlate with, and may be deduced from, the identity of the target genes which GAM1229 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19154] Nucleotide sequences of the GAM1229 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1229 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1229 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1229 are further described hereinbelow with reference to Table Table1.

[19155] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1229 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19156] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1230 (GAM1230) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19157] GAM1230 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1230 was detected is described hereinabove with reference to Figs. 2-8.

[19158] GAM1230 gene, herein designated GAM GENE, and GAM1230 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19159] GAM1230 gene, herein designated GAM GENE, encodes a

GAM1230 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1230 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1230 precursor RNA is designated SEQ ID:1203, and is provided hereinbelow with reference to the sequence listing part.

[19160] GAM1230 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19161] An enzyme complex designated DICER COMPLEX, dices the GAM1230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1230 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1230 RNA is designated SEQ ID:2879, and is provided hereinbelow with reference to the sequence listing part.

[19162] GAM1230 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1230 target RNA, herein designated GAM TARGET RNA. GAM1230 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19163] GAM1230 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1230 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1230 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1230 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1230 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19164] The complementary binding of GAM1230 RNA, herein designated GAM RNA, to target binding sites on GAM1230 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1230 target RNA, herein designated GAM TARGET RNA, into GAM1230 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19165] It is appreciated that GAM1230 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1230 target genes. The mRNA of each one of this plurality of GAM1230 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1230 RNA, herein designated GAM RNA, and which when bound by GAM1230 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1230 target proteins.

[19166] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1230 gene, herein designated GAM GENE, on one or more GAM1230 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[19167] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1230 correlate with, and may be deduced from, the identity of the target genes which GAM1230 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19168] Nucleotide sequences of the GAM1230 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1230 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1230 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1230 are further described hereinbelow with reference to Table Table1.

[19169] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1230 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19170] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1231 (GAM1231) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[19171] GAM1231 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1231 was detected is described hereinabove with reference to Figs. 2-8.

[19172] GAM1231 gene, herein designated GAM GENE, and GAM1231 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19173] GAM1231 gene, herein designated GAM GENE, encodes a GAM1231 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1231 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1231 precursor RNA is designated SEQ ID:1204, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1204 is located at position 2531141 relative to contig NT_006051.13, on chromosome 4.

[19174] GAM1231 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1231 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19175] An enzyme complex designated DICER COMPLEX, dices the GAM1231 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1231 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1231 RNA is designated SEQ ID:2880, and is provided hereinbelow with reference to the sequence listing part.

[19176] GAM1231 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1231 target RNA, herein designated GAM TARGET RNA. GAM1231 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19177] GAM1231 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1231 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1231 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1231 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1231 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19178] The complementary binding of GAM1231 RNA, herein designated GAM RNA, to target binding sites on GAM1231 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1231 target RNA, herein designated GAM TARGET RNA, into GAM1231 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19179] It is appreciated that GAM1231 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1231 target genes. The mRNA of each one of this plurality of GAM1231 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1231 RNA, herein designated GAM RNA, and which when bound by GAM1231 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1231 target proteins.

[19180] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1231 gene, herein designated GAM GENE, on one or more GAM1231 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19181] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1231 correlate with, and may be deduced from, the identity of the target genes which GAM1231 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19182] Nucleotide sequences of the GAM1231 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1231 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1231 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1231 are further described hereinbelow with reference to Table Table1.

[19183] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1231 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19184] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1232 (GAM1232) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19185] GAM1232 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1232 was detected is described hereinabove with reference to Figs. 2-8.

[19186] GAM1232 gene, herein designated GAM GENE, and GAM1232 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19187] GAM1232 gene, herein designated GAM GENE, encodes a GAM1232 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1232 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1232 precursor RNA is designated SEQ ID:1205, and is provided hereinbelow with reference to the sequence listing part.

[19188] GAM1232 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19189] An enzyme complex designated DICER COMPLEX, dices the GAM1232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1232 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1232 RNA is designated SEQ ID:2881, and is provided hereinbelow with reference to the sequence listing part.

[19190] GAM1232 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1232 target RNA, herein designated GAM TARGET RNA. GAM1232 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19191] GAM1232 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1232 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1232 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1232 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1232 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19192] The complementary binding of GAM1232 RNA, herein designated GAM RNA, to target binding sites on GAM1232 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1232 target RNA, herein designated GAM TARGET RNA, into GAM1232 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19193] It is appreciated that GAM1232 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1232 target genes. The mRNA of each one of this

plurality of GAM1232 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1232 RNA, herein designated GAM RNA, and which when bound by GAM1232 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1232 target proteins.

[19194] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1232 gene, herein designated GAM GENE, on one or more GAM1232 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19195] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1232 correlate with, and may be deduced from, the identity of the target genes which GAM1232 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19196] Nucleotide sequences of the GAM1232 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1232 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1232 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1232 are further described hereinbelow with reference to Table Table1.

[19197] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1232 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19198] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1233 (GAM1233) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[19199] GAM1233 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1233 was detected is described hereinabove with reference to Figs. 2-8.

[19200] GAM1233 gene, herein designated GAM GENE, and GAM1233 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19201] GAM1233 gene, herein designated GAM GENE, encodes a GAM1233 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1233 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1233 precursor RNA is designated SEQ ID:1206, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1206 is located at position 14595424 relative to contig NT_010194.13, on chromosome 15.

[19202] GAM1233 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19203] An enzyme complex designated DICER COMPLEX, dices the GAM1233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1233 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1233 RNA is designated SEQ ID:2882, and is provided hereinbelow with reference to the sequence listing part.

[19204] GAM1233 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1233 target RNA, herein designated GAM TARGET RNA. GAM1233 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19205] GAM1233 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1233 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1233 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1233 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1233 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[19206] The complementary binding of GAM1233 RNA, herein designated GAM RNA, to target binding sites on GAM1233 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1233 target RNA, herein designated GAM TARGET RNA, into GAM1233 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19207] It is appreciated that GAM1233 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1233 target genes. The mRNA of each one of this plurality of GAM1233 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1233 RNA, herein designated GAM RNA, and which when bound by GAM1233 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1233 target proteins.

[19208] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1233 gene, herein designated GAM GENE, on one or

more GAM1233 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19209] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1233 correlate with, and may be deduced from, the identity of the target genes which GAM1233 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19210] Nucleotide sequences of the GAM1233 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1233 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1233 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1233 are further de-

scribed hereinbelow with reference to Table Table1.

[19211] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1233 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19212] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1234 (GAM1234) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19213] GAM1234 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1234 was detected is described hereinabove with reference to Figs. 2-8.

[19214] GAM1234 gene, herein designated GAM GENE, and GAM1234 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19215] GAM1234 gene, herein designated GAM GENE, encodes a GAM1234 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1234 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1234 precursor RNA is designated SEQ ID:1207, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1207 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[19216] GAM1234 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19217] An enzyme complex designated DICER COMPLEX, dices the GAM1234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1234 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1234 RNA is designated SEQ ID:2883, and is provided hereinbelow with reference to the sequence listing part.

[19218] GAM1234 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1234 target RNA, herein designated GAM TARGET RNA. GAM1234 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19219] GAM1234 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1234 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1234 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1234 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1234 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19220] The complementary binding of GAM1234 RNA, herein designated GAM RNA, to target binding sites on GAM1234 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1234 target RNA, herein designated GAM TARGET RNA, into GAM1234 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19221] It is appreciated that GAM1234 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1234 target genes. The mRNA of each one of this plurality of GAM1234 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1234 RNA, herein designated GAM RNA, and which when bound by GAM1234 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1234 target proteins.

[19222] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1234 gene, herein designated GAM GENE, on one or more GAM1234 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[19223] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1234 correlate with, and may be deduced from, the identity of the target genes which GAM1234 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19224] Nucleotide sequences of the GAM1234 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1234 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1234 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1234 are further described hereinbelow with reference to Table Table1.

[19225] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1234 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19226] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1235 (GAM1235) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[19227] GAM1235 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1235 was detected is described hereinabove with reference to Figs. 2-8.

[19228] GAM1235 gene, herein designated GAM GENE, and GAM1235 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19229] GAM1235 gene, herein designated GAM GENE, encodes a GAM1235 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1235 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1235 precursor RNA is designated SEQ ID:1208, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1208 is located at position 4544386 relative to contig NT_021953.13, on chromosome 1.

[19230] GAM1235 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1235 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19231] An enzyme complex designated DICER COMPLEX, dices the GAM1235 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1235 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1235 RNA is designated SEQ ID:2884, and is provided hereinbelow with reference to the sequence listing part.

[19232] GAM1235 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1235 target RNA, herein designated GAM TARGET RNA. GAM1235 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19233] GAM1235 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1235 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1235 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1235 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1235 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19234] The complementary binding of GAM1235 RNA, herein designated GAM RNA, to target binding sites on GAM1235 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1235 target RNA, herein designated GAM TARGET RNA, into GAM1235 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19235] It is appreciated that GAM1235 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1235 target genes. The mRNA of each one of this plurality of GAM1235 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1235 RNA, herein designated GAM RNA, and which when bound by GAM1235 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1235 target proteins.

[19236] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1235 gene, herein designated GAM GENE, on one or more GAM1235 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19237] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1235 correlate with, and may be deduced from, the identity of the target genes which GAM1235 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19238] Nucleotide sequences of the GAM1235 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1235 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1235 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1235 are further described hereinbelow with reference to Table Table1.

[19239] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1235 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19240] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1236 (GAM1236) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19241] GAM1236 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1236 was detected is described hereinabove with reference to Figs. 2-8.

[19242] GAM1236 gene, herein designated GAM GENE, and GAM1236 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19243] GAM1236 gene, herein designated GAM GENE, encodes a GAM1236 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1236 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1236 precursor RNA is designated SEQ ID:1209, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1209 is located at position 5428768 relative to contig NT_011568.10, on chromosome X.

[19244] GAM1236 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19245] An enzyme complex designated DICER COMPLEX, dices the GAM1236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1236 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1236 RNA is designated SEQ ID:2885, and is provided hereinbelow with reference to the sequence listing part.

[19246] GAM1236 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1236 target RNA, herein designated GAM TARGET RNA. GAM1236 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19247] GAM1236 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1236 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1236 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1236 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1236 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19248] The complementary binding of GAM1236 RNA, herein designated GAM RNA, to target binding sites on GAM1236 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1236 target RNA, herein designated GAM TARGET RNA, into GAM1236 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19249] It is appreciated that GAM1236 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1236 target genes. The mRNA of each one of this plurality of GAM1236 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1236 RNA, herein designated GAM RNA, and which when bound by GAM1236 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1236 target proteins.

[19250] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1236 gene, herein designated GAM GENE, on one or more GAM1236 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19251] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1236 correlate with, and may be deduced from, the identity of the target genes which GAM1236 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19252] Nucleotide sequences of the GAM1236 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1236 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1236 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1236 are further described hereinbelow with reference to Table Table1.

[19253] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1236 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19254] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1237 (GAM1237) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19255] GAM1237 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1237 was detected is described hereinabove with reference to Figs. 2-8.

[19256] GAM1237 gene, herein designated GAM GENE, and GAM1237 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19257] GAM1237 gene, herein designated GAM GENE, encodes a GAM1237 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1237 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1237 precursor RNA is designated SEQ ID:1210, and is provided hereinbelow with reference to the sequence listing part.

[19258] GAM1237 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19259] An enzyme complex designated DICER COMPLEX, dices the GAM1237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1237 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1237 RNA is designated SEQ ID:2886, and is provided hereinbelow with reference to the sequence listing part.

[19260] GAM1237 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1237 target RNA, herein designated GAM TARGET RNA. GAM1237 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19261] GAM1237 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1237 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1237 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1237 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1237 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[19262] The complementary binding of GAM1237 RNA, herein designated GAM RNA, to target binding sites on GAM1237 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1237 target RNA, herein designated GAM TARGET RNA, into GAM1237 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19263] It is appreciated that GAM1237 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1237 target genes. The mRNA of each one of this plurality of GAM1237 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1237 RNA, herein designated GAM RNA, and which when bound by GAM1237 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1237 target proteins.

[19264] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1237 gene, herein designated GAM GENE, on one or

more GAM1237 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19265] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1237 correlate with, and may be deduced from, the identity of the target genes which GAM1237 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19266] Nucleotide sequences of the GAM1237 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1237 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1237 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1237 are further de-

scribed hereinbelow with reference to Table Table1.

[19267] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1237 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19268] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1238 (GAM1238) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19269] GAM1238 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1238 was detected is described hereinabove with reference to Figs. 2-8.

[19270] GAM1238 gene, herein designated GAM GENE, and GAM1238 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19271] GAM1238 gene, herein designated GAM GENE, encodes a GAM1238 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1238 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1238 precursor RNA is designated SEQ ID:1211, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1211 is located at position 4313929 relative to contig NT_034483.2, on chromosome 2.

[19272] GAM1238 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19273] An enzyme complex designated DICER COMPLEX, dices the GAM1238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1238 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1238 RNA is designated SEQ ID:2887, and is provided hereinbelow with reference to the sequence listing part.

[19274] GAM1238 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1238 target RNA, herein designated GAM TARGET RNA. GAM1238 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19275] GAM1238 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1238 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1238 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1238 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1238 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19276] The complementary binding of GAM1238 RNA, herein designated GAM RNA, to target binding sites on GAM1238 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1238 target RNA, herein designated GAM TARGET RNA, into GAM1238 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19277] It is appreciated that GAM1238 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1238 target genes. The mRNA of each one of this plurality of GAM1238 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1238 RNA, herein designated GAM RNA, and which when bound by GAM1238 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1238 target proteins.

[19278] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1238 gene, herein designated GAM GENE, on one or more GAM1238 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[19279] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1238 correlate with, and may be deduced from, the identity of the target genes which GAM1238 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19280] Nucleotide sequences of the GAM1238 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1238 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1238 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1238 are further described hereinbelow with reference to Table Table1.

[19281] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1238 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19282] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1239 (GAM1239) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[19283] GAM1239 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1239 was detected is described hereinabove with reference to Figs. 2-8.

[19284] GAM1239 gene, herein designated GAM GENE, and GAM1239 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19285] GAM1239 gene, herein designated GAM GENE, encodes a GAM1239 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1239 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1239 precursor RNA is designated SEQ ID:1212, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1212 is located at position 1643563 relative to contig NT_005832.12, on chromosome 3.

[19286] GAM1239 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1239 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19287] An enzyme complex designated DICER COMPLEX, dices the GAM1239 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1239 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 96%) nucleotide sequence of GAM1239 RNA is designated SEQ ID:2888, and is provided hereinbelow with reference to the sequence listing part.

[19288] GAM1239 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1239 target RNA, herein designated GAM TARGET RNA. GAM1239 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19289] GAM1239 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1239 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1239 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1239 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1239 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19290] The complementary binding of GAM1239 RNA, herein designated GAM RNA, to target binding sites on GAM1239 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1239 target RNA, herein designated GAM TARGET RNA, into GAM1239 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19291] It is appreciated that GAM1239 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1239 target genes. The mRNA of each one of this plurality of GAM1239 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1239 RNA, herein designated GAM RNA, and which when bound by GAM1239 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1239 target proteins.

[19292] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1239 gene, herein designated GAM GENE, on one or more GAM1239 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19293] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1239 correlate with, and may be deduced from, the identity of the target genes which GAM1239 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19294] Nucleotide sequences of the GAM1239 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1239 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1239 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1239 are further described hereinbelow with reference to Table Table1.

[19295] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1239 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19296] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1240 (GAM1240) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19297] GAM1240 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1240 was detected is described hereinabove with reference to Figs. 2-8.

[19298] GAM1240 gene, herein designated GAM GENE, and GAM1240 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19299] GAM1240 gene, herein designated GAM GENE, encodes a GAM1240 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1240 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1240 precursor RNA is designated SEQ ID:1213, and is provided hereinbelow with reference to the sequence listing part.

[19300] GAM1240 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19301] An enzyme complex designated DICER COMPLEX, dices the GAM1240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1240 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1240 RNA is designated SEQ ID:2889, and is provided hereinbelow with reference to the sequence listing part.

[19302] GAM1240 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1240 target RNA, herein designated GAM TARGET RNA. GAM1240 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19303] GAM1240 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1240 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1240 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1240 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1240 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19304] The complementary binding of GAM1240 RNA, herein designated GAM RNA, to target binding sites on GAM1240 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1240 target RNA, herein designated GAM TARGET RNA, into GAM1240 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19305] It is appreciated that GAM1240 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1240 target genes. The mRNA of each one of this

plurality of GAM1240 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1240 RNA, herein designated GAM RNA, and which when bound by GAM1240 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1240 target proteins.

[19306] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1240 gene, herein designated GAM GENE, on one or more GAM1240 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19307] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1240 correlate with, and may be deduced from, the identity of the target genes which GAM1240 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19308] Nucleotide sequences of the GAM1240 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1240 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1240 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1240 are further described hereinbelow with reference to Table Table1.

[19309] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1240 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19310] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1241 (GAM1241) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[19311] GAM1241 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1241 was detected is described hereinabove with reference to Figs. 2-8.

[19312] GAM1241 gene, herein designated GAM GENE, and GAM1241 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19313] GAM1241 gene, herein designated GAM GENE, encodes a GAM1241 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1241 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1241 precursor RNA is designated SEQ ID:1214, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1214 is located at position 5792400 relative to contig NT_010498.11, on chromosome 16.

[19314] GAM1241 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19315] An enzyme complex designated DICER COMPLEX, dices the GAM1241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1241 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1241 RNA is designated SEQ ID:2890, and is provided hereinbelow with reference to the sequence listing part.

[19316] GAM1241 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1241 target RNA, herein designated GAM TARGET RNA. GAM1241 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19317] GAM1241 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1241 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1241 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1241 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1241 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[19318] The complementary binding of GAM1241 RNA, herein designated GAM RNA, to target binding sites on GAM1241 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1241 target RNA, herein designated GAM TARGET RNA, into GAM1241 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19319] It is appreciated that GAM1241 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1241 target genes. The mRNA of each one of this plurality of GAM1241 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1241 RNA, herein designated GAM RNA, and which when bound by GAM1241 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1241 target proteins.

[19320] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1241 gene, herein designated GAM GENE, on one or

more GAM1241 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19321] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1241 correlate with, and may be deduced from, the identity of the target genes which GAM1241 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19322] Nucleotide sequences of the GAM1241 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1241 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1241 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1241 are further de-

scribed hereinbelow with reference to Table Table1.

[19323] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1241 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19324] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1242 (GAM1242) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19325] GAM1242 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1242 was detected is described hereinabove with reference to Figs. 2-8.

[19326] GAM1242 gene, herein designated GAM GENE, and GAM1242 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19327] GAM1242 gene, herein designated GAM GENE, encodes a GAM1242 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1242 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1242 precursor RNA is designated SEQ ID:1215, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1215 is located at position 4851356 relative to contig NT_022517.13, on chromosome 3.

[19328] GAM1242 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19329] An enzyme complex designated DICER COMPLEX, dices the GAM1242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1242 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1242 RNA is designated SEQ ID:2891, and is provided hereinbelow with reference to the sequence listing part.

[19330] GAM1242 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1242 target RNA, herein designated GAM TARGET RNA. GAM1242 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19331] GAM1242 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1242 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1242 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1242 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1242 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19332] The complementary binding of GAM1242 RNA, herein designated GAM RNA, to target binding sites on GAM1242 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1242 target RNA, herein designated GAM TARGET RNA, into GAM1242 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19333] It is appreciated that GAM1242 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1242 target genes. The mRNA of each one of this plurality of GAM1242 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1242 RNA, herein designated GAM RNA, and which when bound by GAM1242 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1242 target proteins.

[19334] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1242 gene, herein designated GAM GENE, on one or more GAM1242 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[19335] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1242 correlate with, and may be deduced from, the identity of the target genes which GAM1242 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19336] Nucleotide sequences of the GAM1242 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1242 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1242 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1242 are further described hereinbelow with reference to Table Table1.

[19337] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1242 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19338] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1243 (GAM1243) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[19339] GAM1243 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1243 was detected is described hereinabove with reference to Figs. 2-8.

[19340] GAM1243 gene, herein designated GAM GENE, and GAM1243 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19341] GAM1243 gene, herein designated GAM GENE, encodes a GAM1243 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1243 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1243 precursor RNA is designated SEQ ID:1216, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1216 is located at position 1589540 relative to contig NT_021979.13, on chromosome 1.

[19342] GAM1243 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1243 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19343] An enzyme complex designated DICER COMPLEX, dices the GAM1243 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1243 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1243 RNA is designated SEQ ID:2892, and is provided hereinbelow with reference to the sequence listing part.

[19344] GAM1243 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1243 target RNA, herein designated GAM TARGET RNA. GAM1243 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19345] GAM1243 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1243 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1243 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1243 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1243 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19346] The complementary binding of GAM1243 RNA, herein designated GAM RNA, to target binding sites on GAM1243 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1243 target RNA, herein designated GAM TARGET RNA, into GAM1243 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19347] It is appreciated that GAM1243 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1243 target genes. The mRNA of each one of this plurality of GAM1243 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1243 RNA, herein designated GAM RNA, and which when bound by GAM1243 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1243 target proteins.

[19348] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1243 gene, herein designated GAM GENE, on one or more GAM1243 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19349] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1243 correlate with, and may be deduced from, the identity of the target genes which GAM1243 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19350] Nucleotide sequences of the GAM1243 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1243 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1243 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1243 are further described hereinbelow with reference to Table Table1.

[19351] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1243 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19352] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1244 (GAM1244) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19353] GAM1244 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1244 was detected is described hereinabove with reference to Figs. 2-8.

[19354] GAM1244 gene, herein designated GAM GENE, and GAM1244 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19355] GAM1244 gene, herein designated GAM GENE, encodes a GAM1244 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1244 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1244 precursor RNA is designated SEQ ID:1217, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1217 is located at position 1235151 relative to contig NT_009526.11, on chromosome 12.

[19356] GAM1244 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[19357] SEQ ID:99545 detected in mouse EST Accession BI965972.1.

[19358] SEQ ID:99546 detected in mouse EST Accession AI326210.1.

[19359] SEQ ID:99547 detected in mouse EST Accession BI965652.1.

[19360] GAM1244 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1244 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19361] An enzyme complex designated DICER COMPLEX, dices the GAM1244 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1244 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1244 RNA is designated SEQ ID:2893, and is provided hereinbelow with reference to the sequence listing part.

[19362] GAM1244 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1244 target RNA, herein designated GAM TARGET RNA. GAM1244 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19363] GAM1244 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1244 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1244 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1244 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1244 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19364] The complementary binding of GAM1244 RNA, herein designated GAM RNA, to target binding sites on GAM1244 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1244 target RNA, herein designated GAM TARGET RNA, into GAM1244 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19365] It is appreciated that GAM1244 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1244 target genes. The mRNA of each one of this plurality of GAM1244 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1244 RNA, herein designated GAM RNA, and which when bound by GAM1244 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1244 target proteins.

[19366] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1244 gene, herein designated GAM GENE, on one or more GAM1244 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19367] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1244 correlate with, and may be deduced from, the identity of the target genes which GAM1244 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19368] Nucleotide sequences of the GAM1244 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1244 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1244 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1244 are further described hereinbelow with reference to Table Table1.

[19369] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1244 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19370] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1245 (GAM1245) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19371] GAM1245 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1245 was detected is described hereinabove with reference to Figs. 2-8.

[19372] GAM1245 gene, herein designated GAM GENE, and GAM1245 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19373] GAM1245 gene, herein designated GAM GENE, encodes a GAM1245 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1245 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1245 precursor RNA is designated SEQ ID:1218, and is provided hereinbelow with reference to the sequence listing part.

[19374] GAM1245 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19375] An enzyme complex designated DICER COMPLEX, dices the GAM1245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1245 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1245 RNA is designated SEQ ID:2894, and is provided hereinbelow with reference to the sequence listing part.

[19376] GAM1245 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1245 target RNA, herein designated GAM TARGET RNA. GAM1245 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19377] GAM1245 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1245 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1245 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1245 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1245 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19378] The complementary binding of GAM1245 RNA, herein designated GAM RNA, to target binding sites on GAM1245 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1245 target RNA, herein designated GAM TARGET RNA, into GAM1245 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19379] It is appreciated that GAM1245 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1245 target genes. The mRNA of each one of this

plurality of GAM1245 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1245 RNA, herein designated GAM RNA, and which when bound by GAM1245 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1245 target proteins.

[19380] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1245 gene, herein designated GAM GENE, on one or more GAM1245 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19381] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1245 correlate with, and may be deduced from, the identity of the target genes which GAM1245 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19382] Nucleotide sequences of the GAM1245 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1245 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1245 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1245 are further described hereinbelow with reference to Table Table1.

[19383] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1245 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19384] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1246 (GAM1246) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[19385] GAM1246 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1246 was detected is described hereinabove with reference to Figs. 2-8.

[19386] GAM1246 gene, herein designated GAM GENE, and GAM1246 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19387] GAM1246 gene, herein designated GAM GENE, encodes a GAM1246 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1246 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1246 precursor RNA is designated SEQ ID:1219, and is provided hereinbelow with reference to the sequence listing part.

[19388] GAM1246 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19389] An enzyme complex designated DICER COMPLEX, dices the GAM1246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1246 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1246 RNA is designated SEQ ID:2895, and is provided hereinbelow with reference to the sequence listing part.

[19390] GAM1246 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1246 target RNA, herein designated GAM TARGET RNA. GAM1246 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19391] GAM1246 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1246 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1246 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1246 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1246 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19392] The complementary binding of GAM1246 RNA, herein designated GAM RNA, to target binding sites on GAM1246 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1246 target RNA, herein designated GAM TARGET RNA, into GAM1246 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19393] It is appreciated that GAM1246 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1246 target genes. The mRNA of each one of this plurality of GAM1246 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1246 RNA, herein designated GAM RNA, and which when bound by GAM1246 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1246 target proteins.

[19394] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1246 gene, herein designated GAM GENE, on one or more GAM1246 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19395] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1246 correlate with, and may be deduced from, the identity of the target genes which GAM1246 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19396] Nucleotide sequences of the GAM1246 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1246 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1246 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1246 are further described hereinbelow with reference to Table Table1.

[19397] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1246 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19398] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1247 (GAM1247) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19399] GAM1247 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1247 was detected is described hereinabove with reference to Figs. 2-8.

[19400] GAM1247 gene, herein designated GAM GENE, and GAM1247 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[19401] GAM1247 gene, herein designated GAM GENE, encodes a GAM1247 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1247 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1247 precursor RNA is designated SEQ ID:1220, and is provided hereinbelow with reference to the sequence listing part.

[19402] GAM1247 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19403] An enzyme complex designated DICER COMPLEX, dices the GAM1247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1247 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1247 RNA is designated SEQ ID:2896, and is provided hereinbelow with reference to the sequence listing part.

[19404] GAM1247 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1247 target RNA, herein designated GAM TARGET RNA. GAM1247 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19405] GAM1247 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1247 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1247 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1247 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1247 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19406] The complementary binding of GAM1247 RNA, herein designated GAM RNA, to target binding sites on GAM1247 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1247 target RNA, herein designated GAM TARGET RNA, into GAM1247 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19407] It is appreciated that GAM1247 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1247 target genes. The mRNA of each one of this plurality of GAM1247 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1247 RNA, herein designated GAM RNA, and which when bound by GAM1247 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1247 target proteins.

[19408] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1247 gene, herein designated GAM GENE, on one or more GAM1247 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19409] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1247 correlate with, and may be deduced from, the identity of the target genes which GAM1247 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19410] Nucleotide sequences of the GAM1247 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1247 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1247 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1247 are further described hereinbelow with reference to Table Table1.

[19411] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1247 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19412] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1248 (GAM1248) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19413] GAM1248 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1248 was detected is described hereinabove with reference to Figs. 2-8.

[19414] GAM1248 gene, herein designated GAM GENE, and GAM1248 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19415] GAM1248 gene, herein designated GAM GENE, encodes a GAM1248 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1248 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1248 precursor RNA is designated SEQ ID:1221, and is provided hereinbelow with reference to the sequence listing part.

[19416] GAM1248 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1248 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19417] An enzyme complex designated DICER COMPLEX, dices the GAM1248 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1248 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1248 RNA is designated SEQ ID:2897, and is provided hereinbelow with reference to the sequence listing part.

[19418] GAM1248 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1248 target RNA, herein designated GAM TARGET RNA. GAM1248 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19419] GAM1248 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1248 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1248 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1248 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1248 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19420] The complementary binding of GAM1248 RNA, herein designated GAM RNA, to target binding sites on GAM1248 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1248 target RNA, herein designated GAM TARGET RNA, into GAM1248 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19421] It is appreciated that GAM1248 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1248 target genes. The mRNA of each one of this plurality of GAM1248 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1248 RNA, herein designated GAM RNA, and which when bound by GAM1248 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1248 target proteins.

[19422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1248 gene, herein designated GAM GENE, on one or more GAM1248 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19423] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1248 correlate with, and may be deduced from, the identity of the target genes which GAM1248 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19424] Nucleotide sequences of the GAM1248 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1248 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1248 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1248 are further described hereinbelow with reference to Table Table1.

[19425] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1248 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19426] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1249 (GAM1249) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19427] GAM1249 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1249 was detected is described hereinabove with reference to Figs. 2-8.

[19428] GAM1249 gene, herein designated GAM GENE, and GAM1249 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19429] GAM1249 gene, herein designated GAM GENE, encodes a GAM1249 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1249 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1249 precursor RNA is designated SEQ ID:1222, and is provided hereinbelow with reference to the sequence listing part.

[19430] GAM1249 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19431] An enzyme complex designated DICER COMPLEX, dices the GAM1249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1249 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1249 RNA is designated SEQ ID:2898, and is provided hereinbelow with reference to the sequence listing part.

[19432] GAM1249 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1249 target RNA, herein designated GAM TARGET RNA. GAM1249 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19433] GAM1249 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1249 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1249 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1249 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1249 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19434] The complementary binding of GAM1249 RNA, herein designated GAM RNA, to target binding sites on GAM1249 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1249 target RNA, herein designated GAM TARGET RNA, into GAM1249 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19435] It is appreciated that GAM1249 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1249 target genes. The mRNA of each one of this

plurality of GAM1249 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1249 RNA, herein designated GAM RNA, and which when bound by GAM1249 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1249 target proteins.

[19436] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1249 gene, herein designated GAM GENE, on one or more GAM1249 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19437] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1249 correlate with, and may be deduced from, the identity of the target genes which GAM1249 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19438] Nucleotide sequences of the GAM1249 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1249 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1249 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1249 are further described hereinbelow with reference to Table Table1.

[19439] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1249 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19440] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1250 (GAM1250) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[19441] GAM1250 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1250 was detected is described hereinabove with reference to Figs. 2-8.

[19442] GAM1250 gene, herein designated GAM GENE, and GAM1250 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19443] GAM1250 gene, herein designated GAM GENE, encodes a GAM1250 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1250 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1250 precursor RNA is designated SEQ ID:1223, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1223 is located at position 23908666 relative to contig NT_011512.7, on chromosome 21.

[19444] GAM1250 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19445] An enzyme complex designated DICER COMPLEX, dices the GAM1250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1250 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1250 RNA is designated SEQ ID:2899, and is provided hereinbelow with reference to the sequence listing part.

[19446] GAM1250 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1250 target RNA, herein designated GAM TARGET RNA. GAM1250 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19447] GAM1250 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1250 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1250 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1250 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1250 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[19448] The complementary binding of GAM1250 RNA, herein designated GAM RNA, to target binding sites on GAM1250 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1250 target RNA, herein designated GAM TARGET RNA, into GAM1250 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19449] It is appreciated that GAM1250 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1250 target genes. The mRNA of each one of this plurality of GAM1250 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1250 RNA, herein designated GAM RNA, and which when bound by GAM1250 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1250 target proteins.

[19450] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1250 gene, herein designated GAM GENE, on one or

more GAM1250 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19451] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1250 correlate with, and may be deduced from, the identity of the target genes which GAM1250 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19452] Nucleotide sequences of the GAM1250 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1250 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1250 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1250 are further de-

scribed hereinbelow with reference to Table Table1.

[19453] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1250 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19454] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1251 (GAM1251) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19455] GAM1251 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1251 was detected is described hereinabove with reference to Figs. 2-8.

[19456] GAM1251 gene, herein designated GAM GENE, and GAM1251 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19457] GAM1251 gene, herein designated GAM GENE, encodes a GAM1251 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1251 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1251 precursor RNA is designated SEQ ID:1224, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1224 is located at position 1783572 relative to contig NT_011568.10, on chromosome X.

[19458] GAM1251 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19459] An enzyme complex designated DICER COMPLEX, dices the GAM1251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1251 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1251 RNA is designated SEQ ID:2900, and is provided hereinbelow with reference to the sequence listing part.

[19460] GAM1251 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1251 target RNA, herein designated GAM TARGET RNA. GAM1251 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19461] GAM1251 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1251 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1251 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1251 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1251 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19462] The complementary binding of GAM1251 RNA, herein designated GAM RNA, to target binding sites on GAM1251 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1251 target RNA, herein designated GAM TARGET RNA, into GAM1251 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19463] It is appreciated that GAM1251 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1251 target genes. The mRNA of each one of this plurality of GAM1251 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1251 RNA, herein designated GAM RNA, and which when bound by GAM1251 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1251 target proteins.

[19464] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1251 gene, herein designated GAM GENE, on one or more GAM1251 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[19465] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1251 correlate with, and may be deduced from, the identity of the target genes which GAM1251 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19466] Nucleotide sequences of the GAM1251 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1251 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1251 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1251 are further described hereinbelow with reference to Table Table1.

[19467] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1251 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19468] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1252 (GAM1252) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[19469] GAM1252 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1252 was detected is described hereinabove with reference to Figs. 2-8.

[19470] GAM1252 gene, herein designated GAM GENE, and GAM1252 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19471] GAM1252 gene, herein designated GAM GENE, encodes a GAM1252 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1252 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1252 precursor RNA is designated SEQ ID:1225, and is provided hereinbelow with reference to the sequence listing part.

[19472] GAM1252 has 9 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[19473] SEQ ID:98684 detected in mouse EST Accession BF720106.1.

[19474] SEQ ID:98685 detected in mouse EST Accession BI664024.1.

[19475] SEQ ID:98686 detected in mouse EST Accession AV233075.2.

[19476] SEQ ID:98687 detected in mouse EST Accession BI108742.1.

[19477] SEQ ID:98688 detected in mouse EST Accession BG914410.1.

[19478] SEQ ID:98689 detected in mouse EST Accession BI687742.1.

[19479] SEQ ID:98690 detected in mouse EST Accession AI647910.1.

[19480] SEQ ID:98691 detected in mouse EST Accession BG872884.1.

[19481] SEQ ID:98692 detected in mouse EST Accession BI657279.1.

[19482] GAM1252 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19483] An enzyme complex designated DICER COMPLEX, dices the GAM1252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1252 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1252 RNA is designated SEQ ID:2901, and is provided hereinbelow with reference to the sequence listing part.

[19484] GAM1252 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1252 target RNA, herein designated GAM TARGET RNA. GAM1252 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19485] GAM1252 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1252 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1252 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1252 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1252 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19486] The complementary binding of GAM1252 RNA, herein designated GAM RNA, to target binding sites on GAM1252 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1252 target RNA, herein designated GAM TARGET RNA, into GAM1252 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19487] It is appreciated that GAM1252 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1252 target genes. The mRNA of each one of this plurality of GAM1252 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1252 RNA, herein designated GAM RNA, and which when bound by GAM1252 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1252 target proteins.

[19488] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1252 gene, herein designated GAM GENE, on one or more GAM1252 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19489] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1252 correlate with, and may be deduced from, the identity of the target genes which GAM1252 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19490] Nucleotide sequences of the GAM1252 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1252 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1252 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1252 are further described hereinbelow with reference to Table Table1.

[19491] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1252 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19492] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1253 (GAM1253) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19493] GAM1253 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1253 was detected is described hereinabove with reference to Figs. 2-8.

[19494] GAM1253 gene, herein designated GAM GENE, and GAM1253 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19495] GAM1253 gene, herein designated GAM GENE, encodes a GAM1253 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1253 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1253 precursor RNA is designated SEQ ID:1226, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1226 is located at position 464461 relative to contig NT_010692.9, on chromosome 17.

[19496] GAM1253 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[19497] SEQ ID:99271 detected in mouse EST Accession AA068787.1.

[19498] SEQ ID:99272 detected in mouse EST Accession BE625629.1.

[19499] SEQ ID:100219 detected in mouse EST Accession BI792530.1.

[19500] SEQ ID:100220 detected in mouse EST Accession AA823029.1.

[19501] SEQ ID:100221 detected in mouse EST Accession BE380224.1.

[19502] SEQ ID:100222 detected in mouse EST Accession

BE309708.1.

[19503] SEQ ID:100223 detected in mouse EST Accession BI100916.1.

[19504] SEQ ID:100224 detected in mouse EST Accession BG296866.1.

[19505] GAM1253 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19506] An enzyme complex designated DICER COMPLEX, dices the GAM1253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1253 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 97%) nucleotide sequence of GAM1253 RNA is designated SEQ ID:2902, and is provided hereinbelow with reference to the sequence listing part.

[19507] GAM1253 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1253 target RNA, herein designated GAM TARGET RNA. GAM1253 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19508] GAM1253 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1253 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1253 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1253 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1253 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19509] The complementary binding of GAM1253 RNA, herein designated GAM RNA, to target binding sites on GAM1253 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1253 target RNA, herein designated GAM TARGET RNA, into GAM1253 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19510] It is appreciated that GAM1253 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1253 target genes. The mRNA of each one of this plurality of GAM1253 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1253 RNA, herein designated GAM RNA, and which when bound by GAM1253 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1253 target proteins.

[19511] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1253 gene, herein designated GAM GENE, on one or more GAM1253 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19512] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1253 correlate with, and may

be deduced from, the identity of the target genes which GAM1253 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19513] Nucleotide sequences of the GAM1253 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1253 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1253 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1253 are further described hereinbelow with reference to Table Table1.

[19514] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1253 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19515] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1254 (GAM1254) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19516] GAM1254 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1254 was detected is described hereinabove with reference to Figs. 2-8.

[19517] GAM1254 gene, herein designated GAM GENE, and GAM1254 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19518] GAM1254 gene, herein designated GAM GENE, encodes a GAM1254 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1254 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1254 precursor RNA is designated SEQ ID:1227, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1227 is located at position 365814 relative to contig NT_010799.11, on chromosome 17.

[19519] GAM1254 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[19520] SEQ ID:98868 detected in mouse EST Accession

AA144533.1.

[19521] SEQ ID:98869 detected in mouse EST Accession AA671455.1.

[19522] SEQ ID:98870 detected in mouse EST Accession AW824753.1.

[19523] SEQ ID:98871 detected in mouse EST Accession BE691413.1.

[19524] SEQ ID:98884 detected in mouse EST Accession BE953126.1.

[19525] SEQ ID:98885 detected in mouse EST Accession BE943987.1.

[19526] SEQ ID:98886 detected in mouse EST Accession BG808025.1.

[19527] SEQ ID:98887 detected in mouse EST Accession BG808010.1.

[19528] SEQ ID:98888 detected in mouse EST Accession BG807850.1.

[19529] SEQ ID:98889 detected in mouse EST Accession BG805970.1.

[19530] SEQ ID:98902 detected in mouse EST Accession AW208601.1.

[19531] SEQ ID:98903 detected in mouse EST Accession BB610842.1.

[19532] SEQ ID:98904 detected in mouse EST Accession BB609859.1.

[19533] SEQ ID:98914 detected in mouse EST Accession BE691447.1.

[19534] SEQ ID:98915 detected in mouse EST Accession BG145596.1.

[19535] GAM1254 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19536] An enzyme complex designated DICER COMPLEX, dices the GAM1254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1254 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1254 RNA is designated SEQ ID:2903, and is provided hereinbelow with reference to the sequence listing part.

[19537] GAM1254 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1254 target RNA, herein designated GAM TARGET RNA. GAM1254 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19538] GAM1254 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1254 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1254 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1254 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1254 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19539] The complementary binding of GAM1254 RNA, herein designated GAM RNA, to target binding sites on GAM1254 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1254 target RNA, herein designated GAM TARGET RNA, into GAM1254 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19540] It is appreciated that GAM1254 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1254 target genes. The mRNA of each one of this plurality of GAM1254 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1254 RNA, herein designated GAM RNA, and which when bound by GAM1254 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1254 target proteins.

[19541] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1254 gene, herein designated GAM GENE, on one or more GAM1254 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19542] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1254 correlate with, and may be deduced from, the identity of the target genes which GAM1254 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19543] Nucleotide sequences of the GAM1254 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1254 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1254 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1254 are further described hereinbelow with reference to Table Table1.

[19544] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1254 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19545] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1255 (GAM1255) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19546] GAM1255 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1255 was detected is described hereinabove with reference to Figs. 2-8.

[19547] GAM1255 gene, herein designated GAM GENE, and GAM1255 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19548] GAM1255 gene, herein designated GAM GENE, encodes a GAM1255 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1255 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1255 precursor RNA is designated SEQ ID:1228, and is provided hereinbelow with reference to the sequence listing part.

[19549] GAM1255 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19550] An enzyme complex designated DICER COMPLEX, dices the GAM1255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1255 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1255 RNA is designated SEQ ID:2904, and is provided hereinbelow with reference to the sequence listing part.

[19551] GAM1255 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1255 target RNA, herein designated GAM TARGET RNA. GAM1255 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19552] GAM1255 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1255 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1255 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1255 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1255 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19553] The complementary binding of GAM1255 RNA, herein designated GAM RNA, to target binding sites on GAM1255

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1255 target RNA, herein designated GAM TARGET RNA, into GAM1255 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19554] It is appreciated that GAM1255 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1255 target genes. The mRNA of each one of this plurality of GAM1255 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1255 RNA, herein designated GAM RNA, and which when bound by GAM1255 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1255 target proteins.

[19555] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1255 gene, herein designated GAM GENE, on one or more GAM1255 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19556] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1255 correlate with, and may be deduced from, the identity of the target genes which GAM1255 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19557] Nucleotide sequences of the GAM1255 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1255 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1255 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1255 are further described hereinbelow with reference to Table Table1.

[19558] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1255 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19559] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1256 (GAM1256) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19560] GAM1256 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1256 was detected is described hereinabove with reference to Figs. 2-8.

[19561] GAM1256 gene, herein designated GAM GENE, and GAM1256 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19562] GAM1256 gene, herein designated GAM GENE, encodes a GAM1256 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1256 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1256 precursor RNA is designated SEQ ID:1229, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1229 is located at position 2840909 relative to contig NT_004734.13, on chromosome 1.

[19563] GAM1256 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19564] An enzyme complex designated DICER COMPLEX, dices the GAM1256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1256 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1256 RNA is designated SEQ ID:2905, and is provided hereinbelow with reference to the sequence listing part.

[19565] GAM1256 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1256 target RNA, herein designated GAM TARGET RNA. GAM1256 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19566] GAM1256 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1256 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1256 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1256 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1256 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19567] The complementary binding of GAM1256 RNA, herein designated GAM RNA, to target binding sites on GAM1256 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1256 target RNA, herein designated GAM TARGET RNA, into GAM1256 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19568] It is appreciated that GAM1256 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1256 target genes. The mRNA of each one of this plurality of GAM1256 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1256 RNA, herein designated GAM RNA, and which when bound by GAM1256 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1256 target proteins.

[19569] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1256 gene, herein designated GAM GENE, on one or more GAM1256 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19570] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1256 correlate with, and may

be deduced from, the identity of the target genes which GAM1256 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19571] Nucleotide sequences of the GAM1256 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1256 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1256 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1256 are further described hereinbelow with reference to Table Table1.

[19572] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1256 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19573] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1257 (GAM1257) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19574] GAM1257 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1257 was detected is described hereinabove with reference to Figs. 2-8.

[19575] GAM1257 gene, herein designated GAM GENE, and GAM1257 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19576] GAM1257 gene, herein designated GAM GENE, encodes a GAM1257 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1257 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1257 precursor RNA is designated SEQ ID:1230, and is provided hereinbelow with reference to the sequence listing part.

[19577] GAM1257 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19578] An enzyme complex designated DICER COMPLEX, dices the GAM1257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1257 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1257 RNA is designated SEQ ID:2906, and is provided hereinbelow with reference to the sequence listing part.

[19579] GAM1257 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1257 target RNA, herein designated GAM TARGET RNA. GAM1257 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19580] GAM1257 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1257 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1257 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1257 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1257 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19581] The complementary binding of GAM1257 RNA, herein designated GAM RNA, to target binding sites on GAM1257 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1257 target RNA, herein designated GAM TARGET RNA, into GAM1257 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19582] It is appreciated that GAM1257 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1257 target genes. The mRNA of each one of this plurality of GAM1257 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1257 RNA, herein designated GAM RNA, and which when bound by GAM1257 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1257 target proteins.

[19583] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1257 gene, herein designated GAM GENE, on one or more GAM1257 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19584] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1257 correlate with, and may be deduced from, the identity of the target genes which GAM1257 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19585] Nucleotide sequences of the GAM1257 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1257 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1257 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1257 are further described hereinbelow with reference to Table Table1.

[19586] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1257 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19587] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1258 (GAM1258) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19588] GAM1258 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1258 was detected is described hereinabove with reference to Figs. 2-8.

[19589] GAM1258 gene, herein designated GAM GENE, and GAM1258 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19590] GAM1258 gene, herein designated GAM GENE, encodes a GAM1258 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1258 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1258 precursor RNA is

designated SEQ ID:1231, and is provided hereinbelow with reference to the sequence listing part.

[19591] GAM1258 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19592] An enzyme complex designated DICER COMPLEX, dices the GAM1258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1258 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1258 RNA is designated SEQ ID:2907, and is provided hereinbelow with reference to the sequence

listing part.

[19593] GAM1258 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1258 target RNA, herein designated GAM TARGET RNA. GAM1258 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19594] GAM1258 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1258 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1258 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1258 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1258 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19595] The complementary binding of GAM1258 RNA, herein designated GAM RNA, to target binding sites on GAM1258 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1258 target RNA, herein designated GAM TARGET RNA, into GAM1258 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19596] It is appreciated that GAM1258 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1258 target genes. The mRNA of each one of this plurality of GAM1258 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1258 RNA, herein designated GAM RNA, and which when bound by GAM1258 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1258 target proteins.

[19597] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1258 gene, herein designated GAM GENE, on one or more GAM1258 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19598] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1258 correlate with, and may be deduced from, the identity of the target genes which GAM1258 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19599] Nucleotide sequences of the GAM1258 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1258 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1258 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1258 are further described hereinbelow with reference to Table Table1.

[19600] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1258 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19601] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1259 (GAM1259) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19602] GAM1259 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1259 was detected is described hereinabove with reference to Figs. 2-8.

[19603] GAM1259 gene, herein designated GAM GENE, and GAM1259 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19604] GAM1259 gene, herein designated GAM GENE, encodes a GAM1259 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1259 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1259 precursor RNA is designated SEQ ID:1232, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1232 is located at position 8681475 relative to contig NT_017568.11, on chromosome 9.

[19605] GAM1259 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[19606] An enzyme complex designated DICER COMPLEX, dices the GAM1259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1259 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1259 RNA is designated SEQ ID:2908, and is provided hereinbelow with reference to the sequence listing part.

[19607] GAM1259 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1259 target RNA, herein designated GAM TARGET RNA. GAM1259 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19608] GAM1259 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1259 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1259 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1259 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1259 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19609] The complementary binding of GAM1259 RNA, herein designated GAM RNA, to target binding sites on GAM1259 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1259 target RNA, herein designated GAM TARGET RNA, into GAM1259 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19610] It is appreciated that GAM1259 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1259 target genes. The mRNA of each one of this plurality of GAM1259 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1259 RNA, herein designated GAM RNA, and which when bound by GAM1259 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1259 target proteins.

[19611] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1259 gene, herein designated GAM GENE, on one or more GAM1259 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19612] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1259 correlate with, and may be deduced from, the identity of the target genes which GAM1259 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19613] Nucleotide sequences of the GAM1259 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1259 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1259 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1259 are further described hereinbelow with reference to Table Table1.

[19614] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1259 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19615] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1260 (GAM1260) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19616] GAM1260 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1260 was detected is described hereinabove with reference to Figs. 2-8.

[19617] GAM1260 gene, herein designated GAM GENE, and GAM1260 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19618] GAM1260 gene, herein designated GAM GENE, encodes a GAM1260 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1260 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1260 precursor RNA is designated SEQ ID:1233, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1233 is located at position 5238029 relative to contig NT_010393.11, on chromosome 16.

[19619] GAM1260 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19620] An enzyme complex designated DICER COMPLEX, dices the GAM1260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1260 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1260 RNA is designated SEQ ID:2909, and

is provided hereinbelow with reference to the sequence listing part.

[19621] GAM1260 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1260 target RNA, herein designated GAM TARGET RNA. GAM1260 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19622] GAM1260 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1260 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1260 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1260 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1260 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19623] The complementary binding of GAM1260 RNA, herein designated GAM RNA, to target binding sites on GAM1260 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1260 target RNA, herein designated GAM TARGET RNA, into GAM1260 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19624] It is appreciated that GAM1260 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1260 target genes. The mRNA of each one of this plurality of GAM1260 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1260 RNA, herein designated GAM RNA, and which when bound by

GAM1260 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1260 target proteins.

[19625] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1260 gene, herein designated GAM GENE, on one or more GAM1260 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19626] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1260 correlate with, and may be deduced from, the identity of the target genes which GAM1260 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[19627] Nucleotide sequences of the GAM1260 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1260 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1260 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1260 are further described hereinbelow with reference to Table Table1.

[19628] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1260 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19629] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1261 (GAM1261) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19630] GAM1261 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1261 was detected is described hereinabove

with reference to Figs. 2-8.

[19631] GAM1261 gene, herein designated GAM GENE, and GAM1261 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19632] GAM1261 gene, herein designated GAM GENE, encodes a GAM1261 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1261 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1261 precursor RNA is designated SEQ ID:1234, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1234 is located at position 3757784 relative to contig NT_033898.3, on chromosome 10.

[19633] GAM1261 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19634] An enzyme complex designated DICER COMPLEX, dices the GAM1261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1261 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1261 RNA is designated SEQ ID:2910, and is provided hereinbelow with reference to the sequence listing part.

[19635] GAM1261 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1261 target RNA, herein designated GAM TARGET RNA. GAM1261 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19636] GAM1261 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1261 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1261 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1261 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1261 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19637] The complementary binding of GAM1261 RNA, herein designated GAM RNA, to target binding sites on GAM1261 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1261 target RNA, herein designated GAM TARGET RNA, into GAM1261 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19638] It is appreciated that GAM1261 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1261 target genes. The mRNA of each one of this plurality of GAM1261 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1261 RNA, herein designated GAM RNA, and which when bound by GAM1261 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1261 target proteins.

[19639] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1261 gene, herein designated GAM GENE, on one or more GAM1261 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19640] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1261 correlate with, and may be deduced from, the identity of the target genes which GAM1261 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19641] Nucleotide sequences of the GAM1261 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1261 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1261 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1261 are further described hereinbelow with reference to Table Table1.

[19642] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1261 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19643] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1262 (GAM1262) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19644] GAM1262 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1262 was detected is described hereinabove with reference to Figs. 2-8.

[19645] GAM1262 gene, herein designated GAM GENE, and GAM1262 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19646] GAM1262 gene, herein designated GAM GENE, encodes a GAM1262 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1262 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1262 precursor RNA is

designated SEQ ID:1235, and is provided hereinbelow with reference to the sequence listing part.

[19647] GAM1262 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19648] An enzyme complex designated DICER COMPLEX, dices the GAM1262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1262 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1262 RNA is designated SEQ ID:2911, and is provided hereinbelow with reference to the sequence

listing part.

[19649] GAM1262 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1262 target RNA, herein designated GAM TARGET RNA. GAM1262 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19650] GAM1262 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1262 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1262 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1262 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1262 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19651] The complementary binding of GAM1262 RNA, herein designated GAM RNA, to target binding sites on GAM1262 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1262 target RNA, herein designated GAM TARGET RNA, into GAM1262 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19652] It is appreciated that GAM1262 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1262 target genes. The mRNA of each one of this plurality of GAM1262 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1262 RNA, herein designated GAM RNA, and which when bound by GAM1262 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1262 target proteins.

[19653] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1262 gene, herein designated GAM GENE, on one or more GAM1262 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19654] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1262 correlate with, and may be deduced from, the identity of the target genes which GAM1262 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19655] Nucleotide sequences of the GAM1262 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1262 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1262 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1262 are further described hereinbelow with reference to Table Table1.

[19656] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1262 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19657] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1263 (GAM1263) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19658] GAM1263 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1263 was detected is described hereinabove with reference to Figs. 2-8.

[19659] GAM1263 gene, herein designated GAM GENE, and GAM1263 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19660] GAM1263 gene, herein designated GAM GENE, encodes a GAM1263 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1263 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1263 precursor RNA is designated SEQ ID:1236, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1236 is located at position 365842 relative to contig NT_010799.11, on chromosome 17.

[19661] GAM1263 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[19662] An enzyme complex designated DICER COMPLEX, dices the GAM1263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1263 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1263 RNA is designated SEQ ID:2912, and is provided hereinbelow with reference to the sequence listing part.

[19663] GAM1263 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1263 target RNA, herein designated GAM TARGET RNA. GAM1263 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19664] GAM1263 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1263 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1263 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1263 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1263 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19665] The complementary binding of GAM1263 RNA, herein designated GAM RNA, to target binding sites on GAM1263 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1263 target RNA, herein designated GAM TARGET RNA, into GAM1263 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19666] It is appreciated that GAM1263 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1263 target genes. The mRNA of each one of this plurality of GAM1263 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1263 RNA, herein designated GAM RNA, and which when bound by GAM1263 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1263 target proteins.

[19667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1263 gene, herein designated GAM GENE, on one or more GAM1263 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19668] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1263 correlate with, and may be deduced from, the identity of the target genes which GAM1263 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19669] Nucleotide sequences of the GAM1263 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1263 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1263 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1263 are further described hereinbelow with reference to Table Table1.

[19670] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1263 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19671] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1264 (GAM1264) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19672] GAM1264 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1264 was detected is described hereinabove with reference to Figs. 2-8.

[19673] GAM1264 gene, herein designated GAM GENE, and GAM1264 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19674] GAM1264 gene, herein designated GAM GENE, encodes a GAM1264 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1264 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1264 precursor RNA is designated SEQ ID:1237, and is provided hereinbelow with

reference to the sequence listing part.

[19675] GAM1264 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19676] An enzyme complex designated DICER COMPLEX, dices the GAM1264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1264 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1264 RNA is designated SEQ ID:2913, and is provided hereinbelow with reference to the sequence listing part.

[19677] GAM1264 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1264 target RNA, herein designated GAM TARGET RNA. GAM1264 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19678] GAM1264 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1264 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1264 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1264 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1264 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19679] The complementary binding of GAM1264 RNA, herein designated GAM RNA, to target binding sites on GAM1264 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1264 target RNA, herein designated GAM TARGET RNA, into GAM1264 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19680] It is appreciated that GAM1264 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1264 target genes. The mRNA of each one of this plurality of GAM1264 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1264 RNA, herein designated GAM RNA, and which when bound by GAM1264 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1264

target proteins.

[19681] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1264 gene, herein designated GAM GENE, on one or more GAM1264 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19682] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1264 correlate with, and may be deduced from, the identity of the target genes which GAM1264 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19683] Nucleotide sequences of the GAM1264 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1264 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1264 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1264 are further described hereinbelow with reference to Table Table1.

[19684] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1264 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19685] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1265 (GAM1265) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19686] GAM1265 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1265 was detected is described hereinabove with reference to Figs. 2-8.

[19687] GAM1265 gene, herein designated GAM GENE, and

GAM1265 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19688] GAM1265 gene, herein designated GAM GENE, encodes a GAM1265 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1265 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1265 precursor RNA is designated SEQ ID:1238, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1238 is located at position 33703762 relative to contig NT_007592.11, on chromosome 6.

[19689] GAM1265 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19690] An enzyme complex designated DICER COMPLEX, dices the GAM1265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1265 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1265 RNA is designated SEQ ID:2914, and is provided hereinbelow with reference to the sequence listing part.

[19691] GAM1265 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1265 target RNA, herein designated GAM TARGET RNA. GAM1265 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19692] GAM1265 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1265 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1265 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1265 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1265 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19693] The complementary binding of GAM1265 RNA, herein designated GAM RNA, to target binding sites on GAM1265 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1265 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1265 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19694] It is appreciated that GAM1265 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1265 target genes. The mRNA of each one of this plurality of GAM1265 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1265 RNA, herein designated GAM RNA, and which when bound by GAM1265 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1265 target proteins.

[19695] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1265 gene, herein designated GAM GENE, on one or more GAM1265 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19696] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1265 correlate with, and may be deduced from, the identity of the target genes which GAM1265 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19697] Nucleotide sequences of the GAM1265 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1265 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1265 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1265 are further described hereinbelow with reference to Table Table1.

[19698] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1265 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[19699] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1266 (GAM1266) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19700] GAM1266 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1266 was detected is described hereinabove with reference to Figs. 2-8.

[19701] GAM1266 gene, herein designated GAM GENE, and GAM1266 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19702] GAM1266 gene, herein designated GAM GENE, encodes a GAM1266 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1266 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1266 precursor RNA is designated SEQ ID:1239, and is provided hereinbelow with reference to the sequence listing part.

[19703] GAM1266 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19704] An enzyme complex designated DICER COMPLEX, dices the GAM1266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1266 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1266 RNA is designated SEQ ID:2915, and is provided hereinbelow with reference to the sequence listing part.

[19705] GAM1266 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1266 target RNA, herein designated GAM TARGET RNA. GAM1266 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19706] GAM1266 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1266 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1266 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1266 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1266 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19707] The complementary binding of GAM1266 RNA, herein designated GAM RNA, to target binding sites on GAM1266 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1266 target RNA, herein designated GAM TARGET RNA, into GAM1266 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19708] It is appreciated that GAM1266 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1266 target genes. The mRNA of each one of this plurality of GAM1266 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1266 RNA, herein designated GAM RNA, and which when bound by GAM1266 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1266 target proteins.

[19709] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1266 gene, herein designated GAM GENE, on one or more GAM1266 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19710] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1266 correlate with, and may be deduced from, the identity of the target genes which GAM1266 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19711] Nucleotide sequences of the GAM1266 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1266 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1266 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1266 are further described hereinbelow with reference to Table Table1.

[19712] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1266 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19713] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1267 (GAM1267) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19714] GAM1267 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1267 was detected is described hereinabove with reference to Figs. 2-8.

[19715] GAM1267 gene, herein designated GAM GENE, and GAM1267 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[19716] GAM1267 gene, herein designated GAM GENE, encodes a GAM1267 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1267 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1267 precursor RNA is designated SEQ ID:1240, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1240 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[19717] GAM1267 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19718] An enzyme complex designated DICER COMPLEX, dices

the GAM1267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1267 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1267 RNA is designated SEQ ID:2916, and is provided hereinbelow with reference to the sequence listing part.

[19719] GAM1267 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1267 target RNA, herein designated GAM TARGET RNA. GAM1267 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19720] GAM1267 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1267 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1267 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1267 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1267 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19721] The complementary binding of GAM1267 RNA, herein designated GAM RNA, to target binding sites on GAM1267 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1267 target RNA, herein designated GAM TARGET RNA, into GAM1267 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19722] It is appreciated that GAM1267 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1267 target genes. The mRNA of each one of this plurality of GAM1267 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1267 RNA, herein designated GAM RNA, and which when bound by GAM1267 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1267 target proteins.

[19723] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1267 gene, herein designated GAM GENE, on one or more GAM1267 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19724] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1267 correlate with, and may be deduced from, the identity of the target genes which GAM1267 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19725] Nucleotide sequences of the GAM1267 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1267 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1267 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1267 are further described hereinbelow with reference to Table Table1.

[19726] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1267 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19727] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1268 (GAM1268) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19728] GAM1268 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1268 was detected is described hereinabove with reference to Figs. 2-8.

[19729] GAM1268 gene, herein designated GAM GENE, and GAM1268 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19730] GAM1268 gene, herein designated GAM GENE, encodes a GAM1268 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1268 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1268 precursor RNA is designated SEQ ID:1241, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1241 is located at position 4930710 rela-

tive to contig NT_011568.10, on chromosome X.

[19731] GAM1268 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19732] An enzyme complex designated DICER COMPLEX, dices the GAM1268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1268 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1268 RNA is designated SEQ ID:2917, and is provided hereinbelow with reference to the sequence listing part.

[19733] GAM1268 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1268 target RNA, herein designated GAM TARGET RNA. GAM1268 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19734] GAM1268 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1268 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1268 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1268 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1268 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19735] The complementary binding of GAM1268 RNA, herein designated GAM RNA, to target binding sites on GAM1268 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1268 target RNA, herein designated GAM TARGET RNA, into GAM1268 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19736] It is appreciated that GAM1268 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1268 target genes. The mRNA of each one of this plurality of GAM1268 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1268 RNA, herein designated GAM RNA, and which when bound by GAM1268 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1268

target proteins.

[19737] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1268 gene, herein designated GAM GENE, on one or more GAM1268 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19738] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1268 correlate with, and may be deduced from, the identity of the target genes which GAM1268 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19739] Nucleotide sequences of the GAM1268 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1268 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1268 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1268 are further described hereinbelow with reference to Table Table1.

[19740] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1268 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19741] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1269 (GAM1269) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19742] GAM1269 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1269 was detected is described hereinabove with reference to Figs. 2-8.

[19743] GAM1269 gene, herein designated GAM GENE, and

GAM1269 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19744] GAM1269 gene, herein designated GAM GENE, encodes a GAM1269 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1269 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1269 precursor RNA is designated SEQ ID:1242, and is provided hereinbelow with reference to the sequence listing part.

[19745] GAM1269 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19746] An enzyme complex designated DICER COMPLEX, dices the GAM1269 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1269 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1269 RNA is designated SEQ ID:2918, and is provided hereinbelow with reference to the sequence listing part.

[19747] GAM1269 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1269 target RNA, herein designated GAM TARGET RNA. GAM1269 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19748] GAM1269 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1269 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1269

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1269 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1269 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19749] The complementary binding of GAM1269 RNA, herein designated GAM RNA, to target binding sites on GAM1269 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1269 target RNA, herein designated GAM TARGET RNA, into GAM1269 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[19750] It is appreciated that GAM1269 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1269 target genes. The mRNA of each one of this plurality of GAM1269 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1269 RNA, herein designated GAM RNA, and which when bound by GAM1269 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1269 target proteins.

[19751] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1269 gene, herein designated GAM GENE, on one or more GAM1269 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19752] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1269 correlate with, and may be deduced from, the identity of the target genes which GAM1269 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19753] Nucleotide sequences of the GAM1269 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1269 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1269 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1269 are further described hereinbelow with reference to Table Table1.

[19754] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1269 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19755] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1270 (GAM1270) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19756] GAM1270 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1270 was detected is described hereinabove with reference to Figs. 2-8.

[19757] GAM1270 gene, herein designated GAM GENE, and GAM1270 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19758] GAM1270 gene, herein designated GAM GENE, encodes a GAM1270 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1270 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1270 precursor RNA is designated SEQ ID:1243, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1243 is located at position 11437086 relative to contig NT_011362.7, on chromosome 20.

[19759] GAM1270 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19760] An enzyme complex designated DICER COMPLEX, dices the GAM1270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1270 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1270 RNA is designated SEQ ID:2919, and is provided hereinbelow with reference to the sequence listing part.

[19761] GAM1270 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1270 target RNA, herein designated GAM TARGET RNA. GAM1270 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19762] GAM1270 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1270 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1270 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1270 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1270 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19763] The complementary binding of GAM1270 RNA, herein designated GAM RNA, to target binding sites on GAM1270 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1270 target RNA, herein designated GAM TARGET RNA, into GAM1270 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19764] It is appreciated that GAM1270 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1270 target genes. The mRNA of each one of this plurality of GAM1270 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1270 RNA, herein designated GAM RNA, and which when bound by GAM1270 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1270 target proteins.

[19765] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1270 gene, herein designated GAM GENE, on one or more GAM1270 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19766] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1270 correlate with, and may be deduced from, the identity of the target genes which GAM1270 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19767] Nucleotide sequences of the GAM1270 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1270 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1270 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1270 are further described hereinbelow with reference to Table Table1.

[19768] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1270 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19769] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1271 (GAM1271) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19770] GAM1271 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1271 was detected is described hereinabove with reference to Figs. 2-8.

[19771] GAM1271 gene, herein designated GAM GENE, and GAM1271 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[19772] GAM1271 gene, herein designated GAM GENE, encodes a GAM1271 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1271 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1271 precursor RNA is designated SEQ ID:1244, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1244 is located at position 3434864 relative to contig NT_009714.13, on chromosome 12.

[19773] GAM1271 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98852, which mouse homolog is detected in mouse EST accession BG288438.1.

[19774] GAM1271 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19775] An enzyme complex designated DICER COMPLEX, dices the GAM1271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1271 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1271 RNA is designated SEQ ID:2920, and is provided hereinbelow with reference to the sequence listing part.

[19776] GAM1271 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1271 target RNA, herein designated GAM TARGET RNA. GAM1271 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[19777] GAM1271 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1271 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1271 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1271 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1271 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19778] The complementary binding of GAM1271 RNA, herein

designated GAM RNA, to target binding sites on GAM1271 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1271 target RNA, herein designated GAM TARGET RNA, into GAM1271 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19779] It is appreciated that GAM1271 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1271 target genes. The mRNA of each one of this plurality of GAM1271 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1271 RNA, herein designated GAM RNA, and which when bound by GAM1271 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1271 target proteins.

[19780] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1271 gene, herein designated GAM GENE, on one or more GAM1271 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19781] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1271 correlate with, and may be deduced from, the identity of the target genes which GAM1271 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19782] Nucleotide sequences of the GAM1271 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1271 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1271 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1271 are further described hereinbelow with reference to Table Table1.

[19783] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1271 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19784] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1272 (GAM1272) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19785] GAM1272 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1272 was detected is described hereinabove with reference to Figs. 2-8.

[19786] GAM1272 gene, herein designated GAM GENE, and GAM1272 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19787] GAM1272 gene, herein designated GAM GENE, encodes a GAM1272 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1272 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1272 precursor RNA is designated SEQ ID:1245, and is provided hereinbelow with reference to the sequence listing part.

[19788] GAM1272 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19789] An enzyme complex designated DICER COMPLEX, dices the GAM1272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1272 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1272 RNA is designated SEQ ID:2921, and is provided hereinbelow with reference to the sequence listing part.

[19790] GAM1272 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1272 target RNA, herein designated GAM TARGET RNA. GAM1272 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19791] GAM1272 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1272 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1272 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1272 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1272 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19792] The complementary binding of GAM1272 RNA, herein designated GAM RNA, to target binding sites on GAM1272 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1272 target RNA, herein designated GAM TARGET RNA, into GAM1272 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19793] It is appreciated that GAM1272 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1272 target genes. The mRNA of each one of this plurality of GAM1272 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1272 RNA,

herein designated GAM RNA, and which when bound by GAM1272 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1272 target proteins.

[19794] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1272 gene, herein designated GAM GENE, on one or more GAM1272 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19795] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1272 correlate with, and may be deduced from, the identity of the target genes which

GAM1272 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19796] Nucleotide sequences of the GAM1272 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1272 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1272 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1272 are further described hereinbelow with reference to Table Table1.

[19797] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1272 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19798] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1273 (GAM1273) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19799] GAM1273 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1273 was detected is described hereinabove with reference to Figs. 2-8.

[19800] GAM1273 gene, herein designated GAM GENE, and GAM1273 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19801] GAM1273 gene, herein designated GAM GENE, encodes a GAM1273 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1273 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1273 precursor RNA is designated SEQ ID:1246, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1246 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[19802] GAM1273 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19803] An enzyme complex designated DICER COMPLEX, dices the GAM1273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1273 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1273 RNA is designated SEQ ID:2922, and is provided hereinbelow with reference to the sequence listing part.

[19804] GAM1273 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1273 target RNA, herein designated GAM TARGET RNA. GAM1273 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19805] GAM1273 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1273 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1273 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1273 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1273 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19806] The complementary binding of GAM1273 RNA, herein designated GAM RNA, to target binding sites on GAM1273

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1273 target RNA, herein designated GAM TARGET RNA, into GAM1273 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19807] It is appreciated that GAM1273 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1273 target genes. The mRNA of each one of this plurality of GAM1273 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1273 RNA, herein designated GAM RNA, and which when bound by GAM1273 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1273 target proteins.

[19808] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1273 gene, herein designated GAM GENE, on one or more GAM1273 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19809] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1273 correlate with, and may be deduced from, the identity of the target genes which GAM1273 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19810] Nucleotide sequences of the GAM1273 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1273 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1273 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1273 are further described hereinbelow with reference to Table Table1.

[19811] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1273 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19812] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1274 (GAM1274) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19813] GAM1274 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1274 was detected is described hereinabove with reference to Figs. 2-8.

[19814] GAM1274 gene, herein designated GAM GENE, and GAM1274 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19815] GAM1274 gene, herein designated GAM GENE, encodes a GAM1274 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1274 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1274 precursor RNA is designated SEQ ID:1247, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1247 is located at position 2077051 relative to contig NT_023663.13, on chromosome 8.

[19816] GAM1274 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19817] An enzyme complex designated DICER COMPLEX, dices the GAM1274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1274 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1274 RNA is designated SEQ ID:2923, and is provided hereinbelow with reference to the sequence listing part.

[19818] GAM1274 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1274 target RNA, herein designated GAM TARGET RNA. GAM1274 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19819] GAM1274 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1274 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1274 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1274 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1274 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19820] The complementary binding of GAM1274 RNA, herein designated GAM RNA, to target binding sites on GAM1274 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1274 target RNA, herein designated GAM TARGET RNA, into GAM1274 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19821] It is appreciated that GAM1274 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1274 target genes. The mRNA of each one of this plurality of GAM1274 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1274 RNA, herein designated GAM RNA, and which when bound by GAM1274 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1274 target proteins.

[19822] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1274 gene, herein designated GAM GENE, on one or more GAM1274 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19823] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1274 correlate with, and may

be deduced from, the identity of the target genes which GAM1274 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19824] Nucleotide sequences of the GAM1274 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1274 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1274 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1274 are further described hereinbelow with reference to Table Table1.

[19825] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1274 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19826] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1275 (GAM1275) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19827] GAM1275 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1275 was detected is described hereinabove with reference to Figs. 2-8.

[19828] GAM1275 gene, herein designated GAM GENE, and GAM1275 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19829] GAM1275 gene, herein designated GAM GENE, encodes a GAM1275 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1275 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1275 precursor RNA is designated SEQ ID:1248, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1248 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[19830] GAM1275 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19831] An enzyme complex designated DICER COMPLEX, dices the GAM1275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1275 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1275 RNA is designated SEQ ID:2924, and is provided hereinbelow with reference to the sequence listing part.

[19832] GAM1275 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1275 target RNA, herein designated GAM TARGET RNA. GAM1275 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[19833] GAM1275 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1275 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1275 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1275 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1275 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19834] The complementary binding of GAM1275 RNA, herein

designated GAM RNA, to target binding sites on GAM1275 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1275 target RNA, herein designated GAM TARGET RNA, into GAM1275 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19835] It is appreciated that GAM1275 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1275 target genes. The mRNA of each one of this plurality of GAM1275 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1275 RNA, herein designated GAM RNA, and which when bound by GAM1275 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1275 target proteins.

[19836] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1275 gene, herein designated GAM GENE, on one or more GAM1275 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19837] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1275 correlate with, and may be deduced from, the identity of the target genes which GAM1275 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19838] Nucleotide sequences of the GAM1275 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1275 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1275 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1275 are further described hereinbelow with reference to Table Table1.

[19839] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1275 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19840] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1276 (GAM1276) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19841] GAM1276 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1276 was detected is described hereinabove with reference to Figs. 2-8.

[19842] GAM1276 gene, herein designated GAM GENE, and GAM1276 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19843] GAM1276 gene, herein designated GAM GENE, encodes a GAM1276 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1276 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1276 precursor RNA is designated SEQ ID:1249, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1249 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[19844] GAM1276 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19845] An enzyme complex designated DICER COMPLEX, dices the GAM1276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1276 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1276 RNA is designated SEQ ID:2925, and is provided hereinbelow with reference to the sequence listing part.

[19846] GAM1276 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1276 target RNA, herein designated GAM TARGET RNA. GAM1276 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19847] GAM1276 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1276 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1276 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1276 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1276 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19848] The complementary binding of GAM1276 RNA, herein designated GAM RNA, to target binding sites on GAM1276 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1276 target RNA, herein designated GAM TARGET RNA, into GAM1276 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19849] It is appreciated that GAM1276 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1276 target genes. The mRNA of each one of this plurality of GAM1276 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1276 RNA, herein designated GAM RNA, and which when bound by GAM1276 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1276 target proteins.

[19850] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1276 gene, herein designated GAM GENE, on one or more GAM1276 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19851] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1276 correlate with, and may be deduced from, the identity of the target genes which GAM1276 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19852] Nucleotide sequences of the GAM1276 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1276 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1276 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1276 are further described hereinbelow with reference to Table Table1.

[19853] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1276 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19854] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1277 (GAM1277) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19855] GAM1277 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1277 was detected is described hereinabove with reference to Figs. 2-8.

[19856] GAM1277 gene, herein designated GAM GENE, and GAM1277 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19857] GAM1277 gene, herein designated GAM GENE, encodes a GAM1277 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1277 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1277 precursor RNA is designated SEQ ID:1250, and is provided hereinbelow with reference to the sequence listing part.

[19858] GAM1277 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19859] An enzyme complex designated DICER COMPLEX, dices the GAM1277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1277 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1277 RNA is designated SEQ ID:2926, and is provided hereinbelow with reference to the sequence listing part.

[19860] GAM1277 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1277 target RNA, herein designated GAM TARGET RNA. GAM1277 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19861] GAM1277 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1277 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1277 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1277 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1277 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19862] The complementary binding of GAM1277 RNA, herein designated GAM RNA, to target binding sites on GAM1277

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1277 target RNA, herein designated GAM TARGET RNA, into GAM1277 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19863] It is appreciated that GAM1277 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1277 target genes. The mRNA of each one of this plurality of GAM1277 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1277 RNA, herein designated GAM RNA, and which when bound by GAM1277 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1277 target proteins.

[19864] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1277 gene, herein designated GAM GENE, on one or more GAM1277 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19865] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1277 correlate with, and may be deduced from, the identity of the target genes which GAM1277 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19866] Nucleotide sequences of the GAM1277 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1277 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1277 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1277 are further described hereinbelow with reference to Table Table1.

[19867] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1277 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19868] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1278 (GAM1278) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19869] GAM1278 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1278 was detected is described hereinabove with reference to Figs. 2-8.

[19870] GAM1278 gene, herein designated GAM GENE, and GAM1278 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19871] GAM1278 gene, herein designated GAM GENE, encodes a GAM1278 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1278 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1278 precursor RNA is designated SEQ ID:1251, and is provided hereinbelow with reference to the sequence listing part.

[19872] GAM1278 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19873] An enzyme complex designated DICER COMPLEX, dices the GAM1278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1278 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1278 RNA is designated SEQ ID:2927, and

is provided hereinbelow with reference to the sequence listing part.

[19874] GAM1278 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1278 target RNA, herein designated GAM TARGET RNA. GAM1278 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19875] GAM1278 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1278 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1278 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1278 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1278 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19876] The complementary binding of GAM1278 RNA, herein designated GAM RNA, to target binding sites on GAM1278 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1278 target RNA, herein designated GAM TARGET RNA, into GAM1278 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19877] It is appreciated that GAM1278 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1278 target genes. The mRNA of each one of this plurality of GAM1278 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1278 RNA, herein designated GAM RNA, and which when bound by

GAM1278 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1278 target proteins.

[19878] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1278 gene, herein designated GAM GENE, on one or more GAM1278 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19879] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1278 correlate with, and may be deduced from, the identity of the target genes which GAM1278 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[19880] Nucleotide sequences of the GAM1278 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1278 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1278 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1278 are further described hereinbelow with reference to Table Table1.

[19881] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1278 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19882] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1279 (GAM1279) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19883] GAM1279 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1279 was detected is described hereinabove

with reference to Figs. 2-8.

[19884] GAM1279 gene, herein designated GAM GENE, and GAM1279 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19885] GAM1279 gene, herein designated GAM GENE, encodes a GAM1279 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1279 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1279 precursor RNA is designated SEQ ID:1252, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1252 is located at position 3434852 relative to contig NT_009714.13, on chromosome 12.

[19886] GAM1279 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98633, which mouse homolog is detected in mouse EST accession BG288438.1.

[19887] GAM1279 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1279 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19888] An enzyme complex designated DICER COMPLEX, dices the GAM1279 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1279 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1279 RNA is designated SEQ ID:2928, and is provided hereinbelow with reference to the sequence listing part.

[19889] GAM1279 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1279 target RNA, herein designated GAM TARGET RNA. GAM1279 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19890] GAM1279 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1279 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1279 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1279 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1279 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19891] The complementary binding of GAM1279 RNA, herein designated GAM RNA, to target binding sites on GAM1279 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1279 target RNA, herein designated GAM TARGET RNA, into GAM1279 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19892] It is appreciated that GAM1279 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1279 target genes. The mRNA of each one of this plurality of GAM1279 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1279 RNA, herein designated GAM RNA, and which when bound by GAM1279 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1279 target proteins.

[19893] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1279 gene, herein designated GAM GENE, on one or more GAM1279 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19894] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1279 correlate with, and may be deduced from, the identity of the target genes which GAM1279 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19895] Nucleotide sequences of the GAM1279 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1279 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1279 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1279 are further described hereinbelow with reference to Table Table1.

[19896] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1279 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19897] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1280 (GAM1280) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19898] GAM1280 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1280 was detected is described hereinabove with reference to Figs. 2-8.

[19899] GAM1280 gene, herein designated GAM GENE, and GAM1280 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19900] GAM1280 gene, herein designated GAM GENE, encodes a GAM1280 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1280 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1280 precursor RNA is designated SEQ ID:1253, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1253 is located at position 11375650 relative to contig NT_011520.8, on chromosome 22.

[19901] GAM1280 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19902] An enzyme complex designated DICER COMPLEX, dices the GAM1280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1280 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1280 RNA is designated SEQ ID:2929, and is provided hereinbelow with reference to the sequence listing part.

[19903] GAM1280 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1280 target RNA, herein designated GAM TARGET RNA. GAM1280 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19904] GAM1280 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1280 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1280 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1280 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1280 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19905] The complementary binding of GAM1280 RNA, herein designated GAM RNA, to target binding sites on GAM1280 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1280 target RNA, herein designated GAM TARGET RNA, into GAM1280 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19906] It is appreciated that GAM1280 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1280 target genes. The mRNA of each one of this plurality of GAM1280 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1280 RNA, herein designated GAM RNA, and which when bound by GAM1280 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1280 target proteins.

[19907] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1280 gene, herein designated GAM GENE, on one or more GAM1280 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19908] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1280 correlate with, and may be deduced from, the identity of the target genes which GAM1280 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19909] Nucleotide sequences of the GAM1280 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1280 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1280 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1280 are further described hereinbelow with reference to Table Table1.

[19910] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1280 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19911] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1281 (GAM1281) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19912] GAM1281 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1281 was detected is described hereinabove with reference to Figs. 2-8.

[19913] GAM1281 gene, herein designated GAM GENE, and GAM1281 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19914] GAM1281 gene, herein designated GAM GENE, encodes a GAM1281 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1281 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1281 precursor RNA is designated SEQ ID:1254, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1254 is located at position 532839 relative to contig NT_009575.13, on chromosome 12.

[19915] GAM1281 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1281 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19916] An enzyme complex designated DICER COMPLEX, dices the GAM1281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1281 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1281 RNA is designated SEQ ID:2930, and is provided hereinbelow with reference to the sequence listing part.

[19917] GAM1281 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1281 target RNA, herein designated GAM TARGET

RNA. GAM1281 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19918] GAM1281 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1281 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1281 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1281 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1281 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19919] The complementary binding of GAM1281 RNA, herein designated GAM RNA, to target binding sites on GAM1281 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1281 target RNA, herein designated GAM TARGET RNA, into GAM1281 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19920] It is appreciated that GAM1281 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1281 target genes. The mRNA of each one of this plurality of GAM1281 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1281 RNA, herein designated GAM RNA, and which when bound by GAM1281 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1281 target proteins.

[19921] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1281 gene, herein designated GAM GENE, on one or more GAM1281 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19922] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1281 correlate with, and may be deduced from, the identity of the target genes which GAM1281 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19923] Nucleotide sequences of the GAM1281 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1281 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1281 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1281 are further described hereinbelow with reference to Table Table1.

[19924] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1281 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19925] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1282 (GAM1282) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19926] GAM1282 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1282 was detected is described hereinabove with reference to Figs. 2-8.

[19927] GAM1282 gene, herein designated GAM GENE, and GAM1282 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19928] GAM1282 gene, herein designated GAM GENE, encodes a

GAM1282 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1282 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1282 precursor RNA is designated SEQ ID:1255, and is provided hereinbelow with reference to the sequence listing part.

[19929] GAM1282 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19930] An enzyme complex designated DICER COMPLEX, dices the GAM1282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1282 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1282 RNA is designated SEQ ID:2931, and is provided hereinbelow with reference to the sequence listing part.

[19931] GAM1282 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1282 target RNA, herein designated GAM TARGET RNA. GAM1282 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19932] GAM1282 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1282 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1282 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1282 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1282 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19933] The complementary binding of GAM1282 RNA, herein designated GAM RNA, to target binding sites on GAM1282 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1282 target RNA, herein designated GAM TARGET RNA, into GAM1282 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19934] It is appreciated that GAM1282 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1282 target genes. The mRNA of each one of this plurality of GAM1282 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1282 RNA, herein designated GAM RNA, and which when bound by GAM1282 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1282 target proteins.

[19935] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1282 gene, herein designated GAM GENE, on one or more GAM1282 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[19936] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1282 correlate with, and may be deduced from, the identity of the target genes which GAM1282 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19937] Nucleotide sequences of the GAM1282 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1282 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1282 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1282 are further described hereinbelow with reference to Table Table1.

[19938] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1282 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19939] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1283 (GAM1283) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[19940] GAM1283 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1283 was detected is described hereinabove with reference to Figs. 2-8.

[19941] GAM1283 gene, herein designated GAM GENE, and GAM1283 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19942] GAM1283 gene, herein designated GAM GENE, encodes a GAM1283 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1283 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1283 precursor RNA is designated SEQ ID:1256, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1256 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[19943] GAM1283 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1283 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19944] An enzyme complex designated DICER COMPLEX, dices the GAM1283 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1283 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1283 RNA is designated SEQ ID:2932, and is provided hereinbelow with reference to the sequence listing part.

[19945] GAM1283 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1283 target RNA, herein designated GAM TARGET RNA. GAM1283 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19946] GAM1283 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1283 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1283 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1283 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1283 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19947] The complementary binding of GAM1283 RNA, herein designated GAM RNA, to target binding sites on GAM1283 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1283 target RNA, herein designated GAM TARGET RNA, into GAM1283 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19948] It is appreciated that GAM1283 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1283 target genes. The mRNA of each one of this plurality of GAM1283 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1283 RNA, herein designated GAM RNA, and which when bound by GAM1283 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1283 target proteins.

[19949] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1283 gene, herein designated GAM GENE, on one or more GAM1283 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19950] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1283 correlate with, and may be deduced from, the identity of the target genes which GAM1283 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19951] Nucleotide sequences of the GAM1283 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1283 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1283 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1283 are further described hereinbelow with reference to Table Table1.

[19952] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1283 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19953] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1284 (GAM1284) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19954] GAM1284 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1284 was detected is described hereinabove with reference to Figs. 2-8.

[19955] GAM1284 gene, herein designated GAM GENE, and GAM1284 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19956] GAM1284 gene, herein designated GAM GENE, encodes a GAM1284 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1284 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1284 precursor RNA is designated SEQ ID:1257, and is provided hereinbelow with reference to the sequence listing part.

[19957] GAM1284 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19958] An enzyme complex designated DICER COMPLEX, dices the GAM1284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1284 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1284 RNA is designated SEQ ID:2933, and is provided hereinbelow with reference to the sequence listing part.

[19959] GAM1284 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1284 target RNA, herein designated GAM TARGET RNA. GAM1284 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19960] GAM1284 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1284 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1284 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1284 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1284 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19961] The complementary binding of GAM1284 RNA, herein designated GAM RNA, to target binding sites on GAM1284 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1284 target RNA, herein designated GAM TARGET RNA, into GAM1284 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19962] It is appreciated that GAM1284 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1284 target genes. The mRNA of each one of this

plurality of GAM1284 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1284 RNA, herein designated GAM RNA, and which when bound by GAM1284 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1284 target proteins.

[19963] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1284 gene, herein designated GAM GENE, on one or more GAM1284 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19964] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1284 correlate with, and may be deduced from, the identity of the target genes which GAM1284 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19965] Nucleotide sequences of the GAM1284 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1284 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1284 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1284 are further described hereinbelow with reference to Table Table1.

[19966] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1284 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19967] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1285 (GAM1285) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[19968] GAM1285 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1285 was detected is described hereinabove with reference to Figs. 2-8.

[19969] GAM1285 gene, herein designated GAM GENE, and GAM1285 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19970] GAM1285 gene, herein designated GAM GENE, encodes a GAM1285 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1285 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1285 precursor RNA is designated SEQ ID:1258, and is provided hereinbelow with reference to the sequence listing part.

[19971] GAM1285 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19972] An enzyme complex designated DICER COMPLEX, dices the GAM1285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1285 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1285 RNA is designated SEQ ID:2934, and is provided hereinbelow with reference to the sequence listing part.

[19973] GAM1285 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1285 target RNA, herein designated GAM TARGET RNA. GAM1285 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[19974] GAM1285 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1285 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1285 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1285 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1285 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19975] The complementary binding of GAM1285 RNA, herein

designated GAM RNA, to target binding sites on GAM1285 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1285 target RNA, herein designated GAM TARGET RNA, into GAM1285 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19976] It is appreciated that GAM1285 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1285 target genes. The mRNA of each one of this plurality of GAM1285 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1285 RNA, herein designated GAM RNA, and which when bound by GAM1285 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1285 target proteins.

[19977] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1285 gene, herein designated GAM GENE, on one or more GAM1285 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19978] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1285 correlate with, and may be deduced from, the identity of the target genes which GAM1285 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19979] Nucleotide sequences of the GAM1285 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1285 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1285 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1285 are further described hereinbelow with reference to Table Table1.

[19980] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1285 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19981] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1286 (GAM1286) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19982] GAM1286 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1286 was detected is described hereinabove with reference to Figs. 2-8.

[19983] GAM1286 gene, herein designated GAM GENE, and GAM1286 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19984] GAM1286 gene, herein designated GAM GENE, encodes a GAM1286 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1286 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1286 precursor RNA is designated SEQ ID:1259, and is provided hereinbelow with reference to the sequence listing part.

[19985] GAM1286 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[19986] An enzyme complex designated DICER COMPLEX, dices the GAM1286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1286 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1286 RNA is designated SEQ ID:2935, and is provided hereinbelow with reference to the sequence listing part.

[19987] GAM1286 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1286 target RNA, herein designated GAM TARGET RNA. GAM1286 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[19988] GAM1286 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1286 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1286 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1286 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1286 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[19989] The complementary binding of GAM1286 RNA, herein designated GAM RNA, to target binding sites on GAM1286 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1286 target RNA, herein designated GAM TARGET RNA, into GAM1286 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[19990] It is appreciated that GAM1286 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1286 target genes. The mRNA of each one of this plurality of GAM1286 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1286 RNA,

herein designated GAM RNA, and which when bound by GAM1286 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1286 target proteins.

[19991] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1286 gene, herein designated GAM GENE, on one or more GAM1286 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[19992] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1286 correlate with, and may be deduced from, the identity of the target genes which

GAM1286 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[19993] Nucleotide sequences of the GAM1286 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1286 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1286 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1286 are further described hereinbelow with reference to Table Table1.

[19994] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1286 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[19995] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1287 (GAM1287) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[19996] GAM1287 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1287 was detected is described hereinabove with reference to Figs. 2-8.

[19997] GAM1287 gene, herein designated GAM GENE, and GAM1287 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[19998] GAM1287 gene, herein designated GAM GENE, encodes a GAM1287 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1287 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1287 precursor RNA is designated SEQ ID:1260, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1260 is located at position 7819273 relative to contig NT_023935.13, on chromosome 9.

[19999] GAM1287 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20000] An enzyme complex designated DICER COMPLEX, dices the GAM1287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1287 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1287 RNA is designated SEQ ID:2936, and is provided hereinbelow with reference to the sequence listing part.

[20001] GAM1287 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1287 target RNA, herein designated GAM TARGET RNA. GAM1287 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20002] GAM1287 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1287 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1287 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1287 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1287 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20003] The complementary binding of GAM1287 RNA, herein designated GAM RNA, to target binding sites on GAM1287

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1287 target RNA, herein designated GAM TARGET RNA, into GAM1287 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20004] It is appreciated that GAM1287 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1287 target genes. The mRNA of each one of this plurality of GAM1287 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1287 RNA, herein designated GAM RNA, and which when bound by GAM1287 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1287 target proteins.

[20005] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1287 gene, herein designated GAM GENE, on one or more GAM1287 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20006] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1287 correlate with, and may be deduced from, the identity of the target genes which GAM1287 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20007] Nucleotide sequences of the GAM1287 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1287 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1287 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1287 are further described hereinbelow with reference to Table Table1.

[20008] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1287 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20009] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1288 (GAM1288) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20010] GAM1288 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1288 was detected is described hereinabove with reference to Figs. 2-8.

[20011] GAM1288 gene, herein designated GAM GENE, and GAM1288 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20012] GAM1288 gene, herein designated GAM GENE, encodes a GAM1288 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1288 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1288 precursor RNA is designated SEQ ID:1261, and is provided hereinbelow with reference to the sequence listing part.

[20013] GAM1288 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20014] An enzyme complex designated DICER COMPLEX, dices the GAM1288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1288 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1288 RNA is designated SEQ ID:2937, and

is provided hereinbelow with reference to the sequence listing part.

[20015] GAM1288 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1288 target RNA, herein designated GAM TARGET RNA. GAM1288 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20016] GAM1288 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1288 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1288 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1288 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1288 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20017] The complementary binding of GAM1288 RNA, herein designated GAM RNA, to target binding sites on GAM1288 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1288 target RNA, herein designated GAM TARGET RNA, into GAM1288 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20018] It is appreciated that GAM1288 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1288 target genes. The mRNA of each one of this plurality of GAM1288 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1288 RNA, herein designated GAM RNA, and which when bound by

GAM1288 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1288 target proteins.

[20019] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1288 gene, herein designated GAM GENE, on one or more GAM1288 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20020] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1288 correlate with, and may be deduced from, the identity of the target genes which GAM1288 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[20021] Nucleotide sequences of the GAM1288 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1288 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1288 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1288 are further described hereinbelow with reference to Table Table1.

[20022] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1288 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20023] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1289 (GAM1289) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20024] GAM1289 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1289 was detected is described hereinabove

with reference to Figs. 2-8.

[20025] GAM1289 gene, herein designated GAM GENE, and GAM1289 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20026] GAM1289 gene, herein designated GAM GENE, encodes a GAM1289 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1289 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1289 precursor RNA is designated SEQ ID:1262, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1262 is located at position 6591242 relative to contig NT_011109.13, on chromosome 19.

[20027] GAM1289 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20028] An enzyme complex designated DICER COMPLEX, dices the GAM1289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1289 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1289 RNA is designated SEQ ID:2938, and is provided hereinbelow with reference to the sequence listing part.

[20029] GAM1289 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1289 target RNA, herein designated GAM TARGET RNA. GAM1289 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20030] GAM1289 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1289 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1289 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1289 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1289 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20031] The complementary binding of GAM1289 RNA, herein designated GAM RNA, to target binding sites on GAM1289 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1289 target RNA, herein designated GAM TARGET RNA, into GAM1289 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20032] It is appreciated that GAM1289 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1289 target genes. The mRNA of each one of this plurality of GAM1289 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1289 RNA, herein designated GAM RNA, and which when bound by GAM1289 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1289 target proteins.

[20033] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1289 gene, herein designated GAM GENE, on one or more GAM1289 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20034] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1289 correlate with, and may be deduced from, the identity of the target genes which GAM1289 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20035] Nucleotide sequences of the GAM1289 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1289 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1289 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1289 are further described hereinbelow with reference to Table Table1.

[20036] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1289 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20037] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1290 (GAM1290) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20038] GAM1290 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1290 was detected is described hereinabove with reference to Figs. 2-8.

[20039] GAM1290 gene, herein designated GAM GENE, and GAM1290 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20040] GAM1290 gene, herein designated GAM GENE, encodes a GAM1290 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1290 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1290 precursor RNA is

designated SEQ ID:1263, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1263 is located at position 6591254 relative to contig NT_011109.13, on chromosome 19.

[20041] GAM1290 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20042] An enzyme complex designated DICER COMPLEX, dices the GAM1290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1290 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1290 RNA is designated SEQ ID:2939, and is provided hereinbelow with reference to the sequence listing part.

[20043] GAM1290 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1290 target RNA, herein designated GAM TARGET RNA. GAM1290 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20044] GAM1290 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1290 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1290 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1290 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1290 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20045] The complementary binding of GAM1290 RNA, herein designated GAM RNA, to target binding sites on GAM1290 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1290 target RNA, herein designated GAM TARGET RNA, into GAM1290 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20046] It is appreciated that GAM1290 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1290 target genes. The mRNA of each one of this plurality of GAM1290 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1290 RNA,

herein designated GAM RNA, and which when bound by GAM1290 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1290 target proteins.

[20047] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1290 gene, herein designated GAM GENE, on one or more GAM1290 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20048] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1290 correlate with, and may be deduced from, the identity of the target genes which

GAM1290 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20049] Nucleotide sequences of the GAM1290 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1290 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1290 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1290 are further described hereinbelow with reference to Table Table1.

[20050] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1290 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20051] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1291 (GAM1291) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20052] GAM1291 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1291 was detected is described hereinabove with reference to Figs. 2-8.

[20053] GAM1291 gene, herein designated GAM GENE, and GAM1291 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20054] GAM1291 gene, herein designated GAM GENE, encodes a GAM1291 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1291 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1291 precursor RNA is designated SEQ ID:1264, and is provided hereinbelow with reference to the sequence listing part.

[20055] GAM1291 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[20056] An enzyme complex designated DICER COMPLEX, dices the GAM1291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1291 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1291 RNA is designated SEQ ID:2940, and is provided hereinbelow with reference to the sequence listing part.

[20057] GAM1291 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1291 target RNA, herein designated GAM TARGET RNA. GAM1291 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20058] GAM1291 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1291 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1291 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1291 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1291 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20059] The complementary binding of GAM1291 RNA, herein designated GAM RNA, to target binding sites on GAM1291 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1291 target RNA, herein designated GAM TARGET RNA, into GAM1291 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20060] It is appreciated that GAM1291 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1291 target genes. The mRNA of each one of this plurality of GAM1291 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1291 RNA, herein designated GAM RNA, and which when bound by GAM1291 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1291 target proteins.

[20061] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1291 gene, herein designated GAM GENE, on one or more GAM1291 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20062] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1291 correlate with, and may be deduced from, the identity of the target genes which GAM1291 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20063] Nucleotide sequences of the GAM1291 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1291 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1291 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1291 are further described hereinbelow with reference to Table Table1.

[20064] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1291 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20065] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1292 (GAM1292) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20066] GAM1292 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1292 was detected is described hereinabove with reference to Figs. 2-8.

[20067] GAM1292 gene, herein designated GAM GENE, and GAM1292 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20068] GAM1292 gene, herein designated GAM GENE, encodes a GAM1292 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1292 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1292 precursor RNA is designated SEQ ID:1265, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1265 is located at position 2840909 relative to contig NT_004734.13, on chromosome 1.

[20069] GAM1292 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20070] An enzyme complex designated DICER COMPLEX, dices the GAM1292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1292 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1292 RNA is designated SEQ ID:2941, and

is provided hereinbelow with reference to the sequence listing part.

[20071] GAM1292 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1292 target RNA, herein designated GAM TARGET RNA. GAM1292 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20072] GAM1292 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1292 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1292 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1292 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1292 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20073] The complementary binding of GAM1292 RNA, herein designated GAM RNA, to target binding sites on GAM1292 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1292 target RNA, herein designated GAM TARGET RNA, into GAM1292 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20074] It is appreciated that GAM1292 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1292 target genes. The mRNA of each one of this plurality of GAM1292 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1292 RNA, herein designated GAM RNA, and which when bound by

GAM1292 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1292 target proteins.

[20075] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1292 gene, herein designated GAM GENE, on one or more GAM1292 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20076] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1292 correlate with, and may be deduced from, the identity of the target genes which GAM1292 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[20077] Nucleotide sequences of the GAM1292 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1292 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1292 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1292 are further described hereinbelow with reference to Table Table1.

[20078] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1292 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20079] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1293 (GAM1293) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20080] GAM1293 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1293 was detected is described hereinabove

with reference to Figs. 2-8.

[20081] GAM1293 gene, herein designated GAM GENE, and GAM1293 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20082] GAM1293 gene, herein designated GAM GENE, encodes a GAM1293 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1293 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1293 precursor RNA is designated SEQ ID:1266, and is provided hereinbelow with reference to the sequence listing part.

[20083] GAM1293 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20084] An enzyme complex designated DICER COMPLEX, dices the GAM1293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1293 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1293 RNA is designated SEQ ID:2942, and is provided hereinbelow with reference to the sequence listing part.

[20085] GAM1293 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1293 target RNA, herein designated GAM TARGET RNA. GAM1293 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20086] GAM1293 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1293 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1293 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1293 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1293 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20087] The complementary binding of GAM1293 RNA, herein designated GAM RNA, to target binding sites on GAM1293 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1293 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1293 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20088] It is appreciated that GAM1293 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1293 target genes. The mRNA of each one of this plurality of GAM1293 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1293 RNA, herein designated GAM RNA, and which when bound by GAM1293 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1293 target proteins.

[20089] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1293 gene, herein designated GAM GENE, on one or more GAM1293 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20090] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1293 correlate with, and may be deduced from, the identity of the target genes which GAM1293 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20091] Nucleotide sequences of the GAM1293 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1293 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1293 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1293 are further described hereinbelow with reference to Table Table1.

[20092] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1293 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[20093] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1294 (GAM1294) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20094] GAM1294 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1294 was detected is described hereinabove with reference to Figs. 2-8.

[20095] GAM1294 gene, herein designated GAM GENE, and GAM1294 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20096] GAM1294 gene, herein designated GAM GENE, encodes a GAM1294 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1294 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1294 precursor RNA is designated SEQ ID:1267, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1267 is located at position 4851355 relative to contig NT_022517.13, on chromosome 3.

[20097] GAM1294 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20098] An enzyme complex designated DICER COMPLEX, dices the GAM1294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1294 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1294 RNA is designated SEQ ID:2943, and is provided hereinbelow with reference to the sequence

listing part.

[20099] GAM1294 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1294 target RNA, herein designated GAM TARGET RNA. GAM1294 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20100] GAM1294 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1294 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1294 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1294 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1294 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20101] The complementary binding of GAM1294 RNA, herein designated GAM RNA, to target binding sites on GAM1294 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1294 target RNA, herein designated GAM TARGET RNA, into GAM1294 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20102] It is appreciated that GAM1294 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1294 target genes. The mRNA of each one of this plurality of GAM1294 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1294 RNA, herein designated GAM RNA, and which when bound by GAM1294 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1294 target proteins.

[20103] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1294 gene, herein designated GAM GENE, on one or more GAM1294 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20104] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1294 correlate with, and may be deduced from, the identity of the target genes which GAM1294 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20105] Nucleotide sequences of the GAM1294 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1294 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1294 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1294 are further described hereinbelow with reference to Table Table1.

[20106] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1294 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20107] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1295 (GAM1295) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20108] GAM1295 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1295 was detected is described hereinabove with reference to Figs. 2-8.

[20109] GAM1295 gene, herein designated GAM GENE, and GAM1295 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20110] GAM1295 gene, herein designated GAM GENE, encodes a GAM1295 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1295 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1295 precursor RNA is designated SEQ ID:1268, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1268 is located at position 97146 relative to contig NT_031818.6, on chromosome 8.

[20111] GAM1295 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[20112] SEQ ID:99166 detected in mouse EST Accession AI607221.1.

[20113] SEQ ID:99167 detected in mouse EST Accession BF383680.1.

[20114] SEQ ID:99168 detected in mouse EST Accession AA611163.1.

[20115] SEQ ID:99169 detected in mouse EST Accession BG694663.1.

[20116] SEQ ID:99170 detected in mouse EST Accession BI100878.1.

[20117] SEQ ID:99171 detected in mouse EST Accession AA162040.1.

[20118] SEQ ID:99172 detected in mouse EST Accession AI196919.1.

[20119] SEQ ID:99173 detected in mouse EST Accession BI329737.1.

[20120] GAM1295 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20121] An enzyme complex designated DICER COMPLEX, dices

the GAM1295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1295 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1295 RNA is designated SEQ ID:2944, and is provided hereinbelow with reference to the sequence listing part.

[20122] GAM1295 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1295 target RNA, herein designated GAM TARGET RNA. GAM1295 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20123] GAM1295 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1295 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1295 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1295 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1295 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20124] The complementary binding of GAM1295 RNA, herein designated GAM RNA, to target binding sites on GAM1295 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1295 target RNA, herein designated GAM TARGET RNA, into GAM1295 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20125] It is appreciated that GAM1295 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1295 target genes. The mRNA of each one of this plurality of GAM1295 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1295 RNA, herein designated GAM RNA, and which when bound by GAM1295 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1295 target proteins.

[20126] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1295 gene, herein designated GAM GENE, on one or more GAM1295 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20127] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1295 correlate with, and may be deduced from, the identity of the target genes which GAM1295 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20128] Nucleotide sequences of the GAM1295 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1295 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1295 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1295 are further described hereinbelow with reference to Table Table1.

[20129] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1295 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20130] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1296 (GAM1296) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20131] GAM1296 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1296 was detected is described hereinabove with reference to Figs. 2-8.

[20132] GAM1296 gene, herein designated GAM GENE, and GAM1296 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20133] GAM1296 gene, herein designated GAM GENE, encodes a GAM1296 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1296 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1296 precursor RNA is designated SEQ ID:1269, and is provided hereinbelow with reference to the sequence listing part.

[20134] GAM1296 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20135] An enzyme complex designated DICER COMPLEX, dices the GAM1296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1296 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1296 RNA is designated SEQ ID:2945, and is provided hereinbelow with reference to the sequence listing part.

[20136] GAM1296 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1296 target RNA, herein designated GAM TARGET RNA. GAM1296 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20137] GAM1296 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1296 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1296 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1296 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1296 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20138] The complementary binding of GAM1296 RNA, herein designated GAM RNA, to target binding sites on GAM1296 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1296 target RNA, herein designated GAM TARGET RNA, into GAM1296 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20139] It is appreciated that GAM1296 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1296 target genes. The mRNA of each one of this plurality of GAM1296 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1296 RNA, herein designated GAM RNA, and which when bound by GAM1296 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1296 target proteins.

[20140] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1296 gene, herein designated GAM GENE, on one or more GAM1296 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20141] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1296 correlate with, and may be deduced from, the identity of the target genes which GAM1296 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20142] Nucleotide sequences of the GAM1296 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1296 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1296 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1296 are further described hereinbelow with reference to Table Table1.

[20143] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1296 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20144] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1297 (GAM1297) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20145] GAM1297 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1297 was detected is described hereinabove with reference to Figs. 2-8.

[20146] GAM1297 gene, herein designated GAM GENE, and GAM1297 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20147] GAM1297 gene, herein designated GAM GENE, encodes a GAM1297 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1297 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1297 precursor RNA is designated SEQ ID:1270, and is provided hereinbelow with reference to the sequence listing part.

[20148] GAM1297 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20149] An enzyme complex designated DICER COMPLEX, dices the GAM1297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1297 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1297 RNA is designated SEQ ID:2946, and is provided hereinbelow with reference to the sequence listing part.

[20150] GAM1297 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1297 target RNA, herein designated GAM TARGET RNA. GAM1297 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20151] GAM1297 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1297 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1297 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1297 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1297 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20152] The complementary binding of GAM1297 RNA, herein designated GAM RNA, to target binding sites on GAM1297 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1297 target RNA, herein designated GAM TARGET RNA, into GAM1297 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20153] It is appreciated that GAM1297 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1297 target genes. The mRNA of each one of this plurality of GAM1297 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1297 RNA, herein designated GAM RNA, and which when bound by GAM1297 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1297 target proteins.

[20154] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1297 gene, herein designated GAM GENE, on one or more GAM1297 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20155] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1297 correlate with, and may be deduced from, the identity of the target genes which GAM1297 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20156] Nucleotide sequences of the GAM1297 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1297 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1297 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1297 are further described hereinbelow with reference to Table Table1.

[20157] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1297 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20158] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1298 (GAM1298) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20159] GAM1298 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1298 was detected is described hereinabove with reference to Figs. 2-8.

[20160] GAM1298 gene, herein designated GAM GENE, and GAM1298 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20161] GAM1298 gene, herein designated GAM GENE, encodes a GAM1298 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1298 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1298 precursor RNA is designated SEQ ID:1271, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1271 is located at position 2349693 relative to contig NT_021907.13, on chromosome 1.

[20162] GAM1298 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1298 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20163] An enzyme complex designated DICER COMPLEX, dices the GAM1298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1298 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1298 RNA is designated SEQ ID:2947, and is provided hereinbelow with reference to the sequence listing part.

[20164] GAM1298 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1298 target RNA, herein designated GAM TARGET

RNA. GAM1298 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20165] GAM1298 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1298 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1298 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1298 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1298 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20166] The complementary binding of GAM1298 RNA, herein designated GAM RNA, to target binding sites on GAM1298 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1298 target RNA, herein designated GAM TARGET RNA, into GAM1298 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20167] It is appreciated that GAM1298 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1298 target genes. The mRNA of each one of this plurality of GAM1298 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1298 RNA, herein designated GAM RNA, and which when bound by GAM1298 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1298 target proteins.

[20168] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1298 gene, herein designated GAM GENE, on one or more GAM1298 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20169] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1298 correlate with, and may be deduced from, the identity of the target genes which GAM1298 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20170] Nucleotide sequences of the GAM1298 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1298 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1298 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1298 are further described hereinbelow with reference to Table Table1.

[20171] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1298 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20172] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1299 (GAM1299) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20173] GAM1299 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1299 was detected is described hereinabove with reference to Figs. 2-8.

[20174] GAM1299 gene, herein designated GAM GENE, and GAM1299 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20175] GAM1299 gene, herein designated GAM GENE, encodes a

GAM1299 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1299 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1299 precursor RNA is designated SEQ ID:1272, and is provided hereinbelow with reference to the sequence listing part.

[20176] GAM1299 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20177] An enzyme complex designated DICER COMPLEX, dices the GAM1299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1299 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1299 RNA is designated SEQ ID:2948, and is provided hereinbelow with reference to the sequence listing part.

[20178] GAM1299 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1299 target RNA, herein designated GAM TARGET RNA. GAM1299 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20179] GAM1299 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1299 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1299 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1299 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1299 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20180] The complementary binding of GAM1299 RNA, herein designated GAM RNA, to target binding sites on GAM1299 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1299 target RNA, herein designated GAM TARGET RNA, into GAM1299 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20181] It is appreciated that GAM1299 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1299 target genes. The mRNA of each one of this plurality of GAM1299 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1299 RNA, herein designated GAM RNA, and which when bound by GAM1299 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1299 target proteins.

[20182] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1299 gene, herein designated GAM GENE, on one or more GAM1299 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[20183] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1299 correlate with, and may be deduced from, the identity of the target genes which GAM1299 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20184] Nucleotide sequences of the GAM1299 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1299 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1299 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1299 are further described hereinbelow with reference to Table Table1.

[20185] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1299 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20186] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1300 (GAM1300) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[20187] GAM1300 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1300 was detected is described hereinabove with reference to Figs. 2-8.

[20188] GAM1300 gene, herein designated GAM GENE, and GAM1300 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20189] GAM1300 gene, herein designated GAM GENE, encodes a GAM1300 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1300 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1300 precursor RNA is designated SEQ ID:1273, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1273 is located at position 8271493 relative to contig NT_011109.13, on chromosome 19.

[20190] GAM1300 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1300 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20191] An enzyme complex designated DICER COMPLEX, dices the GAM1300 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1300 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1300 RNA is designated SEQ ID:2949, and is provided hereinbelow with reference to the sequence listing part.

[20192] GAM1300 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1300 target RNA, herein designated GAM TARGET RNA. GAM1300 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20193] GAM1300 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1300 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1300 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1300 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1300 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20194] The complementary binding of GAM1300 RNA, herein designated GAM RNA, to target binding sites on GAM1300 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1300 target RNA, herein designated GAM TARGET RNA, into GAM1300 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20195] It is appreciated that GAM1300 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1300 target genes. The mRNA of each one of this plurality of GAM1300 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1300 RNA, herein designated GAM RNA, and which when bound by GAM1300 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1300 target proteins.

[20196] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1300 gene, herein designated GAM GENE, on one or more GAM1300 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20197] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1300 correlate with, and may be deduced from, the identity of the target genes which GAM1300 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20198] Nucleotide sequences of the GAM1300 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1300 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1300 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1300 are further described hereinbelow with reference to Table Table1.

[20199] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1300 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20200] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1301 (GAM1301) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20201] GAM1301 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1301 was detected is described hereinabove with reference to Figs. 2-8.

[20202] GAM1301 gene, herein designated GAM GENE, and GAM1301 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20203] GAM1301 gene, herein designated GAM GENE, encodes a GAM1301 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1301 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1301 precursor RNA is designated SEQ ID:1274, and is provided hereinbelow with reference to the sequence listing part.

[20204] GAM1301 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20205] An enzyme complex designated DICER COMPLEX, dices the GAM1301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1301 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1301 RNA is designated SEQ ID:2950, and is provided hereinbelow with reference to the sequence listing part.

[20206] GAM1301 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1301 target RNA, herein designated GAM TARGET RNA. GAM1301 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20207] GAM1301 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1301 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1301 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1301 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1301 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20208] The complementary binding of GAM1301 RNA, herein designated GAM RNA, to target binding sites on GAM1301 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1301 target RNA, herein designated GAM TARGET RNA, into GAM1301 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20209] It is appreciated that GAM1301 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1301 target genes. The mRNA of each one of this

plurality of GAM1301 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1301 RNA, herein designated GAM RNA, and which when bound by GAM1301 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1301 target proteins.

[20210] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1301 gene, herein designated GAM GENE, on one or more GAM1301 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20211] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1301 correlate with, and may be deduced from, the identity of the target genes which GAM1301 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20212] Nucleotide sequences of the GAM1301 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1301 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1301 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1301 are further described hereinbelow with reference to Table Table1.

[20213] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1301 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20214] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1302 (GAM1302) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[20215] GAM1302 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1302 was detected is described hereinabove with reference to Figs. 2-8.

[20216] GAM1302 gene, herein designated GAM GENE, and GAM1302 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20217] GAM1302 gene, herein designated GAM GENE, encodes a GAM1302 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1302 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1302 precursor RNA is designated SEQ ID:1275, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1275 is located at position 25819164 relative to contig NT_007933.10, on chromosome 7.

[20218] GAM1302 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20219] An enzyme complex designated DICER COMPLEX, dices the GAM1302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1302 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1302 RNA is designated SEQ ID:2951, and is provided hereinbelow with reference to the sequence listing part.

[20220] GAM1302 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1302 target RNA, herein designated GAM TARGET RNA. GAM1302 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20221] GAM1302 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1302 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1302 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1302 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1302 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[20222] The complementary binding of GAM1302 RNA, herein designated GAM RNA, to target binding sites on GAM1302 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1302 target RNA, herein designated GAM TARGET RNA, into GAM1302 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20223] It is appreciated that GAM1302 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1302 target genes. The mRNA of each one of this plurality of GAM1302 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1302 RNA, herein designated GAM RNA, and which when bound by GAM1302 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1302 target proteins.

[20224] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1302 gene, herein designated GAM GENE, on one or

more GAM1302 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20225] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1302 correlate with, and may be deduced from, the identity of the target genes which GAM1302 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20226] Nucleotide sequences of the GAM1302 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1302 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1302 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1302 are further de-

scribed hereinbelow with reference to Table Table1.

[20227] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1302 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20228] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1303 (GAM1303) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20229] GAM1303 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1303 was detected is described hereinabove with reference to Figs. 2-8.

[20230] GAM1303 gene, herein designated GAM GENE, and GAM1303 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20231] GAM1303 gene, herein designated GAM GENE, encodes a GAM1303 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1303 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1303 precursor RNA is designated SEQ ID:1276, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1276 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[20232] GAM1303 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20233] An enzyme complex designated DICER COMPLEX, dices the GAM1303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1303 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1303 RNA is designated SEQ ID:2952, and is provided hereinbelow with reference to the sequence listing part.

[20234] GAM1303 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1303 target RNA, herein designated GAM TARGET RNA. GAM1303 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20235] GAM1303 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1303 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1303 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1303 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1303 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20236] The complementary binding of GAM1303 RNA, herein designated GAM RNA, to target binding sites on GAM1303 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1303 target RNA, herein designated GAM TARGET RNA, into GAM1303 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20237] It is appreciated that GAM1303 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1303 target genes. The mRNA of each one of this plurality of GAM1303 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1303 RNA, herein designated GAM RNA, and which when bound by GAM1303 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1303 target proteins.

[20238] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1303 gene, herein designated GAM GENE, on one or more GAM1303 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[20239] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1303 correlate with, and may be deduced from, the identity of the target genes which GAM1303 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20240] Nucleotide sequences of the GAM1303 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1303 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1303 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1303 are further described hereinbelow with reference to Table Table1.

[20241] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1303 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20242] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1304 (GAM1304) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[20243] GAM1304 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1304 was detected is described hereinabove with reference to Figs. 2-8.

[20244] GAM1304 gene, herein designated GAM GENE, and GAM1304 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20245] GAM1304 gene, herein designated GAM GENE, encodes a GAM1304 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1304 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1304 precursor RNA is designated SEQ ID:1277, and is provided hereinbelow with reference to the sequence listing part.

[20246] GAM1304 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20247] An enzyme complex designated DICER COMPLEX, dices the GAM1304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1304 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1304 RNA is designated SEQ ID:2953, and is provided hereinbelow with reference to the sequence listing part.

[20248] GAM1304 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1304 target RNA, herein designated GAM TARGET RNA. GAM1304 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20249] GAM1304 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1304 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1304 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1304 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1304 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20250] The complementary binding of GAM1304 RNA, herein designated GAM RNA, to target binding sites on GAM1304 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1304 target RNA, herein designated GAM TARGET RNA, into GAM1304 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20251] It is appreciated that GAM1304 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1304 target genes. The mRNA of each one of this plurality of GAM1304 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1304 RNA, herein designated GAM RNA, and which when bound by GAM1304 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1304 target proteins.

[20252] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1304 gene, herein designated GAM GENE, on one or more GAM1304 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20253] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1304 correlate with, and may be deduced from, the identity of the target genes which GAM1304 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20254] Nucleotide sequences of the GAM1304 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1304 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1304 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1304 are further described hereinbelow with reference to Table Table1.

[20255] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1304 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20256] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1305 (GAM1305) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20257] GAM1305 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1305 was detected is described hereinabove with reference to Figs. 2-8.

[20258] GAM1305 gene, herein designated GAM GENE, and GAM1305 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20259] GAM1305 gene, herein designated GAM GENE, encodes a GAM1305 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1305 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1305 precursor RNA is designated SEQ ID:1278, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1278 is located at position 439985 relative to contig NT_009759.13, on chromosome 12.

[20260] GAM1305 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20261] An enzyme complex designated DICER COMPLEX, dices the GAM1305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1305 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1305 RNA is designated SEQ ID:2954, and is provided hereinbelow with reference to the sequence listing part.

[20262] GAM1305 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1305 target RNA, herein designated GAM TARGET RNA. GAM1305 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20263] GAM1305 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1305 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1305 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1305 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1305 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20264] The complementary binding of GAM1305 RNA, herein designated GAM RNA, to target binding sites on GAM1305 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1305 target RNA, herein designated GAM TARGET RNA, into GAM1305 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20265] It is appreciated that GAM1305 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1305 target genes. The mRNA of each one of this

plurality of GAM1305 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1305 RNA, herein designated GAM RNA, and which when bound by GAM1305 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1305 target proteins.

[20266] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1305 gene, herein designated GAM GENE, on one or more GAM1305 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20267] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1305 correlate with, and may be deduced from, the identity of the target genes which GAM1305 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20268] Nucleotide sequences of the GAM1305 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1305 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1305 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1305 are further described hereinbelow with reference to Table Table1.

[20269] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1305 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20270] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1306 (GAM1306) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[20271] GAM1306 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1306 was detected is described hereinabove with reference to Figs. 2-8.

[20272] GAM1306 gene, herein designated GAM GENE, and GAM1306 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20273] GAM1306 gene, herein designated GAM GENE, encodes a GAM1306 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1306 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1306 precursor RNA is designated SEQ ID:1279, and is provided hereinbelow with reference to the sequence listing part.

[20274] GAM1306 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20275] An enzyme complex designated DICER COMPLEX, dices the GAM1306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1306 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1306 RNA is designated SEQ ID:2955, and is provided hereinbelow with reference to the sequence listing part.

[20276] GAM1306 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1306 target RNA, herein designated GAM TARGET RNA. GAM1306 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[20277] GAM1306 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1306 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1306 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1306 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1306 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20278] The complementary binding of GAM1306 RNA, herein

designated GAM RNA, to target binding sites on GAM1306 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1306 target RNA, herein designated GAM TARGET RNA, into GAM1306 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20279] It is appreciated that GAM1306 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1306 target genes. The mRNA of each one of this plurality of GAM1306 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1306 RNA, herein designated GAM RNA, and which when bound by GAM1306 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1306 target proteins.

[20280] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1306 gene, herein designated GAM GENE, on one or more GAM1306 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20281] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1306 correlate with, and may be deduced from, the identity of the target genes which GAM1306 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20282] Nucleotide sequences of the GAM1306 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1306 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1306 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1306 are further described hereinbelow with reference to Table Table1.

[20283] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1306 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20284] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1307 (GAM1307) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20285] GAM1307 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1307 was detected is described hereinabove with reference to Figs. 2-8.

[20286] GAM1307 gene, herein designated GAM GENE, and GAM1307 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20287] GAM1307 gene, herein designated GAM GENE, encodes a GAM1307 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1307 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1307 precursor RNA is designated SEQ ID:1280, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1280 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[20288] GAM1307 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20289] An enzyme complex designated DICER COMPLEX, dices the GAM1307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1307 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1307 RNA is designated SEQ ID:2956, and is provided hereinbelow with reference to the sequence listing part.

[20290] GAM1307 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1307 target RNA, herein designated GAM TARGET RNA. GAM1307 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20291] GAM1307 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1307 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1307 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1307 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1307 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20292] The complementary binding of GAM1307 RNA, herein designated GAM RNA, to target binding sites on GAM1307 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1307 target RNA, herein designated GAM TARGET RNA, into GAM1307 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20293] It is appreciated that GAM1307 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1307 target genes. The mRNA of each one of this plurality of GAM1307 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1307 RNA, herein designated GAM RNA, and which when bound by GAM1307 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1307 target proteins.

[20294] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1307 gene, herein designated GAM GENE, on one or more GAM1307 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20295] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1307 correlate with, and may be deduced from, the identity of the target genes which GAM1307 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20296] Nucleotide sequences of the GAM1307 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1307 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1307 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1307 are further described hereinbelow with reference to Table Table1.

[20297] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1307 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20298] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1308 (GAM1308) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20299] GAM1308 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1308 was detected is described hereinabove with reference to Figs. 2-8.

[20300] GAM1308 gene, herein designated GAM GENE, and GAM1308 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20301] GAM1308 gene, herein designated GAM GENE, encodes a GAM1308 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1308 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1308 precursor RNA is designated SEQ ID:1281, and is provided hereinbelow with reference to the sequence listing part.

[20302] GAM1308 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20303] An enzyme complex designated DICER COMPLEX, dices the GAM1308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1308 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1308 RNA is designated SEQ ID:2957, and is provided hereinbelow with reference to the sequence listing part.

[20304] GAM1308 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1308 target RNA, herein designated GAM TARGET RNA. GAM1308 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20305] GAM1308 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1308 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1308 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1308 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1308 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20306] The complementary binding of GAM1308 RNA, herein designated GAM RNA, to target binding sites on GAM1308

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1308 target RNA, herein designated GAM TARGET RNA, into GAM1308 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20307] It is appreciated that GAM1308 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1308 target genes. The mRNA of each one of this plurality of GAM1308 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1308 RNA, herein designated GAM RNA, and which when bound by GAM1308 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1308 target proteins.

[20308] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1308 gene, herein designated GAM GENE, on one or more GAM1308 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20309] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1308 correlate with, and may be deduced from, the identity of the target genes which GAM1308 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20310] Nucleotide sequences of the GAM1308 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1308 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1308 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1308 are further described hereinbelow with reference to Table Table1.

[20311] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1308 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20312] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1309 (GAM1309) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20313] GAM1309 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1309 was detected is described hereinabove with reference to Figs. 2-8.

[20314] GAM1309 gene, herein designated GAM GENE, and GAM1309 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20315] GAM1309 gene, herein designated GAM GENE, encodes a GAM1309 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1309 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1309 precursor RNA is designated SEQ ID:1282, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1282 is located at position 280464 relative to contig NT_007758.8, on chromosome 7.

[20316] GAM1309 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20317] An enzyme complex designated DICER COMPLEX, dices the GAM1309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1309 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1309 RNA is designated SEQ ID:2958, and is provided hereinbelow with reference to the sequence listing part.

[20318] GAM1309 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1309 target RNA, herein designated GAM TARGET RNA. GAM1309 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20319] GAM1309 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1309 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1309 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1309 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1309 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20320] The complementary binding of GAM1309 RNA, herein designated GAM RNA, to target binding sites on GAM1309 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1309 target RNA, herein designated GAM TARGET RNA, into GAM1309 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20321] It is appreciated that GAM1309 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1309 target genes. The mRNA of each one of this plurality of GAM1309 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1309 RNA, herein designated GAM RNA, and which when bound by GAM1309 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1309 target proteins.

[20322] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1309 gene, herein designated GAM GENE, on one or more GAM1309 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20323] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1309 correlate with, and may

be deduced from, the identity of the target genes which GAM1309 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20324] Nucleotide sequences of the GAM1309 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1309 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1309 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1309 are further described hereinbelow with reference to Table Table1.

[20325] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1309 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20326] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1310 (GAM1310) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20327] GAM1310 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1310 was detected is described hereinabove with reference to Figs. 2-8.

[20328] GAM1310 gene, herein designated GAM GENE, and GAM1310 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20329] GAM1310 gene, herein designated GAM GENE, encodes a GAM1310 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1310 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1310 precursor RNA is designated SEQ ID:1283, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1283 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[20330] GAM1310 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20331] An enzyme complex designated DICER COMPLEX, dices the GAM1310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1310 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1310 RNA is designated SEQ ID:2959, and is provided hereinbelow with reference to the sequence listing part.

[20332] GAM1310 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1310 target RNA, herein designated GAM TARGET RNA. GAM1310 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[20333] GAM1310 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1310 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1310 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1310 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1310 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20334] The complementary binding of GAM1310 RNA, herein

designated GAM RNA, to target binding sites on GAM1310 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1310 target RNA, herein designated GAM TARGET RNA, into GAM1310 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20335] It is appreciated that GAM1310 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1310 target genes. The mRNA of each one of this plurality of GAM1310 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1310 RNA, herein designated GAM RNA, and which when bound by GAM1310 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1310 target proteins.

[20336] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1310 gene, herein designated GAM GENE, on one or more GAM1310 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20337] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1310 correlate with, and may be deduced from, the identity of the target genes which GAM1310 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20338] Nucleotide sequences of the GAM1310 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1310 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1310 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1310 are further described hereinbelow with reference to Table Table1.

[20339] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1310 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20340] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1311 (GAM1311) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20341] GAM1311 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1311 was detected is described hereinabove with reference to Figs. 2-8.

[20342] GAM1311 gene, herein designated GAM GENE, and GAM1311 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20343] GAM1311 gene, herein designated GAM GENE, encodes a GAM1311 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1311 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1311 precursor RNA is designated SEQ ID:1284, and is provided hereinbelow with reference to the sequence listing part.

[20344] GAM1311 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20345] An enzyme complex designated DICER COMPLEX, dices the GAM1311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1311 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1311 RNA is designated SEQ ID:2960, and is provided hereinbelow with reference to the sequence listing part.

[20346] GAM1311 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1311 target RNA, herein designated GAM TARGET RNA. GAM1311 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20347] GAM1311 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1311 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1311 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1311 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1311 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20348] The complementary binding of GAM1311 RNA, herein designated GAM RNA, to target binding sites on GAM1311 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1311 target RNA, herein designated GAM TARGET RNA, into GAM1311 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20349] It is appreciated that GAM1311 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1311 target genes. The mRNA of each one of this plurality of GAM1311 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1311 RNA,

herein designated GAM RNA, and which when bound by GAM1311 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1311 target proteins.

[20350] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1311 gene, herein designated GAM GENE, on one or more GAM1311 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20351] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1311 correlate with, and may be deduced from, the identity of the target genes which

GAM1311 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20352] Nucleotide sequences of the GAM1311 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1311 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1311 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1311 are further described hereinbelow with reference to Table Table1.

[20353] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1311 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20354] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1312 (GAM1312) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20355] GAM1312 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1312 was detected is described hereinabove with reference to Figs. 2-8.

[20356] GAM1312 gene, herein designated GAM GENE, and GAM1312 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20357] GAM1312 gene, herein designated GAM GENE, encodes a GAM1312 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1312 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1312 precursor RNA is designated SEQ ID:1285, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1285 is located at position 174362 relative to contig NT_007819.11, on chromosome 7.

[20358] GAM1312 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20359] An enzyme complex designated DICER COMPLEX, dices the GAM1312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1312 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1312 RNA is designated SEQ ID:2961, and is provided hereinbelow with reference to the sequence listing part.

[20360] GAM1312 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1312 target RNA, herein designated GAM TARGET RNA. GAM1312 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20361] GAM1312 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1312 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1312 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1312 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1312 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20362] The complementary binding of GAM1312 RNA, herein designated GAM RNA, to target binding sites on GAM1312

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1312 target RNA, herein designated GAM TARGET RNA, into GAM1312 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20363] It is appreciated that GAM1312 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1312 target genes. The mRNA of each one of this plurality of GAM1312 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1312 RNA, herein designated GAM RNA, and which when bound by GAM1312 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1312 target proteins.

[20364] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1312 gene, herein designated GAM GENE, on one or more GAM1312 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20365] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1312 correlate with, and may be deduced from, the identity of the target genes which GAM1312 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20366] Nucleotide sequences of the GAM1312 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1312 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1312 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1312 are further described hereinbelow with reference to Table Table1.

[20367] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1312 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20368] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1313 (GAM1313) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20369] GAM1313 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1313 was detected is described hereinabove with reference to Figs. 2-8.

[20370] GAM1313 gene, herein designated GAM GENE, and GAM1313 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20371] GAM1313 gene, herein designated GAM GENE, encodes a GAM1313 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1313 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1313 precursor RNA is designated SEQ ID:1286, and is provided hereinbelow with reference to the sequence listing part.

[20372] GAM1313 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20373] An enzyme complex designated DICER COMPLEX, dices the GAM1313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1313 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1313 RNA is designated SEQ ID:2962, and

is provided hereinbelow with reference to the sequence listing part.

[20374] GAM1313 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1313 target RNA, herein designated GAM TARGET RNA. GAM1313 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20375] GAM1313 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1313 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1313 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1313 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1313 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20376] The complementary binding of GAM1313 RNA, herein designated GAM RNA, to target binding sites on GAM1313 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1313 target RNA, herein designated GAM TARGET RNA, into GAM1313 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20377] It is appreciated that GAM1313 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1313 target genes. The mRNA of each one of this plurality of GAM1313 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1313 RNA, herein designated GAM RNA, and which when bound by

GAM1313 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1313 target proteins.

[20378] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1313 gene, herein designated GAM GENE, on one or more GAM1313 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20379] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1313 correlate with, and may be deduced from, the identity of the target genes which GAM1313 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[20380] Nucleotide sequences of the GAM1313 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1313 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1313 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1313 are further described hereinbelow with reference to Table Table1.

[20381] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1313 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20382] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1314 (GAM1314) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20383] GAM1314 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1314 was detected is described hereinabove

with reference to Figs. 2-8.

[20384] GAM1314 gene, herein designated GAM GENE, and GAM1314 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20385] GAM1314 gene, herein designated GAM GENE, encodes a GAM1314 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1314 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1314 precursor RNA is designated SEQ ID:1287, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1287 is located at position 13329170 relative to contig NT_033899.3, on chromosome 11.

[20386] GAM1314 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20387] An enzyme complex designated DICER COMPLEX, dices the GAM1314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1314 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1314 RNA is designated SEQ ID:2963, and is provided hereinbelow with reference to the sequence listing part.

[20388] GAM1314 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1314 target RNA, herein designated GAM TARGET RNA. GAM1314 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20389] GAM1314 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1314 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1314 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1314 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1314 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20390] The complementary binding of GAM1314 RNA, herein designated GAM RNA, to target binding sites on GAM1314 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1314 target RNA, herein designated GAM TARGET RNA, into GAM1314 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20391] It is appreciated that GAM1314 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1314 target genes. The mRNA of each one of this plurality of GAM1314 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1314 RNA, herein designated GAM RNA, and which when bound by GAM1314 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1314 target proteins.

[20392] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1314 gene, herein designated GAM GENE, on one or more GAM1314 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20393] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1314 correlate with, and may be deduced from, the identity of the target genes which GAM1314 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20394] Nucleotide sequences of the GAM1314 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1314 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1314 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1314 are further described hereinbelow with reference to Table Table1.

[20395] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1314 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20396] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1315 (GAM1315) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20397] GAM1315 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1315 was detected is described hereinabove with reference to Figs. 2-8.

[20398] GAM1315 gene, herein designated GAM GENE, and GAM1315 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20399] GAM1315 gene, herein designated GAM GENE, encodes a GAM1315 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1315 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1315 precursor RNA is

designated SEQ ID:1288, and is provided hereinbelow with reference to the sequence listing part.

[20400] GAM1315 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20401] An enzyme complex designated DICER COMPLEX, dices the GAM1315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1315 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1315 RNA is designated SEQ ID:2964, and is provided hereinbelow with reference to the sequence

listing part.

[20402] GAM1315 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1315 target RNA, herein designated GAM TARGET RNA. GAM1315 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20403] GAM1315 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1315 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1315 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1315 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1315 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20404] The complementary binding of GAM1315 RNA, herein designated GAM RNA, to target binding sites on GAM1315 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1315 target RNA, herein designated GAM TARGET RNA, into GAM1315 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20405] It is appreciated that GAM1315 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1315 target genes. The mRNA of each one of this plurality of GAM1315 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1315 RNA, herein designated GAM RNA, and which when bound by GAM1315 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1315 target proteins.

[20406] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1315 gene, herein designated GAM GENE, on one or more GAM1315 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20407] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1315 correlate with, and may be deduced from, the identity of the target genes which GAM1315 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20408] Nucleotide sequences of the GAM1315 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1315 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1315 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1315 are further described hereinbelow with reference to Table Table1.

[20409] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1315 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20410] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1316 (GAM1316) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[20411] GAM1316 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1316 was detected is described hereinabove with reference to Figs. 2-8.

[20412] GAM1316 gene, herein designated GAM GENE, and GAM1316 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20413] GAM1316 gene, herein designated GAM GENE, encodes a GAM1316 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1316 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1316 precursor RNA is designated SEQ ID:1289, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1289 is located at position 3434864 relative to contig NT_009714.13, on chromosome 12.

[20414] GAM1316 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99358, which mouse homolog is detected in

mouse EST accession BG288438.1.

[20415] GAM1316 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20416] An enzyme complex designated DICER COMPLEX, dices the GAM1316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1316 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1316 RNA is designated SEQ ID:2965, and is provided hereinbelow with reference to the sequence listing part.

[20417] GAM1316 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1316 target RNA, herein designated GAM TARGET RNA. GAM1316 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20418] GAM1316 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1316 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1316 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1316 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1316 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20419] The complementary binding of GAM1316 RNA, herein designated GAM RNA, to target binding sites on GAM1316 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1316 target RNA, herein designated GAM TARGET RNA, into GAM1316 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20420] It is appreciated that GAM1316 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1316 target genes. The mRNA of each one of this plurality of GAM1316 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1316 RNA, herein designated GAM RNA, and which when bound by GAM1316 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1316

target proteins.

[20421] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1316 gene, herein designated GAM GENE, on one or more GAM1316 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20422] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1316 correlate with, and may be deduced from, the identity of the target genes which GAM1316 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20423] Nucleotide sequences of the GAM1316 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1316 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1316 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1316 are further described hereinbelow with reference to Table Table1.

[20424] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1316 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20425] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1317 (GAM1317) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20426] GAM1317 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1317 was detected is described hereinabove with reference to Figs. 2-8.

[20427] GAM1317 gene, herein designated GAM GENE, and

GAM1317 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20428] GAM1317 gene, herein designated GAM GENE, encodes a GAM1317 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1317 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1317 precursor RNA is designated SEQ ID:1290, and is provided hereinbelow with reference to the sequence listing part.

[20429] GAM1317 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20430] An enzyme complex designated DICER COMPLEX, dices the GAM1317 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1317 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1317 RNA is designated SEQ ID:2966, and is provided hereinbelow with reference to the sequence listing part.

[20431] GAM1317 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1317 target RNA, herein designated GAM TARGET RNA. GAM1317 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20432] GAM1317 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1317 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1317

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1317 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1317 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20433] The complementary binding of GAM1317 RNA, herein designated GAM RNA, to target binding sites on GAM1317 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1317 target RNA, herein designated GAM TARGET RNA, into GAM1317 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[20434] It is appreciated that GAM1317 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1317 target genes. The mRNA of each one of this plurality of GAM1317 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1317 RNA, herein designated GAM RNA, and which when bound by GAM1317 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1317 target proteins.

[20435] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1317 gene, herein designated GAM GENE, on one or more GAM1317 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20436] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1317 correlate with, and may be deduced from, the identity of the target genes which GAM1317 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20437] Nucleotide sequences of the GAM1317 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1317 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1317 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1317 are further described hereinbelow with reference to Table Table1.

[20438] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1317 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20439] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1318 (GAM1318) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20440] GAM1318 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1318 was detected is described hereinabove with reference to Figs. 2-8.

[20441] GAM1318 gene, herein designated GAM GENE, and GAM1318 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20442] GAM1318 gene, herein designated GAM GENE, encodes a GAM1318 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1318 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1318 precursor RNA is designated SEQ ID:1291, and is provided hereinbelow with reference to the sequence listing part.

[20443] GAM1318 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1318 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20444] An enzyme complex designated DICER COMPLEX, dices the GAM1318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1318 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1318 RNA is designated SEQ ID:2967, and is provided hereinbelow with reference to the sequence listing part.

[20445] GAM1318 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1318 target RNA, herein designated GAM TARGET

RNA. GAM1318 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20446] GAM1318 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1318 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1318 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1318 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1318 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20447] The complementary binding of GAM1318 RNA, herein designated GAM RNA, to target binding sites on GAM1318 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1318 target RNA, herein designated GAM TARGET RNA, into GAM1318 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20448] It is appreciated that GAM1318 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1318 target genes. The mRNA of each one of this plurality of GAM1318 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1318 RNA, herein designated GAM RNA, and which when bound by GAM1318 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1318 target proteins.

[20449] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1318 gene, herein designated GAM GENE, on one or more GAM1318 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20450] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1318 correlate with, and may be deduced from, the identity of the target genes which GAM1318 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20451] Nucleotide sequences of the GAM1318 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1318 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1318 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1318 are further described hereinbelow with reference to Table Table1.

[20452] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1318 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20453] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1319 (GAM1319) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20454] GAM1319 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1319 was detected is described hereinabove with reference to Figs. 2-8.

[20455] GAM1319 gene, herein designated GAM GENE, and GAM1319 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20456] GAM1319 gene, herein designated GAM GENE, encodes a

GAM1319 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1319 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1319 precursor RNA is designated SEQ ID:1292, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1292 is located at position 4851374 relative to contig NT_022517.13, on chromosome 3.

[20457] GAM1319 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20458] An enzyme complex designated DICER COMPLEX, dices the GAM1319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1319 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1319 RNA is designated SEQ ID:2968, and is provided hereinbelow with reference to the sequence listing part.

[20459] GAM1319 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1319 target RNA, herein designated GAM TARGET RNA. GAM1319 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20460] GAM1319 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1319 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1319 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1319 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1319 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20461] The complementary binding of GAM1319 RNA, herein designated GAM RNA, to target binding sites on GAM1319 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1319 target RNA, herein designated GAM TARGET RNA, into GAM1319 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20462] It is appreciated that GAM1319 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1319 target genes. The mRNA of each one of this plurality of GAM1319 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1319 RNA, herein designated GAM RNA, and which when bound by GAM1319 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1319 target proteins.

[20463] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1319 gene, herein designated GAM GENE, on one or more GAM1319 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20464] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1319 correlate with, and may be deduced from, the identity of the target genes which GAM1319 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20465] Nucleotide sequences of the GAM1319 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1319 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1319 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1319 are further described hereinbelow with reference to Table Table1.

[20466] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1319 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20467] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1320 (GAM1320) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20468] GAM1320 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1320 was detected is described hereinabove with reference to Figs. 2-8.

[20469] GAM1320 gene, herein designated GAM GENE, and GAM1320 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20470] GAM1320 gene, herein designated GAM GENE, encodes a GAM1320 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1320 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1320 precursor RNA is designated SEQ ID:1293, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1293 is located at position 18703627 relative to contig NT_005403.11, on chromosome 2.

[20471] GAM1320 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20472] An enzyme complex designated DICER COMPLEX, dices the GAM1320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1320 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1320 RNA is designated SEQ ID:2969, and is provided hereinbelow with reference to the sequence listing part.

[20473] GAM1320 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1320 target RNA, herein designated GAM TARGET RNA. GAM1320 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20474] GAM1320 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1320 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1320 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1320 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1320 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20475] The complementary binding of GAM1320 RNA, herein designated GAM RNA, to target binding sites on GAM1320 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1320 target RNA, herein designated GAM TARGET RNA, into GAM1320 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20476] It is appreciated that GAM1320 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1320 target genes. The mRNA of each one of this plurality of GAM1320 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1320 RNA, herein designated GAM RNA, and which when bound by GAM1320 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1320 target proteins.

[20477] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1320 gene, herein designated GAM GENE, on one or more GAM1320 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20478] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1320 correlate with, and may be deduced from, the identity of the target genes which GAM1320 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20479] Nucleotide sequences of the GAM1320 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1320 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1320 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1320 are further described hereinbelow with reference to Table Table1.

[20480] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1320 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20481] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1321 (GAM1321) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20482] GAM1321 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1321 was detected is described hereinabove with reference to Figs. 2-8.

[20483] GAM1321 gene, herein designated GAM GENE, and GAM1321 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20484] GAM1321 gene, herein designated GAM GENE, encodes a GAM1321 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1321 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1321 precursor RNA is designated SEQ ID:1294, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1294 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[20485] GAM1321 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20486] An enzyme complex designated DICER COMPLEX, dices the GAM1321 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1321 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1321 RNA is designated SEQ ID:2970, and is provided hereinbelow with reference to the sequence listing part.

[20487] GAM1321 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1321 target RNA, herein designated GAM TARGET RNA. GAM1321 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20488] GAM1321 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1321 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1321

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1321 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1321 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20489] The complementary binding of GAM1321 RNA, herein designated GAM RNA, to target binding sites on GAM1321 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1321 target RNA, herein designated GAM TARGET RNA, into GAM1321 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[20490] It is appreciated that GAM1321 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1321 target genes. The mRNA of each one of this plurality of GAM1321 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1321 RNA, herein designated GAM RNA, and which when bound by GAM1321 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1321 target proteins.

[20491] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1321 gene, herein designated GAM GENE, on one or more GAM1321 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20492] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1321 correlate with, and may be deduced from, the identity of the target genes which GAM1321 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20493] Nucleotide sequences of the GAM1321 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1321 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1321 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1321 are further described hereinbelow with reference to Table Table1.

[20494] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1321 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20495] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1322 (GAM1322) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20496] GAM1322 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1322 was detected is described hereinabove with reference to Figs. 2-8.

[20497] GAM1322 gene, herein designated GAM GENE, and GAM1322 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20498] GAM1322 gene, herein designated GAM GENE, encodes a GAM1322 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1322 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1322 precursor RNA is designated SEQ ID:1295, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1295 is located at position 1402763 relative to contig NT_035427.2, on chromosome 17.

[20499] GAM1322 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20500] An enzyme complex designated DICER COMPLEX, dices the GAM1322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1322 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1322 RNA is designated SEQ ID:2971, and is provided hereinbelow with reference to the sequence listing part.

[20501] GAM1322 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1322 target RNA, herein designated GAM TARGET RNA. GAM1322 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20502] GAM1322 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1322 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1322 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1322 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1322 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20503] The complementary binding of GAM1322 RNA, herein designated GAM RNA, to target binding sites on GAM1322 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1322 target RNA, herein designated GAM TARGET RNA, into GAM1322 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20504] It is appreciated that GAM1322 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1322 target genes. The mRNA of each one of this plurality of GAM1322 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1322 RNA, herein designated GAM RNA, and which when bound by GAM1322 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1322 target proteins.

[20505] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1322 gene, herein designated GAM GENE, on one or more GAM1322 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20506] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1322 correlate with, and may be deduced from, the identity of the target genes which GAM1322 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20507] Nucleotide sequences of the GAM1322 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1322 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1322 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1322 are further described hereinbelow with reference to Table Table1.

[20508] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1322 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20509] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1323 (GAM1323) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20510] GAM1323 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1323 was detected is described hereinabove with reference to Figs. 2-8.

[20511] GAM1323 gene, herein designated GAM GENE, and GAM1323 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[20512] GAM1323 gene, herein designated GAM GENE, encodes a GAM1323 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1323 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1323 precursor RNA is designated SEQ ID:1296, and is provided hereinbelow with reference to the sequence listing part.

[20513] GAM1323 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20514] An enzyme complex designated DICER COMPLEX, dices the GAM1323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1323 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1323 RNA is designated SEQ ID:2972, and is provided hereinbelow with reference to the sequence listing part.

[20515] GAM1323 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1323 target RNA, herein designated GAM TARGET RNA. GAM1323 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20516] GAM1323 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1323 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1323 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1323 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1323 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20517] The complementary binding of GAM1323 RNA, herein designated GAM RNA, to target binding sites on GAM1323 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1323 target RNA, herein designated GAM TARGET RNA, into GAM1323 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20518] It is appreciated that GAM1323 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1323 target genes. The mRNA of each one of this plurality of GAM1323 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1323 RNA, herein designated GAM RNA, and which when bound by GAM1323 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1323 target proteins.

[20519] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1323 gene, herein designated GAM GENE, on one or more GAM1323 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20520] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1323 correlate with, and may be deduced from, the identity of the target genes which GAM1323 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20521] Nucleotide sequences of the GAM1323 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1323 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1323 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1323 are further described hereinbelow with reference to Table Table1.

[20522] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1323 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20523] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1324 (GAM1324) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20524] GAM1324 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1324 was detected is described hereinabove with reference to Figs. 2-8.

[20525] GAM1324 gene, herein designated GAM GENE, and GAM1324 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20526] GAM1324 gene, herein designated GAM GENE, encodes a GAM1324 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1324 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1324 precursor RNA is designated SEQ ID:1297, and is provided hereinbelow with reference to the sequence listing part.

[20527] GAM1324 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1324 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20528] An enzyme complex designated DICER COMPLEX, dices the GAM1324 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1324 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1324 RNA is designated SEQ ID:2973, and is provided hereinbelow with reference to the sequence listing part.

[20529] GAM1324 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1324 target RNA, herein designated GAM TARGET RNA. GAM1324 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20530] GAM1324 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1324 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1324 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1324 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1324 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20531] The complementary binding of GAM1324 RNA, herein designated GAM RNA, to target binding sites on GAM1324 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1324 target RNA, herein designated GAM TARGET RNA, into GAM1324 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20532] It is appreciated that GAM1324 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1324 target genes. The mRNA of each one of this plurality of GAM1324 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1324 RNA, herein designated GAM RNA, and which when bound by GAM1324 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1324 target proteins.

[20533] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1324 gene, herein designated GAM GENE, on one or more GAM1324 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20534] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1324 correlate with, and may be deduced from, the identity of the target genes which GAM1324 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20535] Nucleotide sequences of the GAM1324 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1324 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1324 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1324 are further described hereinbelow with reference to Table Table1.

[20536] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1324 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20537] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1325 (GAM1325) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20538] GAM1325 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1325 was detected is described hereinabove with reference to Figs. 2-8.

[20539] GAM1325 gene, herein designated GAM GENE, and GAM1325 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20540] GAM1325 gene, herein designated GAM GENE, encodes a GAM1325 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1325 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1325 precursor RNA is designated SEQ ID:1298, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1298 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[20541] GAM1325 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20542] An enzyme complex designated DICER COMPLEX, dices the GAM1325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1325 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1325 RNA is designated SEQ ID:2974, and is provided hereinbelow with reference to the sequence listing part.

[20543] GAM1325 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1325 target RNA, herein designated GAM TARGET RNA. GAM1325 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20544] GAM1325 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1325 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1325 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1325 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1325 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20545] The complementary binding of GAM1325 RNA, herein designated GAM RNA, to target binding sites on GAM1325 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1325 target RNA, herein designated GAM TARGET RNA, into GAM1325 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20546] It is appreciated that GAM1325 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1325 target genes. The mRNA of each one of this plurality of GAM1325 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1325 RNA, herein designated GAM RNA, and which when bound by GAM1325 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1325 target proteins.

[20547] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1325 gene, herein designated GAM GENE, on one or more GAM1325 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20548] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1325 correlate with, and may be deduced from, the identity of the target genes which GAM1325 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20549] Nucleotide sequences of the GAM1325 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1325 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1325 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1325 are further described hereinbelow with reference to Table Table1.

[20550] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1325 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20551] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1326 (GAM1326) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20552] GAM1326 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1326 was detected is described hereinabove with reference to Figs. 2-8.

[20553] GAM1326 gene, herein designated GAM GENE, and GAM1326 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20554] GAM1326 gene, herein designated GAM GENE, encodes a GAM1326 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1326 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1326 precursor RNA is designated SEQ ID:1299, and is provided hereinbelow with reference to the sequence listing part.

[20555] GAM1326 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20556] An enzyme complex designated DICER COMPLEX, dices the GAM1326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1326 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1326 RNA is designated SEQ ID:2975, and is provided hereinbelow with reference to the sequence listing part.

[20557] GAM1326 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1326 target RNA, herein designated GAM TARGET RNA. GAM1326 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20558] GAM1326 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1326 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1326 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1326 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1326 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[20559] The complementary binding of GAM1326 RNA, herein designated GAM RNA, to target binding sites on GAM1326 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1326 target RNA, herein designated GAM TARGET RNA, into GAM1326 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20560] It is appreciated that GAM1326 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1326 target genes. The mRNA of each one of this plurality of GAM1326 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1326 RNA, herein designated GAM RNA, and which when bound by GAM1326 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1326 target proteins.

[20561] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1326 gene, herein designated GAM GENE, on one or

more GAM1326 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20562] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1326 correlate with, and may be deduced from, the identity of the target genes which GAM1326 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20563] Nucleotide sequences of the GAM1326 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1326 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1326 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1326 are further de-

scribed hereinbelow with reference to Table Table1.

[20564] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1326 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20565] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1327 (GAM1327) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20566] GAM1327 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1327 was detected is described hereinabove with reference to Figs. 2-8.

[20567] GAM1327 gene, herein designated GAM GENE, and GAM1327 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20568] GAM1327 gene, herein designated GAM GENE, encodes a GAM1327 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1327 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1327 precursor RNA is designated SEQ ID:1300, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1300 is located at position 320694 relative to contig NT_028054.10, on chromosome 1.

[20569] GAM1327 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20570] An enzyme complex designated DICER COMPLEX, dices the GAM1327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1327 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1327 RNA is designated SEQ ID:2976, and is provided hereinbelow with reference to the sequence listing part.

[20571] GAM1327 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1327 target RNA, herein designated GAM TARGET RNA. GAM1327 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20572] GAM1327 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1327 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1327 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1327 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1327 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20573] The complementary binding of GAM1327 RNA, herein designated GAM RNA, to target binding sites on GAM1327 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1327 target RNA, herein designated GAM TARGET RNA, into GAM1327 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20574] It is appreciated that GAM1327 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1327 target genes. The mRNA of each one of this plurality of GAM1327 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1327 RNA, herein designated GAM RNA, and which when bound by GAM1327 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1327 target proteins.

[20575] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1327 gene, herein designated GAM GENE, on one or more GAM1327 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[20576] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1327 correlate with, and may be deduced from, the identity of the target genes which GAM1327 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20577] Nucleotide sequences of the GAM1327 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1327 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1327 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1327 are further described hereinbelow with reference to Table Table1.

[20578] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1327 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20579] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1328 (GAM1328) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[20580] GAM1328 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1328 was detected is described hereinabove with reference to Figs. 2-8.

[20581] GAM1328 gene, herein designated GAM GENE, and GAM1328 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20582] GAM1328 gene, herein designated GAM GENE, encodes a GAM1328 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1328 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1328 precursor RNA is designated SEQ ID:1301, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1301 is located at position 755880 relative to contig NT_005416.8, on chromosome 2.

[20583] GAM1328 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1328 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20584] An enzyme complex designated DICER COMPLEX, dices the GAM1328 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1328 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1328 RNA is designated SEQ ID:2977, and is provided hereinbelow with reference to the sequence listing part.

[20585] GAM1328 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1328 target RNA, herein designated GAM TARGET RNA. GAM1328 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20586] GAM1328 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1328 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1328 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1328 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1328 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20587] The complementary binding of GAM1328 RNA, herein designated GAM RNA, to target binding sites on GAM1328 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1328 target RNA, herein designated GAM TARGET RNA, into GAM1328 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20588] It is appreciated that GAM1328 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1328 target genes. The mRNA of each one of this plurality of GAM1328 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1328 RNA, herein designated GAM RNA, and which when bound by GAM1328 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1328 target proteins.

[20589] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1328 gene, herein designated GAM GENE, on one or more GAM1328 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20590] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1328 correlate with, and may be deduced from, the identity of the target genes which GAM1328 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20591] Nucleotide sequences of the GAM1328 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1328 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1328 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1328 are further described hereinbelow with reference to Table Table1.

[20592] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1328 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20593] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1329 (GAM1329) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20594] GAM1329 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1329 was detected is described hereinabove with reference to Figs. 2-8.

[20595] GAM1329 gene, herein designated GAM GENE, and GAM1329 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20596] GAM1329 gene, herein designated GAM GENE, encodes a GAM1329 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1329 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1329 precursor RNA is designated SEQ ID:1302, and is provided hereinbelow with reference to the sequence listing part.

[20597] GAM1329 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20598] An enzyme complex designated DICER COMPLEX, dices the GAM1329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1329 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1329 RNA is designated SEQ ID:2978, and is provided hereinbelow with reference to the sequence listing part.

[20599] GAM1329 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1329 target RNA, herein designated GAM TARGET RNA. GAM1329 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20600] GAM1329 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1329 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1329 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1329 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1329 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20601] The complementary binding of GAM1329 RNA, herein designated GAM RNA, to target binding sites on GAM1329 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1329 target RNA, herein designated GAM TARGET RNA, into GAM1329 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20602] It is appreciated that GAM1329 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1329 target genes. The mRNA of each one of this

plurality of GAM1329 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1329 RNA, herein designated GAM RNA, and which when bound by GAM1329 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1329 target proteins.

[20603] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1329 gene, herein designated GAM GENE, on one or more GAM1329 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20604] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1329 correlate with, and may be deduced from, the identity of the target genes which GAM1329 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20605] Nucleotide sequences of the GAM1329 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1329 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1329 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1329 are further described hereinbelow with reference to Table Table1.

[20606] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1329 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20607] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1330 (GAM1330) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[20608] GAM1330 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1330 was detected is described hereinabove with reference to Figs. 2-8.

[20609] GAM1330 gene, herein designated GAM GENE, and GAM1330 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20610] GAM1330 gene, herein designated GAM GENE, encodes a GAM1330 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1330 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1330 precursor RNA is designated SEQ ID:1303, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1303 is located at position 76647 relative to contig NT_033000.3, on chromosome 2.

[20611] GAM1330 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20612] An enzyme complex designated DICER COMPLEX, dices the GAM1330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1330 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1330 RNA is designated SEQ ID:2979, and is provided hereinbelow with reference to the sequence listing part.

[20613] GAM1330 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1330 target RNA, herein designated GAM TARGET RNA. GAM1330 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20614] GAM1330 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1330 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1330 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1330 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1330 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[20615] The complementary binding of GAM1330 RNA, herein designated GAM RNA, to target binding sites on GAM1330 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1330 target RNA, herein designated GAM TARGET RNA, into GAM1330 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20616] It is appreciated that GAM1330 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1330 target genes. The mRNA of each one of this plurality of GAM1330 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1330 RNA, herein designated GAM RNA, and which when bound by GAM1330 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1330 target proteins.

[20617] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1330 gene, herein designated GAM GENE, on one or

more GAM1330 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20618] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1330 correlate with, and may be deduced from, the identity of the target genes which GAM1330 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20619] Nucleotide sequences of the GAM1330 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1330 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1330 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1330 are further de-

scribed hereinbelow with reference to Table Table1.

[20620] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1330 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20621] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1331 (GAM1331) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20622] GAM1331 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1331 was detected is described hereinabove with reference to Figs. 2-8.

[20623] GAM1331 gene, herein designated GAM GENE, and GAM1331 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20624] GAM1331 gene, herein designated GAM GENE, encodes a GAM1331 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1331 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1331 precursor RNA is designated SEQ ID:1304, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1304 is located at position 2835366 relative to contig NT_006431.11, on chromosome 5.

[20625] GAM1331 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20626] An enzyme complex designated DICER COMPLEX, dices the GAM1331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1331 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1331 RNA is designated SEQ ID:2980, and is provided hereinbelow with reference to the sequence listing part.

[20627] GAM1331 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1331 target RNA, herein designated GAM TARGET RNA. GAM1331 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20628] GAM1331 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1331 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1331 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1331 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1331 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20629] The complementary binding of GAM1331 RNA, herein designated GAM RNA, to target binding sites on GAM1331 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1331 target RNA, herein designated GAM TARGET RNA, into GAM1331 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20630] It is appreciated that GAM1331 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1331 target genes. The mRNA of each one of this plurality of GAM1331 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1331 RNA, herein designated GAM RNA, and which when bound by GAM1331 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1331 target proteins.

[20631] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1331 gene, herein designated GAM GENE, on one or more GAM1331 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[20632] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1331 correlate with, and may be deduced from, the identity of the target genes which GAM1331 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20633] Nucleotide sequences of the GAM1331 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1331 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1331 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1331 are further described hereinbelow with reference to Table Table1.

[20634] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1331 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20635] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1332 (GAM1332) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[20636] GAM1332 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1332 was detected is described hereinabove with reference to Figs. 2-8.

[20637] GAM1332 gene, herein designated GAM GENE, and GAM1332 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20638] GAM1332 gene, herein designated GAM GENE, encodes a GAM1332 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1332 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1332 precursor RNA is designated SEQ ID:1305, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1305 is located at position 1235063 relative to contig NT_009526.11, on chromosome 12.

[20639] GAM1332 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences

of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[20640] SEQ ID:99203 detected in mouse EST Accession BI965652.1.

[20641] SEQ ID:99208 detected in mouse EST Accession BI965972.1.

[20642] SEQ ID:99209 detected in mouse EST Accession AI326210.1.

[20643] GAM1332 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20644] An enzyme complex designated DICER COMPLEX, dices the GAM1332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1332 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1332 RNA is designated SEQ ID:2981, and is provided hereinbelow with reference to the sequence listing part.

[20645] GAM1332 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1332 target RNA, herein designated GAM TARGET RNA. GAM1332 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20646] GAM1332 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1332 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1332 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1332 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1332 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20647] The complementary binding of GAM1332 RNA, herein designated GAM RNA, to target binding sites on GAM1332 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1332 target RNA, herein designated GAM TARGET RNA, into GAM1332 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20648] It is appreciated that GAM1332 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1332 target genes. The mRNA of each one of this plurality of GAM1332 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1332 RNA, herein designated GAM RNA, and which when bound by GAM1332 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1332 target proteins.

[20649] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1332 gene, herein designated GAM GENE, on one or more GAM1332 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[20650] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1332 correlate with, and may be deduced from, the identity of the target genes which GAM1332 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20651] Nucleotide sequences of the GAM1332 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1332 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1332 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1332 are further described hereinbelow with reference to Table Table1.

[20652] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1332 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20653] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1333 (GAM1333) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[20654] GAM1333 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1333 was detected is described hereinabove with reference to Figs. 2-8.

[20655] GAM1333 gene, herein designated GAM GENE, and GAM1333 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20656] GAM1333 gene, herein designated GAM GENE, encodes a GAM1333 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1333 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1333 precursor RNA is designated SEQ ID:1306, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1306 is located at position 4851355 relative to contig NT_022517.13, on chromosome 3.

[20657] GAM1333 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1333 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20658] An enzyme complex designated DICER COMPLEX, dices the GAM1333 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1333 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1333 RNA is designated SEQ ID:2982, and is provided hereinbelow with reference to the sequence listing part.

[20659] GAM1333 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1333 target RNA, herein designated GAM TARGET RNA. GAM1333 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20660] GAM1333 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1333 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1333 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1333 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1333 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20661] The complementary binding of GAM1333 RNA, herein designated GAM RNA, to target binding sites on GAM1333 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1333 target RNA, herein designated GAM TARGET RNA, into GAM1333 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20662] It is appreciated that GAM1333 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1333 target genes. The mRNA of each one of this plurality of GAM1333 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1333 RNA, herein designated GAM RNA, and which when bound by GAM1333 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1333 target proteins.

[20663] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1333 gene, herein designated GAM GENE, on one or more GAM1333 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20664] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1333 correlate with, and may be deduced from, the identity of the target genes which GAM1333 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20665] Nucleotide sequences of the GAM1333 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1333 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1333 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1333 are further described hereinbelow with reference to Table Table1.

[20666] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1333 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20667] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1334 (GAM1334) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20668] GAM1334 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1334 was detected is described hereinabove with reference to Figs. 2-8.

[20669] GAM1334 gene, herein designated GAM GENE, and GAM1334 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20670] GAM1334 gene, herein designated GAM GENE, encodes a GAM1334 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1334 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1334 precursor RNA is designated SEQ ID:1307, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1307 is located at position 446287 relative to contig NT_022140.11, on chromosome 2.

[20671] GAM1334 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20672] An enzyme complex designated DICER COMPLEX, dices the GAM1334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1334 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1334 RNA is designated SEQ ID:2983, and is provided hereinbelow with reference to the sequence listing part.

[20673] GAM1334 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1334 target RNA, herein designated GAM TARGET RNA. GAM1334 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20674] GAM1334 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1334 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1334 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1334 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1334 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20675] The complementary binding of GAM1334 RNA, herein designated GAM RNA, to target binding sites on GAM1334 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1334 target RNA, herein designated GAM TARGET RNA, into GAM1334 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20676] It is appreciated that GAM1334 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1334 target genes. The mRNA of each one of this plurality of GAM1334 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1334 RNA, herein designated GAM RNA, and which when bound by GAM1334 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1334 target proteins.

[20677] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1334 gene, herein designated GAM GENE, on one or more GAM1334 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20678] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1334 correlate with, and may be deduced from, the identity of the target genes which GAM1334 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20679] Nucleotide sequences of the GAM1334 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1334 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1334 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1334 are further described hereinbelow with reference to Table Table1.

[20680] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1334 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20681] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1335 (GAM1335) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20682] GAM1335 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1335 was detected is described hereinabove with reference to Figs. 2-8.

[20683] GAM1335 gene, herein designated GAM GENE, and GAM1335 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20684] GAM1335 gene, herein designated GAM GENE, encodes a GAM1335 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1335 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1335 precursor RNA is designated SEQ ID:1308, and is provided hereinbelow with reference to the sequence listing part.

[20685] GAM1335 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20686] An enzyme complex designated DICER COMPLEX, dices the GAM1335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1335 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1335 RNA is designated SEQ ID:2984, and is provided hereinbelow with reference to the sequence listing part.

[20687] GAM1335 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1335 target RNA, herein designated GAM TARGET RNA. GAM1335 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20688] GAM1335 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1335 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1335 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1335 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1335 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[20689] The complementary binding of GAM1335 RNA, herein designated GAM RNA, to target binding sites on GAM1335 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1335 target RNA, herein designated GAM TARGET RNA, into GAM1335 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20690] It is appreciated that GAM1335 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1335 target genes. The mRNA of each one of this plurality of GAM1335 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1335 RNA, herein designated GAM RNA, and which when bound by GAM1335 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1335 target proteins.

[20691] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1335 gene, herein designated GAM GENE, on one or

more GAM1335 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20692] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1335 correlate with, and may be deduced from, the identity of the target genes which GAM1335 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20693] Nucleotide sequences of the GAM1335 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1335 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1335 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1335 are further de-

scribed hereinbelow with reference to Table Table1.

[20694] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1335 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20695] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1336 (GAM1336) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20696] GAM1336 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1336 was detected is described hereinabove with reference to Figs. 2-8.

[20697] GAM1336 gene, herein designated GAM GENE, and GAM1336 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20698] GAM1336 gene, herein designated GAM GENE, encodes a GAM1336 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1336 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1336 precursor RNA is designated SEQ ID:1309, and is provided hereinbelow with reference to the sequence listing part.

[20699] GAM1336 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20700] An enzyme complex designated DICER COMPLEX, dices the GAM1336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1336 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1336 RNA is designated SEQ ID:2985, and is provided hereinbelow with reference to the sequence listing part.

[20701] GAM1336 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1336 target RNA, herein designated GAM TARGET RNA. GAM1336 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20702] GAM1336 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1336 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1336 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1336 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1336 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20703] The complementary binding of GAM1336 RNA, herein designated GAM RNA, to target binding sites on GAM1336 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1336 target RNA, herein designated GAM TARGET RNA, into GAM1336 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20704] It is appreciated that GAM1336 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1336 target genes. The mRNA of each one of this plurality of GAM1336 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1336 RNA, herein designated GAM RNA, and which when bound by GAM1336 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1336 target proteins.

[20705] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1336 gene, herein designated GAM GENE, on one or more GAM1336 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20706] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1336 correlate with, and may be deduced from, the identity of the target genes which GAM1336 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20707] Nucleotide sequences of the GAM1336 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1336 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1336 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1336 are further described hereinbelow with reference to Table Table1.

[20708] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1336 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20709] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1337 (GAM1337) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20710] GAM1337 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1337 was detected is described hereinabove with reference to Figs. 2-8.

[20711] GAM1337 gene, herein designated GAM GENE, and GAM1337 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20712] GAM1337 gene, herein designated GAM GENE, encodes a GAM1337 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1337 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1337 precursor RNA is designated SEQ ID:1310, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1310 is located at position 1757609 relative to contig NT_005526.12, on chromosome 3.

[20713] GAM1337 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20714] An enzyme complex designated DICER COMPLEX, dices the GAM1337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1337 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1337 RNA is designated SEQ ID:2986, and is provided hereinbelow with reference to the sequence listing part.

[20715] GAM1337 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1337 target RNA, herein designated GAM TARGET RNA. GAM1337 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20716] GAM1337 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1337 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1337 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1337 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1337 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20717] The complementary binding of GAM1337 RNA, herein designated GAM RNA, to target binding sites on GAM1337 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1337 target RNA, herein designated GAM TARGET RNA, into GAM1337 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20718] It is appreciated that GAM1337 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1337 target genes. The mRNA of each one of this plurality of GAM1337 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1337 RNA, herein designated GAM RNA, and which when bound by GAM1337 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1337 target proteins.

[20719] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1337 gene, herein designated GAM GENE, on one or more GAM1337 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20720] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1337 correlate with, and may be deduced from, the identity of the target genes which GAM1337 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20721] Nucleotide sequences of the GAM1337 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1337 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1337 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1337 are further described hereinbelow with reference to Table Table1.

[20722] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1337 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20723] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1338 (GAM1338) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20724] GAM1338 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1338 was detected is described hereinabove with reference to Figs. 2-8.

[20725] GAM1338 gene, herein designated GAM GENE, and GAM1338 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20726] GAM1338 gene, herein designated GAM GENE, encodes a GAM1338 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1338 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1338 precursor RNA is designated SEQ ID:1311, and is provided hereinbelow with reference to the sequence listing part.

[20727] GAM1338 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20728] An enzyme complex designated DICER COMPLEX, dices the GAM1338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1338 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1338 RNA is designated SEQ ID:2987, and is provided hereinbelow with reference to the sequence listing part.

[20729] GAM1338 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1338 target RNA, herein designated GAM TARGET RNA. GAM1338 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20730] GAM1338 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1338 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1338 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1338 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1338 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20731] The complementary binding of GAM1338 RNA, herein designated GAM RNA, to target binding sites on GAM1338 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1338 target RNA, herein designated GAM TARGET RNA, into GAM1338 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20732] It is appreciated that GAM1338 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1338 target genes. The mRNA of each one of this plurality of GAM1338 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1338 RNA, herein designated GAM RNA, and which when bound by GAM1338 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1338 target proteins.

[20733] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1338 gene, herein designated GAM GENE, on one or more GAM1338 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20734] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1338 correlate with, and may

be deduced from, the identity of the target genes which GAM1338 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20735] Nucleotide sequences of the GAM1338 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1338 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1338 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1338 are further described hereinbelow with reference to Table Table1.

[20736] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1338 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20737] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1339 (GAM1339) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20738] GAM1339 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1339 was detected is described hereinabove with reference to Figs. 2-8.

[20739] GAM1339 gene, herein designated GAM GENE, and GAM1339 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20740] GAM1339 gene, herein designated GAM GENE, encodes a GAM1339 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1339 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1339 precursor RNA is designated SEQ ID:1312, and is provided hereinbelow with reference to the sequence listing part.

[20741] GAM1339 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20742] An enzyme complex designated DICER COMPLEX, dices the GAM1339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1339 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1339 RNA is designated SEQ ID:2988, and is provided hereinbelow with reference to the sequence listing part.

[20743] GAM1339 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1339 target RNA, herein designated GAM TARGET RNA. GAM1339 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20744] GAM1339 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1339 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1339 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1339 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1339 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20745] The complementary binding of GAM1339 RNA, herein designated GAM RNA, to target binding sites on GAM1339 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1339 target RNA, herein designated GAM TARGET RNA, into GAM1339 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20746] It is appreciated that GAM1339 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1339 target genes. The mRNA of each one of this plurality of GAM1339 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1339 RNA, herein designated GAM RNA, and which when bound by GAM1339 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1339 target proteins.

[20747] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1339 gene, herein designated GAM GENE, on one or more GAM1339 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20748] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1339 correlate with, and may be deduced from, the identity of the target genes which GAM1339 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20749] Nucleotide sequences of the GAM1339 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1339 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1339 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1339 are further described hereinbelow with reference to Table Table1.

[20750] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1339 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20751] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1340 (GAM1340) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20752] GAM1340 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1340 was detected is described hereinabove with reference to Figs. 2-8.

[20753] GAM1340 gene, herein designated GAM GENE, and GAM1340 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20754] GAM1340 gene, herein designated GAM GENE, encodes a GAM1340 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1340 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1340 precursor RNA is

designated SEQ ID:1313, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1313 is located at position 36924270 relative to contig NT_007592.11, on chromosome 6.

[20755] GAM1340 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20756] An enzyme complex designated DICER COMPLEX, dices the GAM1340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1340 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1340 RNA is designated SEQ ID:2989, and is provided hereinbelow with reference to the sequence listing part.

[20757] GAM1340 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1340 target RNA, herein designated GAM TARGET RNA. GAM1340 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20758] GAM1340 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1340 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1340 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1340 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1340 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20759] The complementary binding of GAM1340 RNA, herein designated GAM RNA, to target binding sites on GAM1340 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1340 target RNA, herein designated GAM TARGET RNA, into GAM1340 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20760] It is appreciated that GAM1340 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1340 target genes. The mRNA of each one of this plurality of GAM1340 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1340 RNA,

herein designated GAM RNA, and which when bound by GAM1340 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1340 target proteins.

[20761] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1340 gene, herein designated GAM GENE, on one or more GAM1340 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20762] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1340 correlate with, and may be deduced from, the identity of the target genes which

GAM1340 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20763] Nucleotide sequences of the GAM1340 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1340 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1340 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1340 are further described hereinbelow with reference to Table Table1.

[20764] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1340 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20765] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1341 (GAM1341) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20766] GAM1341 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1341 was detected is described hereinabove with reference to Figs. 2-8.

[20767] GAM1341 gene, herein designated GAM GENE, and GAM1341 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20768] GAM1341 gene, herein designated GAM GENE, encodes a GAM1341 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1341 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1341 precursor RNA is designated SEQ ID:1314, and is provided hereinbelow with reference to the sequence listing part.

[20769] GAM1341 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[20770] An enzyme complex designated DICER COMPLEX, dices the GAM1341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1341 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1341 RNA is designated SEQ ID:2990, and is provided hereinbelow with reference to the sequence listing part.

[20771] GAM1341 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1341 target RNA, herein designated GAM TARGET RNA. GAM1341 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20772] GAM1341 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1341 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1341 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1341 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1341 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20773] The complementary binding of GAM1341 RNA, herein designated GAM RNA, to target binding sites on GAM1341 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1341 target RNA, herein designated GAM TARGET RNA, into GAM1341 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20774] It is appreciated that GAM1341 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1341 target genes. The mRNA of each one of this plurality of GAM1341 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1341 RNA, herein designated GAM RNA, and which when bound by GAM1341 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1341 target proteins.

[20775] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1341 gene, herein designated GAM GENE, on one or more GAM1341 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20776] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1341 correlate with, and may be deduced from, the identity of the target genes which GAM1341 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20777] Nucleotide sequences of the GAM1341 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1341 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1341 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1341 are further described hereinbelow with reference to Table Table1.

[20778] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1341 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20779] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1342 (GAM1342) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20780] GAM1342 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1342 was detected is described hereinabove with reference to Figs. 2-8.

[20781] GAM1342 gene, herein designated GAM GENE, and GAM1342 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20782] GAM1342 gene, herein designated GAM GENE, encodes a GAM1342 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1342 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1342 precursor RNA is designated SEQ ID:1315, and is provided hereinbelow with

reference to the sequence listing part.

[20783] GAM1342 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20784] An enzyme complex designated DICER COMPLEX, dices the GAM1342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1342 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1342 RNA is designated SEQ ID:2991, and is provided hereinbelow with reference to the sequence listing part.

[20785] GAM1342 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1342 target RNA, herein designated GAM TARGET RNA. GAM1342 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20786] GAM1342 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1342 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1342 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1342 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1342 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20787] The complementary binding of GAM1342 RNA, herein designated GAM RNA, to target binding sites on GAM1342 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1342 target RNA, herein designated GAM TARGET RNA, into GAM1342 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20788] It is appreciated that GAM1342 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1342 target genes. The mRNA of each one of this plurality of GAM1342 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1342 RNA, herein designated GAM RNA, and which when bound by GAM1342 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1342

target proteins.

[20789] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1342 gene, herein designated GAM GENE, on one or more GAM1342 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20790] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1342 correlate with, and may be deduced from, the identity of the target genes which GAM1342 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20791] Nucleotide sequences of the GAM1342 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1342 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1342 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1342 are further described hereinbelow with reference to Table Table1.

[20792] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1342 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20793] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1343 (GAM1343) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20794] GAM1343 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1343 was detected is described hereinabove with reference to Figs. 2-8.

[20795] GAM1343 gene, herein designated GAM GENE, and

GAM1343 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20796] GAM1343 gene, herein designated GAM GENE, encodes a GAM1343 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1343 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1343 precursor RNA is designated SEQ ID:1316, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1316 is located at position 2485260 relative to contig NT_029419.8, on chromosome 12.

[20797] GAM1343 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20798] An enzyme complex designated DICER COMPLEX, dices the GAM1343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1343 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1343 RNA is designated SEQ ID:2992, and is provided hereinbelow with reference to the sequence listing part.

[20799] GAM1343 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1343 target RNA, herein designated GAM TARGET RNA. GAM1343 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20800] GAM1343 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1343 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1343 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1343 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1343 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20801] The complementary binding of GAM1343 RNA, herein designated GAM RNA, to target binding sites on GAM1343 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1343 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1343 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20802] It is appreciated that GAM1343 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1343 target genes. The mRNA of each one of this plurality of GAM1343 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1343 RNA, herein designated GAM RNA, and which when bound by GAM1343 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1343 target proteins.

[20803] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1343 gene, herein designated GAM GENE, on one or more GAM1343 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20804] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1343 correlate with, and may be deduced from, the identity of the target genes which GAM1343 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20805] Nucleotide sequences of the GAM1343 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1343 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1343 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1343 are further described hereinbelow with reference to Table Table1.

[20806] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1343 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[20807] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1344 (GAM1344) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20808] GAM1344 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1344 was detected is described hereinabove with reference to Figs. 2-8.

[20809] GAM1344 gene, herein designated GAM GENE, and GAM1344 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20810] GAM1344 gene, herein designated GAM GENE, encodes a GAM1344 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1344 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1344 precursor RNA is designated SEQ ID:1317, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1317 is located at position 4284578 relative to contig NT_034874.2, on chromosome 6.

[20811] GAM1344 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20812] An enzyme complex designated DICER COMPLEX, dices the GAM1344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1344 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1344 RNA is designated SEQ ID:2993, and is provided hereinbelow with reference to the sequence

listing part.

[20813] GAM1344 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1344 target RNA, herein designated GAM TARGET RNA. GAM1344 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20814] GAM1344 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1344 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1344 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1344 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1344 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20815] The complementary binding of GAM1344 RNA, herein designated GAM RNA, to target binding sites on GAM1344 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1344 target RNA, herein designated GAM TARGET RNA, into GAM1344 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20816] It is appreciated that GAM1344 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1344 target genes. The mRNA of each one of this plurality of GAM1344 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1344 RNA, herein designated GAM RNA, and which when bound by GAM1344 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1344 target proteins.

[20817] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1344 gene, herein designated GAM GENE, on one or more GAM1344 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20818] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1344 correlate with, and may be deduced from, the identity of the target genes which GAM1344 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20819] Nucleotide sequences of the GAM1344 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1344 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1344 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1344 are further described hereinbelow with reference to Table Table1.

[20820] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1344 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20821] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1345 (GAM1345) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20822] GAM1345 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1345 was detected is described hereinabove with reference to Figs. 2-8.

[20823] GAM1345 gene, herein designated GAM GENE, and GAM1345 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20824] GAM1345 gene, herein designated GAM GENE, encodes a GAM1345 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1345 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1345 precursor RNA is designated SEQ ID:1318, and is provided hereinbelow with reference to the sequence listing part.

[20825] GAM1345 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98658, which mouse homolog is detected in mouse EST accession BI903259.1.

[20826] GAM1345 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20827] An enzyme complex designated DICER COMPLEX, dices the GAM1345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1345 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1345 RNA is designated SEQ ID:2994, and is provided hereinbelow with reference to the sequence listing part.

[20828] GAM1345 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1345 target RNA, herein designated GAM TARGET RNA. GAM1345 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[20829] GAM1345 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1345 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1345 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1345 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1345 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20830] The complementary binding of GAM1345 RNA, herein

designated GAM RNA, to target binding sites on GAM1345 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1345 target RNA, herein designated GAM TARGET RNA, into GAM1345 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20831] It is appreciated that GAM1345 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1345 target genes. The mRNA of each one of this plurality of GAM1345 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1345 RNA, herein designated GAM RNA, and which when bound by GAM1345 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1345 target proteins.

[20832] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1345 gene, herein designated GAM GENE, on one or more GAM1345 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20833] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1345 correlate with, and may be deduced from, the identity of the target genes which GAM1345 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20834] Nucleotide sequences of the GAM1345 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1345 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1345 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1345 are further described hereinbelow with reference to Table Table1.

[20835] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1345 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20836] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1346 (GAM1346) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20837] GAM1346 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1346 was detected is described hereinabove with reference to Figs. 2-8.

[20838] GAM1346 gene, herein designated GAM GENE, and GAM1346 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20839] GAM1346 gene, herein designated GAM GENE, encodes a GAM1346 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1346 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1346 precursor RNA is designated SEQ ID:1319, and is provided hereinbelow with reference to the sequence listing part.

[20840] GAM1346 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20841] An enzyme complex designated DICER COMPLEX, dices the GAM1346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1346 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1346 RNA is designated SEQ ID:2995, and is provided hereinbelow with reference to the sequence listing part.

[20842] GAM1346 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1346 target RNA, herein designated GAM TARGET RNA. GAM1346 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20843] GAM1346 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1346 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1346 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1346 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1346 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20844] The complementary binding of GAM1346 RNA, herein designated GAM RNA, to target binding sites on GAM1346 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1346 target RNA, herein designated GAM TARGET RNA, into GAM1346 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20845] It is appreciated that GAM1346 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1346 target genes. The mRNA of each one of this plurality of GAM1346 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1346 RNA,

herein designated GAM RNA, and which when bound by GAM1346 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1346 target proteins.

[20846] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1346 gene, herein designated GAM GENE, on one or more GAM1346 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20847] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1346 correlate with, and may be deduced from, the identity of the target genes which

GAM1346 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20848] Nucleotide sequences of the GAM1346 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1346 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1346 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1346 are further described hereinbelow with reference to Table Table1.

[20849] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1346 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20850] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1347 (GAM1347) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20851] GAM1347 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1347 was detected is described hereinabove with reference to Figs. 2-8.

[20852] GAM1347 gene, herein designated GAM GENE, and GAM1347 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20853] GAM1347 gene, herein designated GAM GENE, encodes a GAM1347 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1347 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1347 precursor RNA is designated SEQ ID:1320, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1320 is located at position 23535227 relative to contig NT_033899.3, on chromosome 11.

[20854] GAM1347 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[20855] SEQ ID:97974 detected in mouse EST Accession BI714485.1.

[20856] SEQ ID:97975 detected in mouse EST Accession BE368829.1.

[20857] GAM1347 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20858] An enzyme complex designated DICER COMPLEX, dices the GAM1347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1347 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1347 RNA is designated SEQ ID:2996, and is provided hereinbelow with reference to the sequence

listing part.

[20859] GAM1347 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1347 target RNA, herein designated GAM TARGET RNA. GAM1347 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20860] GAM1347 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1347 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1347 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1347 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1347 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20861] The complementary binding of GAM1347 RNA, herein designated GAM RNA, to target binding sites on GAM1347 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1347 target RNA, herein designated GAM TARGET RNA, into GAM1347 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20862] It is appreciated that GAM1347 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1347 target genes. The mRNA of each one of this plurality of GAM1347 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1347 RNA, herein designated GAM RNA, and which when bound by GAM1347 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1347 target proteins.

[20863] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1347 gene, herein designated GAM GENE, on one or more GAM1347 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20864] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1347 correlate with, and may be deduced from, the identity of the target genes which GAM1347 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20865] Nucleotide sequences of the GAM1347 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1347 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1347 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1347 are further described hereinbelow with reference to Table Table1.

[20866] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1347 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20867] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1348 (GAM1348) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20868] GAM1348 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1348 was detected is described hereinabove with reference to Figs. 2-8.

[20869] GAM1348 gene, herein designated GAM GENE, and GAM1348 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20870] GAM1348 gene, herein designated GAM GENE, encodes a GAM1348 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1348 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1348 precursor RNA is designated SEQ ID:1321, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1321 is located at position 716274 relative to contig NT_006111.13, on chromosome 4.

[20871] GAM1348 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[20872] An enzyme complex designated DICER COMPLEX, dices the GAM1348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1348 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1348 RNA is designated SEQ ID:2997, and is provided hereinbelow with reference to the sequence listing part.

[20873] GAM1348 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1348 target RNA, herein designated GAM TARGET RNA. GAM1348 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20874] GAM1348 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1348 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1348 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1348 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1348 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20875] The complementary binding of GAM1348 RNA, herein designated GAM RNA, to target binding sites on GAM1348 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1348 target RNA, herein designated GAM TARGET RNA, into GAM1348 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20876] It is appreciated that GAM1348 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1348 target genes. The mRNA of each one of this plurality of GAM1348 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1348 RNA, herein designated GAM RNA, and which when bound by GAM1348 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1348 target proteins.

[20877] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1348 gene, herein designated GAM GENE, on one or more GAM1348 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20878] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1348 correlate with, and may be deduced from, the identity of the target genes which GAM1348 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20879] Nucleotide sequences of the GAM1348 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1348 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1348 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1348 are further described hereinbelow with reference to Table Table1.

[20880] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1348 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20881] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1349 (GAM1349) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20882] GAM1349 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1349 was detected is described hereinabove with reference to Figs. 2-8.

[20883] GAM1349 gene, herein designated GAM GENE, and GAM1349 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20884] GAM1349 gene, herein designated GAM GENE, encodes a GAM1349 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1349 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1349 precursor RNA is designated SEQ ID:1322, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1322 is located at position 21008687 relative to contig NT_034874.2, on chromosome 6.

[20885] GAM1349 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20886] An enzyme complex designated DICER COMPLEX, dices the GAM1349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1349 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1349 RNA is designated SEQ ID:2998, and

is provided hereinbelow with reference to the sequence listing part.

[20887] GAM1349 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1349 target RNA, herein designated GAM TARGET RNA. GAM1349 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20888] GAM1349 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1349 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1349 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1349 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1349 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20889] The complementary binding of GAM1349 RNA, herein designated GAM RNA, to target binding sites on GAM1349 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1349 target RNA, herein designated GAM TARGET RNA, into GAM1349 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20890] It is appreciated that GAM1349 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1349 target genes. The mRNA of each one of this plurality of GAM1349 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1349 RNA, herein designated GAM RNA, and which when bound by

GAM1349 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1349 target proteins.

[20891] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1349 gene, herein designated GAM GENE, on one or more GAM1349 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20892] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1349 correlate with, and may be deduced from, the identity of the target genes which GAM1349 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[20893] Nucleotide sequences of the GAM1349 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1349 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1349 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1349 are further described hereinbelow with reference to Table Table1.

[20894] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1349 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20895] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1350 (GAM1350) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20896] GAM1350 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1350 was detected is described hereinabove

with reference to Figs. 2-8.

[20897] GAM1350 gene, herein designated GAM GENE, and GAM1350 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20898] GAM1350 gene, herein designated GAM GENE, encodes a GAM1350 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1350 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1350 precursor RNA is designated SEQ ID:1323, and is provided hereinbelow with reference to the sequence listing part.

[20899] GAM1350 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20900] An enzyme complex designated DICER COMPLEX, dices the GAM1350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1350 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1350 RNA is designated SEQ ID:2999, and is provided hereinbelow with reference to the sequence listing part.

[20901] GAM1350 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1350 target RNA, herein designated GAM TARGET RNA. GAM1350 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20902] GAM1350 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1350 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1350 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1350 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1350 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20903] The complementary binding of GAM1350 RNA, herein designated GAM RNA, to target binding sites on GAM1350 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1350 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1350 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20904] It is appreciated that GAM1350 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1350 target genes. The mRNA of each one of this plurality of GAM1350 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1350 RNA, herein designated GAM RNA, and which when bound by GAM1350 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1350 target proteins.

[20905] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1350 gene, herein designated GAM GENE, on one or more GAM1350 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20906] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1350 correlate with, and may be deduced from, the identity of the target genes which GAM1350 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20907] Nucleotide sequences of the GAM1350 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1350 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1350 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1350 are further described hereinbelow with reference to Table Table1.

[20908] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1350 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[20909] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1351 (GAM1351) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20910] GAM1351 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1351 was detected is described hereinabove with reference to Figs. 2-8.

[20911] GAM1351 gene, herein designated GAM GENE, and GAM1351 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20912] GAM1351 gene, herein designated GAM GENE, encodes a GAM1351 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1351 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1351 precursor RNA is designated SEQ ID:1324, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1324 is located at position 7678827 relative to contig NT_004852.13, on chromosome 1.

[20913] GAM1351 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20914] An enzyme complex designated DICER COMPLEX, dices the GAM1351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1351 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1351 RNA is designated SEQ ID:3000, and is provided hereinbelow with reference to the sequence

listing part.

[20915] GAM1351 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1351 target RNA, herein designated GAM TARGET RNA. GAM1351 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20916] GAM1351 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1351 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1351 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1351 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1351 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20917] The complementary binding of GAM1351 RNA, herein designated GAM RNA, to target binding sites on GAM1351 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1351 target RNA, herein designated GAM TARGET RNA, into GAM1351 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20918] It is appreciated that GAM1351 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1351 target genes. The mRNA of each one of this plurality of GAM1351 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1351 RNA, herein designated GAM RNA, and which when bound by GAM1351 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1351 target proteins.

[20919] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1351 gene, herein designated GAM GENE, on one or more GAM1351 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20920] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1351 correlate with, and may be deduced from, the identity of the target genes which GAM1351 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20921] Nucleotide sequences of the GAM1351 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1351 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1351 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1351 are further described hereinbelow with reference to Table Table1.

[20922] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1351 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20923] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1352 (GAM1352) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20924] GAM1352 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1352 was detected is described hereinabove with reference to Figs. 2-8.

[20925] GAM1352 gene, herein designated GAM GENE, and GAM1352 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20926] GAM1352 gene, herein designated GAM GENE, encodes a GAM1352 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1352 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1352 precursor RNA is designated SEQ ID:1325, and is provided hereinbelow with reference to the sequence listing part.

[20927] GAM1352 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20928] An enzyme complex designated DICER COMPLEX, dices

the GAM1352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1352 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1352 RNA is designated SEQ ID:3001, and is provided hereinbelow with reference to the sequence listing part.

[20929] GAM1352 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1352 target RNA, herein designated GAM TARGET RNA. GAM1352 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20930] GAM1352 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1352 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1352 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1352 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1352 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20931] The complementary binding of GAM1352 RNA, herein designated GAM RNA, to target binding sites on GAM1352 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1352 target RNA, herein designated GAM TARGET RNA, into GAM1352 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20932] It is appreciated that GAM1352 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1352 target genes. The mRNA of each one of this plurality of GAM1352 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1352 RNA, herein designated GAM RNA, and which when bound by GAM1352 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1352 target proteins.

[20933] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1352 gene, herein designated GAM GENE, on one or more GAM1352 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20934] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1352 correlate with, and may be deduced from, the identity of the target genes which GAM1352 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20935] Nucleotide sequences of the GAM1352 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1352 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1352 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1352 are further described hereinbelow with reference to Table Table1.

[20936] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1352 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20937] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1353 (GAM1353) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20938] GAM1353 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1353 was detected is described hereinabove with reference to Figs. 2-8.

[20939] GAM1353 gene, herein designated GAM GENE, and GAM1353 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20940] GAM1353 gene, herein designated GAM GENE, encodes a GAM1353 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1353 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1353 precursor RNA is designated SEQ ID:1326, and is provided hereinbelow with reference to the sequence listing part.

[20941] GAM1353 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[20942] An enzyme complex designated DICER COMPLEX, dices the GAM1353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1353 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1353 RNA is designated SEQ ID:3002, and is provided hereinbelow with reference to the sequence listing part.

[20943] GAM1353 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1353 target RNA, herein designated GAM TARGET RNA. GAM1353 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[20944] GAM1353 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1353 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1353 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1353 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1353 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[20945] The complementary binding of GAM1353 RNA, herein designated GAM RNA, to target binding sites on GAM1353 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1353 target RNA, herein designated GAM TARGET RNA, into GAM1353 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[20946] It is appreciated that GAM1353 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1353 target genes. The mRNA of each one of this plurality of GAM1353 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1353 RNA, herein designated GAM RNA, and which when bound by GAM1353 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1353 target proteins.

[20947] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1353 gene, herein designated GAM GENE, on one or more GAM1353 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[20948] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1353 correlate with, and may be deduced from, the identity of the target genes which GAM1353 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[20949] Nucleotide sequences of the GAM1353 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1353 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1353 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1353 are further described hereinbelow with reference to Table Table1.

[20950] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1353 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[20951] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1354 (GAM1354) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[20952] GAM1354 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1354 was detected is described hereinabove with reference to Figs. 2-8.

[20953] GAM1354 gene, herein designated GAM GENE, and GAM1354 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[20954] GAM1354 gene, herein designated GAM GENE, encodes a GAM1354 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1354 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1354 precursor RNA is designated SEQ ID:1327, and is provided hereinbelow with reference to the sequence listing part.

[20955] GAM1354 has 52 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[20956] SEQ ID:98768 detected in mouse EST Accession W16182.1.

[20957] SEQ ID:98769 detected in mouse EST Accession BF450285.1.

[20958] SEQ ID:98770 detected in mouse EST Accession AW110985.1.

[20959] SEQ ID:98771 detected in mouse EST Accession AA764472.1.

[20960] SEQ ID:98772 detected in mouse EST Accession

AW908422.1.

[20961] SEQ ID:98773 detected in mouse EST Accession AW322040.1.

[20962] SEQ ID:98774 detected in mouse EST Accession AW987156.1.

[20963] SEQ ID:98775 detected in mouse EST Accession BE335469.1.

[20964] SEQ ID:98776 detected in mouse EST Accession AA270973.1.

[20965] SEQ ID:98777 detected in mouse EST Accession BE690578.1.

[20966] SEQ ID:98778 detected in mouse EST Accession BE199228.1.

[20967] SEQ ID:98779 detected in mouse EST Accession BE650065.1.

[20968] SEQ ID:98780 detected in mouse EST Accession AW018407.1.

[20969] SEQ ID:98781 detected in mouse EST Accession BF227510.1.

[20970] SEQ ID:98782 detected in mouse EST Accession AA239428.1.

[20971] SEQ ID:98783 detected in mouse EST Accession AA238246.1.

[20972] SEQ ID:98784 detected in mouse EST Accession AA230354.1.

[20973] SEQ ID:98785 detected in mouse EST Accession AW110984.1.

[20974] SEQ ID:98786 detected in mouse EST Accession AW909366.1.

[20975] SEQ ID:98787 detected in mouse EST Accession BI111409.1.

[20976] SEQ ID:98788 detected in mouse EST Accession AI255679.1.

[20977] SEQ ID:98789 detected in mouse EST Accession BE199152.1.

[20978] SEQ ID:98790 detected in mouse EST Accession BF227614.1.

[20979] SEQ ID:98791 detected in mouse EST Accession BI248794.1.

[20980] SEQ ID:98792 detected in mouse EST Accession AI785459.1.

[20981] SEQ ID:98793 detected in mouse EST Accession AI152470.1.

[20982] SEQ ID:98794 detected in mouse EST Accession AW241043.1.

[20983] SEQ ID:98795 detected in mouse EST Accession

BF116785.1.

[20984] SEQ ID:98796 detected in mouse EST Accession BE624221.1.

[20985] SEQ ID:98797 detected in mouse EST Accession AW018398.1.

[20986] SEQ ID:98798 detected in mouse EST Accession BF226299.1.

[20987] SEQ ID:98799 detected in mouse EST Accession AI323769.1.

[20988] SEQ ID:98800 detected in mouse EST Accession BF179498.1.

[20989] SEQ ID:98801 detected in mouse EST Accession AW209037.1.

[20990] SEQ ID:98802 detected in mouse EST Accession AW701118.1.

[20991] SEQ ID:98803 detected in mouse EST Accession AI646857.1.

[20992] SEQ ID:98804 detected in mouse EST Accession AW212849.1.

[20993] SEQ ID:98805 detected in mouse EST Accession AI747413.1.

[20994] SEQ ID:98806 detected in mouse EST Accession BI246484.1.

[20995] SEQ ID:98807 detected in mouse EST Accession AI114892.1.

[20996] SEQ ID:98808 detected in mouse EST Accession AI194959.1.

[20997] SEQ ID:98809 detected in mouse EST Accession BI250124.1.

[20998] SEQ ID:98810 detected in mouse EST Accession BE689976.1.

[20999] SEQ ID:98811 detected in mouse EST Accession BF020203.1.

[21000] SEQ ID:98812 detected in mouse EST Accession AW989706.1.

[21001] SEQ ID:98813 detected in mouse EST Accession BI110254.1.

[21002] SEQ ID:98814 detected in mouse EST Accession AA237404.1.

[21003] SEQ ID:98815 detected in mouse EST Accession BE690148.1.

[21004] SEQ ID:98816 detected in mouse EST Accession BE692663.1.

[21005] SEQ ID:98817 detected in mouse EST Accession AA237479.1.

[21006] SEQ ID:98818 detected in mouse EST Accession

AW113760.1.

[21007] SEQ ID:98819 detected in mouse EST Accession AI195467.1.

[21008] GAM1354 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21009] An enzyme complex designated DICER COMPLEX, dices the GAM1354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1354 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1354 RNA is designated SEQ ID:3003, and

is provided hereinbelow with reference to the sequence listing part.

[21010] GAM1354 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1354 target RNA, herein designated GAM TARGET RNA. GAM1354 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21011] GAM1354 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1354 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1354 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1354 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1354 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21012] The complementary binding of GAM1354 RNA, herein designated GAM RNA, to target binding sites on GAM1354 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1354 target RNA, herein designated GAM TARGET RNA, into GAM1354 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21013] It is appreciated that GAM1354 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1354 target genes. The mRNA of each one of this plurality of GAM1354 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1354 RNA, herein designated GAM RNA, and which when bound by

GAM1354 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1354 target proteins.

[21014] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1354 gene, herein designated GAM GENE, on one or more GAM1354 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21015] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1354 correlate with, and may be deduced from, the identity of the target genes which GAM1354 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[21016] Nucleotide sequences of the GAM1354 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1354 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1354 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1354 are further described hereinbelow with reference to Table Table1.

[21017] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1354 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21018] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1355 (GAM1355) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21019] GAM1355 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1355 was detected is described hereinabove

with reference to Figs. 2-8.

[21020] GAM1355 gene, herein designated GAM GENE, and GAM1355 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21021] GAM1355 gene, herein designated GAM GENE, encodes a GAM1355 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1355 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1355 precursor RNA is designated SEQ ID:1328, and is provided hereinbelow with reference to the sequence listing part.

[21022] GAM1355 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21023] An enzyme complex designated DICER COMPLEX, dices the GAM1355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1355 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1355 RNA is designated SEQ ID:3004, and is provided hereinbelow with reference to the sequence listing part.

[21024] GAM1355 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1355 target RNA, herein designated GAM TARGET RNA. GAM1355 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21025] GAM1355 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1355 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1355 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1355 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1355 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21026] The complementary binding of GAM1355 RNA, herein designated GAM RNA, to target binding sites on GAM1355 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1355 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1355 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21027] It is appreciated that GAM1355 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1355 target genes. The mRNA of each one of this plurality of GAM1355 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1355 RNA, herein designated GAM RNA, and which when bound by GAM1355 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1355 target proteins.

[21028] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1355 gene, herein designated GAM GENE, on one or more GAM1355 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21029] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1355 correlate with, and may be deduced from, the identity of the target genes which GAM1355 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21030] Nucleotide sequences of the GAM1355 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1355 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1355 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1355 are further described hereinbelow with reference to Table Table1.

[21031] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1355 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[21032] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1356 (GAM1356) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21033] GAM1356 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1356 was detected is described hereinabove with reference to Figs. 2-8.

[21034] GAM1356 gene, herein designated GAM GENE, and GAM1356 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21035] GAM1356 gene, herein designated GAM GENE, encodes a GAM1356 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1356 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1356 precursor RNA is designated SEQ ID:1329, and is provided hereinbelow with reference to the sequence listing part.

[21036] GAM1356 has 52 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[21037] SEQ ID:98697 detected in mouse EST Accession W16182.1.

[21038] SEQ ID:98698 detected in mouse EST Accession AA237404.1.

[21039] SEQ ID:98699 detected in mouse EST Accession BE692663.1.

[21040] SEQ ID:98700 detected in mouse EST Accession AA237479.1.

[21041] SEQ ID:98701 detected in mouse EST Accession BE689976.1.

[21042] SEQ ID:98702 detected in mouse EST Accession BF020203.1.

[21043] SEQ ID:98703 detected in mouse EST Accession AW989706.1.

[21044] SEQ ID:98704 detected in mouse EST Accession BI110254.1.

[21045] SEQ ID:98705 detected in mouse EST Accession AW322040.1.

[21046] SEQ ID:98706 detected in mouse EST Accession AW987156.1.

[21047] SEQ ID:98707 detected in mouse EST Accession BE335469.1.

[21048] SEQ ID:98708 detected in mouse EST Accession BF116785.1.

[21049] SEQ ID:98709 detected in mouse EST Accession BE690578.1.

[21050] SEQ ID:98710 detected in mouse EST Accession BE624221.1.

[21051] SEQ ID:98711 detected in mouse EST Accession BE199228.1.

[21052] SEQ ID:98712 detected in mouse EST Accession BE650065.1.

[21053] SEQ ID:98713 detected in mouse EST Accession AW018407.1.

[21054] SEQ ID:98714 detected in mouse EST Accession BF227510.1.

[21055] SEQ ID:98715 detected in mouse EST Accession AW018398.1.

[21056] SEQ ID:98716 detected in mouse EST Accession AA238246.1.

[21057] SEQ ID:98717 detected in mouse EST Accession

AA230354.1.

[21058] SEQ ID:98718 detected in mouse EST Accession BF226299.1.

[21059] SEQ ID:98719 detected in mouse EST Accession AW909366.1.

[21060] SEQ ID:98720 detected in mouse EST Accession BI111409.1.

[21061] SEQ ID:98721 detected in mouse EST Accession AI255679.1.

[21062] SEQ ID:98722 detected in mouse EST Accession BE199152.1.

[21063] SEQ ID:98723 detected in mouse EST Accession BF227614.1.

[21064] SEQ ID:98724 detected in mouse EST Accession AI323769.1.

[21065] SEQ ID:98725 detected in mouse EST Accession BF179498.1.

[21066] SEQ ID:98726 detected in mouse EST Accession AW209037.1.

[21067] SEQ ID:98727 detected in mouse EST Accession AI195467.1.

[21068] SEQ ID:98728 detected in mouse EST Accession AI747413.1.

[21069] SEQ ID:98729 detected in mouse EST Accession BI246484.1.

[21070] SEQ ID:98730 detected in mouse EST Accession AI114892.1.

[21071] SEQ ID:98731 detected in mouse EST Accession AW110985.1.

[21072] SEQ ID:98732 detected in mouse EST Accession AA764472.1.

[21073] SEQ ID:98733 detected in mouse EST Accession AA239428.1.

[21074] SEQ ID:98734 detected in mouse EST Accession AW113760.1.

[21075] SEQ ID:98735 detected in mouse EST Accession AW110984.1.

[21076] SEQ ID:98736 detected in mouse EST Accession BI248794.1.

[21077] SEQ ID:98737 detected in mouse EST Accession AI785459.1.

[21078] SEQ ID:98738 detected in mouse EST Accession AW701118.1.

[21079] SEQ ID:98739 detected in mouse EST Accession AI646857.1.

[21080] SEQ ID:98740 detected in mouse EST Accession

AW212849.1.

[21081] SEQ ID:98741 detected in mouse EST Accession AI194959.1.

[21082] SEQ ID:98742 detected in mouse EST Accession BI250124.1.

[21083] SEQ ID:98743 detected in mouse EST Accession BF450285.1.

[21084] SEQ ID:98744 detected in mouse EST Accession BE690148.1.

[21085] SEQ ID:98745 detected in mouse EST Accession AW908422.1.

[21086] SEQ ID:98746 detected in mouse EST Accession AI152470.1.

[21087] SEQ ID:98747 detected in mouse EST Accession AW241043.1.

[21088] SEQ ID:98748 detected in mouse EST Accession AA270973.1.

[21089] GAM1356 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21090] An enzyme complex designated DICER COMPLEX, dices the GAM1356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1356 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1356 RNA is designated SEQ ID:3005, and is provided hereinbelow with reference to the sequence listing part.

[21091] GAM1356 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1356 target RNA, herein designated GAM TARGET RNA. GAM1356 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[21092] GAM1356 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1356 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1356 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1356 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1356 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21093] The complementary binding of GAM1356 RNA, herein

designated GAM RNA, to target binding sites on GAM1356 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1356 target RNA, herein designated GAM TARGET RNA, into GAM1356 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21094] It is appreciated that GAM1356 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1356 target genes. The mRNA of each one of this plurality of GAM1356 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1356 RNA, herein designated GAM RNA, and which when bound by GAM1356 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1356 target proteins.

[21095] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1356 gene, herein designated GAM GENE, on one or more GAM1356 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21096] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1356 correlate with, and may be deduced from, the identity of the target genes which GAM1356 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21097] Nucleotide sequences of the GAM1356 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1356 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1356 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1356 are further described hereinbelow with reference to Table Table1.

[21098] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1356 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21099] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1357 (GAM1357) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21100] GAM1357 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1357 was detected is described hereinabove with reference to Figs. 2-8.

[21101] GAM1357 gene, herein designated GAM GENE, and GAM1357 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21102] GAM1357 gene, herein designated GAM GENE, encodes a GAM1357 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1357 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1357 precursor RNA is designated SEQ ID:1330, and is provided hereinbelow with reference to the sequence listing part.

[21103] GAM1357 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21104] An enzyme complex designated DICER COMPLEX, dices the GAM1357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1357 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1357 RNA is designated SEQ ID:3006, and is provided hereinbelow with reference to the sequence listing part.

[21105] GAM1357 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1357 target RNA, herein designated GAM TARGET RNA. GAM1357 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21106] GAM1357 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1357 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1357 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1357 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1357 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21107] The complementary binding of GAM1357 RNA, herein designated GAM RNA, to target binding sites on GAM1357 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1357 target RNA, herein designated GAM TARGET RNA, into GAM1357 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21108] It is appreciated that GAM1357 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1357 target genes. The mRNA of each one of this plurality of GAM1357 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1357 RNA,

herein designated GAM RNA, and which when bound by GAM1357 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1357 target proteins.

[21109] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1357 gene, herein designated GAM GENE, on one or more GAM1357 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21110] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1357 correlate with, and may be deduced from, the identity of the target genes which

GAM1357 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21111] Nucleotide sequences of the GAM1357 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1357 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1357 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1357 are further described hereinbelow with reference to Table Table1.

[21112] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1357 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21113] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1358 (GAM1358) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21114] GAM1358 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1358 was detected is described hereinabove with reference to Figs. 2-8.

[21115] GAM1358 gene, herein designated GAM GENE, and GAM1358 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21116] GAM1358 gene, herein designated GAM GENE, encodes a GAM1358 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1358 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1358 precursor RNA is designated SEQ ID:1331, and is provided hereinbelow with reference to the sequence listing part.

[21117] GAM1358 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[21118] An enzyme complex designated DICER COMPLEX, dices the GAM1358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1358 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1358 RNA is designated SEQ ID:3007, and is provided hereinbelow with reference to the sequence listing part.

[21119] GAM1358 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1358 target RNA, herein designated GAM TARGET RNA. GAM1358 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21120] GAM1358 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1358 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1358 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1358 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1358 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21121] The complementary binding of GAM1358 RNA, herein designated GAM RNA, to target binding sites on GAM1358 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1358 target RNA, herein designated GAM TARGET RNA, into GAM1358 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21122] It is appreciated that GAM1358 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1358 target genes. The mRNA of each one of this plurality of GAM1358 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1358 RNA, herein designated GAM RNA, and which when bound by GAM1358 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1358 target proteins.

[21123] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1358 gene, herein designated GAM GENE, on one or more GAM1358 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21124] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1358 correlate with, and may be deduced from, the identity of the target genes which GAM1358 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21125] Nucleotide sequences of the GAM1358 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1358 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1358 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1358 are further described hereinbelow with reference to Table Table1.

[21126] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1358 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21127] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1359 (GAM1359) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21128] GAM1359 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1359 was detected is described hereinabove with reference to Figs. 2-8.

[21129] GAM1359 gene, herein designated GAM GENE, and GAM1359 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21130] GAM1359 gene, herein designated GAM GENE, encodes a GAM1359 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1359 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1359 precursor RNA is designated SEQ ID:1332, and is provided hereinbelow with

reference to the sequence listing part.

[21131] GAM1359 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21132] An enzyme complex designated DICER COMPLEX, dices the GAM1359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1359 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1359 RNA is designated SEQ ID:3008, and is provided hereinbelow with reference to the sequence listing part.

[21133] GAM1359 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1359 target RNA, herein designated GAM TARGET RNA. GAM1359 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21134] GAM1359 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1359 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1359 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1359 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1359 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21135] The complementary binding of GAM1359 RNA, herein designated GAM RNA, to target binding sites on GAM1359 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1359 target RNA, herein designated GAM TARGET RNA, into GAM1359 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21136] It is appreciated that GAM1359 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1359 target genes. The mRNA of each one of this plurality of GAM1359 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1359 RNA, herein designated GAM RNA, and which when bound by GAM1359 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1359

target proteins.

[21137] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1359 gene, herein designated GAM GENE, on one or more GAM1359 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21138] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1359 correlate with, and may be deduced from, the identity of the target genes which GAM1359 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21139] Nucleotide sequences of the GAM1359 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1359 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1359 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1359 are further described hereinbelow with reference to Table Table1.

[21140] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1359 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21141] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1360 (GAM1360) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21142] GAM1360 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1360 was detected is described hereinabove with reference to Figs. 2-8.

[21143] GAM1360 gene, herein designated GAM GENE, and

GAM1360 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21144] GAM1360 gene, herein designated GAM GENE, encodes a GAM1360 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1360 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1360 precursor RNA is designated SEQ ID:1333, and is provided hereinbelow with reference to the sequence listing part.

[21145] GAM1360 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21146] An enzyme complex designated DICER COMPLEX, dices the GAM1360 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1360 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1360 RNA is designated SEQ ID:3009, and is provided hereinbelow with reference to the sequence listing part.

[21147] GAM1360 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1360 target RNA, herein designated GAM TARGET RNA. GAM1360 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21148] GAM1360 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1360 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1360

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1360 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1360 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21149] The complementary binding of GAM1360 RNA, herein designated GAM RNA, to target binding sites on GAM1360 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1360 target RNA, herein designated GAM TARGET RNA, into GAM1360 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[21150] It is appreciated that GAM1360 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1360 target genes. The mRNA of each one of this plurality of GAM1360 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1360 RNA, herein designated GAM RNA, and which when bound by GAM1360 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1360 target proteins.

[21151] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1360 gene, herein designated GAM GENE, on one or more GAM1360 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21152] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1360 correlate with, and may be deduced from, the identity of the target genes which GAM1360 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21153] Nucleotide sequences of the GAM1360 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1360 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1360 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1360 are further described hereinbelow with reference to Table Table1.

[21154] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1360 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21155] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1361 (GAM1361) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21156] GAM1361 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1361 was detected is described hereinabove with reference to Figs. 2-8.

[21157] GAM1361 gene, herein designated GAM GENE, and GAM1361 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21158] GAM1361 gene, herein designated GAM GENE, encodes a GAM1361 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1361 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1361 precursor RNA is designated SEQ ID:1334, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1334 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[21159] GAM1361 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21160] An enzyme complex designated DICER COMPLEX, dices the GAM1361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1361 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1361 RNA is designated SEQ ID:3010, and is provided hereinbelow with reference to the sequence listing part.

[21161] GAM1361 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1361 target RNA, herein designated GAM TARGET RNA. GAM1361 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21162] GAM1361 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1361 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1361 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1361 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1361 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21163] The complementary binding of GAM1361 RNA, herein designated GAM RNA, to target binding sites on GAM1361 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1361 target RNA, herein designated GAM TARGET RNA, into GAM1361 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21164] It is appreciated that GAM1361 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1361 target genes. The mRNA of each one of this plurality of GAM1361 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1361 RNA, herein designated GAM RNA, and which when bound by GAM1361 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1361 target proteins.

[21165] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1361 gene, herein designated GAM GENE, on one or more GAM1361 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21166] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1361 correlate with, and may be deduced from, the identity of the target genes which GAM1361 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21167] Nucleotide sequences of the GAM1361 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1361 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1361 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1361 are further described hereinbelow with reference to Table Table1.

[21168] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1361 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21169] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1362 (GAM1362) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21170] GAM1362 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1362 was detected is described hereinabove with reference to Figs. 2-8.

[21171] GAM1362 gene, herein designated GAM GENE, and GAM1362 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[21172] GAM1362 gene, herein designated GAM GENE, encodes a GAM1362 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1362 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1362 precursor RNA is designated SEQ ID:1335, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1335 is located at position 7933233 relative to contig NT_033899.3, on chromosome 11.

[21173] GAM1362 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98421, which mouse homolog is detected in mouse EST accession BI411194.1.

[21174] GAM1362 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21175] An enzyme complex designated DICER COMPLEX, dices the GAM1362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1362 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1362 RNA is designated SEQ ID:3011, and is provided hereinbelow with reference to the sequence listing part.

[21176] GAM1362 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1362 target RNA, herein designated GAM TARGET RNA. GAM1362 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[21177] GAM1362 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1362 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1362 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1362 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1362 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21178] The complementary binding of GAM1362 RNA, herein

designated GAM RNA, to target binding sites on GAM1362 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1362 target RNA, herein designated GAM TARGET RNA, into GAM1362 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21179] It is appreciated that GAM1362 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1362 target genes. The mRNA of each one of this plurality of GAM1362 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1362 RNA, herein designated GAM RNA, and which when bound by GAM1362 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1362 target proteins.

[21180] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1362 gene, herein designated GAM GENE, on one or more GAM1362 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21181] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1362 correlate with, and may be deduced from, the identity of the target genes which GAM1362 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21182] Nucleotide sequences of the GAM1362 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1362 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1362 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1362 are further described hereinbelow with reference to Table Table1.

[21183] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1362 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21184] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1363 (GAM1363) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21185] GAM1363 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1363 was detected is described hereinabove with reference to Figs. 2-8.

[21186] GAM1363 gene, herein designated GAM GENE, and GAM1363 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21187] GAM1363 gene, herein designated GAM GENE, encodes a GAM1363 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1363 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1363 precursor RNA is designated SEQ ID:1336, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1336 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[21188] GAM1363 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21189] An enzyme complex designated DICER COMPLEX, dices the GAM1363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1363 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1363 RNA is designated SEQ ID:3012, and is provided hereinbelow with reference to the sequence listing part.

[21190] GAM1363 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1363 target RNA, herein designated GAM TARGET RNA. GAM1363 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21191] GAM1363 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1363 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1363 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1363 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1363 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21192] The complementary binding of GAM1363 RNA, herein designated GAM RNA, to target binding sites on GAM1363 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1363 target RNA, herein designated GAM TARGET RNA, into GAM1363 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21193] It is appreciated that GAM1363 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1363 target genes. The mRNA of each one of this plurality of GAM1363 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1363 RNA, herein designated GAM RNA, and which when bound by GAM1363 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1363 target proteins.

[21194] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1363 gene, herein designated GAM GENE, on one or more GAM1363 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21195] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1363 correlate with, and may be deduced from, the identity of the target genes which GAM1363 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21196] Nucleotide sequences of the GAM1363 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1363 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1363 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1363 are further described hereinbelow with reference to Table Table1.

[21197] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1363 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21198] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1364 (GAM1364) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21199] GAM1364 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1364 was detected is described hereinabove with reference to Figs. 2-8.

[21200] GAM1364 gene, herein designated GAM GENE, and GAM1364 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21201] GAM1364 gene, herein designated GAM GENE, encodes a GAM1364 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1364 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1364 precursor RNA is designated SEQ ID:1337, and is provided hereinbelow with reference to the sequence listing part.

[21202] GAM1364 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21203] An enzyme complex designated DICER COMPLEX, dices the GAM1364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1364 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1364 RNA is designated SEQ ID:3013, and is provided hereinbelow with reference to the sequence listing part.

[21204] GAM1364 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1364 target RNA, herein designated GAM TARGET RNA. GAM1364 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21205] GAM1364 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1364 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1364 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1364 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1364 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21206] The complementary binding of GAM1364 RNA, herein designated GAM RNA, to target binding sites on GAM1364

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1364 target RNA, herein designated GAM TARGET RNA, into GAM1364 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21207] It is appreciated that GAM1364 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1364 target genes. The mRNA of each one of this plurality of GAM1364 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1364 RNA, herein designated GAM RNA, and which when bound by GAM1364 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1364 target proteins.

[21208] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1364 gene, herein designated GAM GENE, on one or more GAM1364 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21209] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1364 correlate with, and may be deduced from, the identity of the target genes which GAM1364 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21210] Nucleotide sequences of the GAM1364 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1364 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1364 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1364 are further described hereinbelow with reference to Table Table1.

[21211] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1364 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21212] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1365 (GAM1365) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21213] GAM1365 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1365 was detected is described hereinabove with reference to Figs. 2-8.

[21214] GAM1365 gene, herein designated GAM GENE, and GAM1365 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21215] GAM1365 gene, herein designated GAM GENE, encodes a GAM1365 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1365 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1365 precursor RNA is designated SEQ ID:1338, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1338 is located at position 21515931 relative to contig NT_008705.13, on chromosome 10.

[21216] GAM1365 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21217] An enzyme complex designated DICER COMPLEX, dices the GAM1365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1365 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1365 RNA is designated SEQ ID:3014, and is provided hereinbelow with reference to the sequence listing part.

[21218] GAM1365 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1365 target RNA, herein designated GAM TARGET RNA. GAM1365 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21219] GAM1365 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1365 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1365 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1365 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1365 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21220] The complementary binding of GAM1365 RNA, herein designated GAM RNA, to target binding sites on GAM1365 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1365 target RNA, herein designated GAM TARGET RNA, into GAM1365 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21221] It is appreciated that GAM1365 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1365 target genes. The mRNA of each one of this plurality of GAM1365 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1365 RNA, herein designated GAM RNA, and which when bound by GAM1365 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1365 target proteins.

[21222] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1365 gene, herein designated GAM GENE, on one or more GAM1365 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21223] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1365 correlate with, and may

be deduced from, the identity of the target genes which GAM1365 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21224] Nucleotide sequences of the GAM1365 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1365 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1365 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1365 are further described hereinbelow with reference to Table Table1.

[21225] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1365 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21226] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1366 (GAM1366) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21227] GAM1366 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1366 was detected is described hereinabove with reference to Figs. 2-8.

[21228] GAM1366 gene, herein designated GAM GENE, and GAM1366 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21229] GAM1366 gene, herein designated GAM GENE, encodes a GAM1366 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1366 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1366 precursor RNA is designated SEQ ID:1339, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1339 is located at position 3263798 relative to contig NT_028392.4, on chromosome 20.

[21230] GAM1366 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21231] An enzyme complex designated DICER COMPLEX, dices the GAM1366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1366 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1366 RNA is designated SEQ ID:3015, and is provided hereinbelow with reference to the sequence listing part.

[21232] GAM1366 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1366 target RNA, herein designated GAM TARGET RNA. GAM1366 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[21233] GAM1366 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1366 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1366 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1366 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1366 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21234] The complementary binding of GAM1366 RNA, herein

designated GAM RNA, to target binding sites on GAM1366 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1366 target RNA, herein designated GAM TARGET RNA, into GAM1366 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21235] It is appreciated that GAM1366 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1366 target genes. The mRNA of each one of this plurality of GAM1366 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1366 RNA, herein designated GAM RNA, and which when bound by GAM1366 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1366 target proteins.

[21236] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1366 gene, herein designated GAM GENE, on one or more GAM1366 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21237] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1366 correlate with, and may be deduced from, the identity of the target genes which GAM1366 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21238] Nucleotide sequences of the GAM1366 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1366 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1366 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1366 are further described hereinbelow with reference to Table Table1.

[21239] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1366 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21240] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1367 (GAM1367) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21241] GAM1367 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1367 was detected is described hereinabove with reference to Figs. 2-8.

[21242] GAM1367 gene, herein designated GAM GENE, and GAM1367 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21243] GAM1367 gene, herein designated GAM GENE, encodes a GAM1367 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1367 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1367 precursor RNA is designated SEQ ID:1340, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1340 is located at position 3434852 relative to contig NT_009714.13, on chromosome 12.

[21244] GAM1367 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98683, which mouse homolog is detected in mouse EST accession BG288438.1.

[21245] GAM1367 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21246] An enzyme complex designated DICER COMPLEX, dices the GAM1367 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1367 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1367 RNA is designated SEQ ID:3016, and is provided hereinbelow with reference to the sequence listing part.

[21247] GAM1367 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1367 target RNA, herein designated GAM TARGET RNA. GAM1367 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21248] GAM1367 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1367 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1367

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1367 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1367 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21249] The complementary binding of GAM1367 RNA, herein designated GAM RNA, to target binding sites on GAM1367 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1367 target RNA, herein designated GAM TARGET RNA, into GAM1367 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[21250] It is appreciated that GAM1367 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1367 target genes. The mRNA of each one of this plurality of GAM1367 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1367 RNA, herein designated GAM RNA, and which when bound by GAM1367 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1367 target proteins.

[21251] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1367 gene, herein designated GAM GENE, on one or more GAM1367 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21252] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1367 correlate with, and may be deduced from, the identity of the target genes which GAM1367 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21253] Nucleotide sequences of the GAM1367 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1367 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1367 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1367 are further described hereinbelow with reference to Table Table1.

[21254] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1367 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21255] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1368 (GAM1368) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21256] GAM1368 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1368 was detected is described hereinabove with reference to Figs. 2-8.

[21257] GAM1368 gene, herein designated GAM GENE, and GAM1368 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21258] GAM1368 gene, herein designated GAM GENE, encodes a GAM1368 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1368 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1368 precursor RNA is designated SEQ ID:1341, and is provided hereinbelow with reference to the sequence listing part.

[21259] GAM1368 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1368 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21260] An enzyme complex designated DICER COMPLEX, dices the GAM1368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1368 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1368 RNA is designated SEQ ID:3017, and is provided hereinbelow with reference to the sequence listing part.

[21261] GAM1368 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1368 target RNA, herein designated GAM TARGET

RNA. GAM1368 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21262] GAM1368 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1368 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1368 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1368 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1368 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21263] The complementary binding of GAM1368 RNA, herein designated GAM RNA, to target binding sites on GAM1368 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1368 target RNA, herein designated GAM TARGET RNA, into GAM1368 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21264] It is appreciated that GAM1368 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1368 target genes. The mRNA of each one of this plurality of GAM1368 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1368 RNA, herein designated GAM RNA, and which when bound by GAM1368 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1368 target proteins.

[21265] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1368 gene, herein designated GAM GENE, on one or more GAM1368 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21266] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1368 correlate with, and may be deduced from, the identity of the target genes which GAM1368 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21267] Nucleotide sequences of the GAM1368 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1368 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1368 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1368 are further described hereinbelow with reference to Table Table1.

[21268] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1368 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21269] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1369 (GAM1369) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21270] GAM1369 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1369 was detected is described hereinabove with reference to Figs. 2-8.

[21271] GAM1369 gene, herein designated GAM GENE, and GAM1369 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21272] GAM1369 gene, herein designated GAM GENE, encodes a

GAM1369 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1369 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1369 precursor RNA is designated SEQ ID:1342, and is provided hereinbelow with reference to the sequence listing part.

[21273] GAM1369 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21274] An enzyme complex designated DICER COMPLEX, dices the GAM1369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1369 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1369 RNA is designated SEQ ID:3018, and is provided hereinbelow with reference to the sequence listing part.

[21275] GAM1369 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1369 target RNA, herein designated GAM TARGET RNA. GAM1369 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21276] GAM1369 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1369 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1369 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1369 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1369 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21277] The complementary binding of GAM1369 RNA, herein designated GAM RNA, to target binding sites on GAM1369 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1369 target RNA, herein designated GAM TARGET RNA, into GAM1369 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21278] It is appreciated that GAM1369 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1369 target genes. The mRNA of each one of this plurality of GAM1369 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1369 RNA, herein designated GAM RNA, and which when bound by GAM1369 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1369 target proteins.

[21279] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1369 gene, herein designated GAM GENE, on one or more GAM1369 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[21280] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1369 correlate with, and may be deduced from, the identity of the target genes which GAM1369 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21281] Nucleotide sequences of the GAM1369 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1369 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1369 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1369 are further described hereinbelow with reference to Table Table1.

[21282] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1369 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21283] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1370 (GAM1370) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[21284] GAM1370 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1370 was detected is described hereinabove with reference to Figs. 2-8.

[21285] GAM1370 gene, herein designated GAM GENE, and GAM1370 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21286] GAM1370 gene, herein designated GAM GENE, encodes a GAM1370 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1370 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1370 precursor RNA is designated SEQ ID:1343, and is provided hereinbelow with reference to the sequence listing part.

[21287] GAM1370 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21288] An enzyme complex designated DICER COMPLEX, dices the GAM1370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1370 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1370 RNA is designated SEQ ID:3019, and is provided hereinbelow with reference to the sequence listing part.

[21289] GAM1370 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1370 target RNA, herein designated GAM TARGET RNA. GAM1370 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21290] GAM1370 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1370 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1370 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1370 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1370 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21291] The complementary binding of GAM1370 RNA, herein designated GAM RNA, to target binding sites on GAM1370 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1370 target RNA, herein designated GAM TARGET RNA, into GAM1370 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21292] It is appreciated that GAM1370 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1370 target genes. The mRNA of each one of this plurality of GAM1370 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1370 RNA, herein designated GAM RNA, and which when bound by GAM1370 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1370 target proteins.

[21293] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1370 gene, herein designated GAM GENE, on one or more GAM1370 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21294] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1370 correlate with, and may be deduced from, the identity of the target genes which GAM1370 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21295] Nucleotide sequences of the GAM1370 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1370 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1370 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1370 are further described hereinbelow with reference to Table Table1.

[21296] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1370 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21297] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1371 (GAM1371) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21298] GAM1371 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1371 was detected is described hereinabove with reference to Figs. 2-8.

[21299] GAM1371 gene, herein designated GAM GENE, and GAM1371 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21300] GAM1371 gene, herein designated GAM GENE, encodes a GAM1371 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1371 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1371 precursor RNA is designated SEQ ID:1344, and is provided hereinbelow with reference to the sequence listing part.

[21301] GAM1371 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21302] An enzyme complex designated DICER COMPLEX, dices the GAM1371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1371 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1371 RNA is designated SEQ ID:3020, and is provided hereinbelow with reference to the sequence listing part.

[21303] GAM1371 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1371 target RNA, herein designated GAM TARGET RNA. GAM1371 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21304] GAM1371 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1371 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1371 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1371 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1371 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21305] The complementary binding of GAM1371 RNA, herein designated GAM RNA, to target binding sites on GAM1371 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1371 target RNA, herein designated GAM TARGET RNA, into GAM1371 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21306] It is appreciated that GAM1371 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1371 target genes. The mRNA of each one of this plurality of GAM1371 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1371 RNA, herein designated GAM RNA, and which when bound by GAM1371 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1371 target proteins.

[21307] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1371 gene, herein designated GAM GENE, on one or more GAM1371 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21308] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1371 correlate with, and may

be deduced from, the identity of the target genes which GAM1371 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21309] Nucleotide sequences of the GAM1371 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1371 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1371 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1371 are further described hereinbelow with reference to Table Table1.

[21310] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1371 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21311] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1372 (GAM1372) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21312] GAM1372 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1372 was detected is described hereinabove with reference to Figs. 2-8.

[21313] GAM1372 gene, herein designated GAM GENE, and GAM1372 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21314] GAM1372 gene, herein designated GAM GENE, encodes a GAM1372 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1372 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1372 precursor RNA is designated SEQ ID:1345, and is provided hereinbelow with reference to the sequence listing part.

[21315] GAM1372 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21316] An enzyme complex designated DICER COMPLEX, dices the GAM1372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1372 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1372 RNA is designated SEQ ID:3021, and is provided hereinbelow with reference to the sequence listing part.

[21317] GAM1372 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1372 target RNA, herein designated GAM TARGET RNA. GAM1372 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21318] GAM1372 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1372 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1372 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1372 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1372 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21319] The complementary binding of GAM1372 RNA, herein designated GAM RNA, to target binding sites on GAM1372 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1372 target RNA, herein designated GAM TARGET RNA, into GAM1372 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21320] It is appreciated that GAM1372 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1372 target genes. The mRNA of each one of this plurality of GAM1372 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1372 RNA, herein designated GAM RNA, and which when bound by GAM1372 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1372 target proteins.

[21321] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1372 gene, herein designated GAM GENE, on one or more GAM1372 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21322] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1372 correlate with, and may be deduced from, the identity of the target genes which GAM1372 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21323] Nucleotide sequences of the GAM1372 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1372 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1372 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1372 are further described hereinbelow with reference to Table Table1.

[21324] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1372 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21325] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1373 (GAM1373) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21326] GAM1373 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1373 was detected is described hereinabove with reference to Figs. 2-8.

[21327] GAM1373 gene, herein designated GAM GENE, and GAM1373 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21328] GAM1373 gene, herein designated GAM GENE, encodes a GAM1373 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1373 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1373 precursor RNA is

designated SEQ ID:1346, and is provided hereinbelow with reference to the sequence listing part.

[21329] GAM1373 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21330] An enzyme complex designated DICER COMPLEX, dices the GAM1373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1373 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1373 RNA is designated SEQ ID:3022, and is provided hereinbelow with reference to the sequence

listing part.

[21331] GAM1373 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1373 target RNA, herein designated GAM TARGET RNA. GAM1373 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21332] GAM1373 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1373 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1373 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1373 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1373 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21333] The complementary binding of GAM1373 RNA, herein designated GAM RNA, to target binding sites on GAM1373 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1373 target RNA, herein designated GAM TARGET RNA, into GAM1373 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21334] It is appreciated that GAM1373 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1373 target genes. The mRNA of each one of this plurality of GAM1373 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1373 RNA, herein designated GAM RNA, and which when bound by GAM1373 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1373 target proteins.

[21335] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1373 gene, herein designated GAM GENE, on one or more GAM1373 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21336] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1373 correlate with, and may be deduced from, the identity of the target genes which GAM1373 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21337] Nucleotide sequences of the GAM1373 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1373 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1373 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1373 are further described hereinbelow with reference to Table Table1.

[21338] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1373 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21339] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1374 (GAM1374) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21340] GAM1374 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1374 was detected is described hereinabove with reference to Figs. 2-8.

[21341] GAM1374 gene, herein designated GAM GENE, and GAM1374 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21342] GAM1374 gene, herein designated GAM GENE, encodes a GAM1374 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1374 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1374 precursor RNA is designated SEQ ID:1347, and is provided hereinbelow with reference to the sequence listing part.

[21343] GAM1374 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21344] An enzyme complex designated DICER COMPLEX, dices

the GAM1374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1374 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1374 RNA is designated SEQ ID:3023, and is provided hereinbelow with reference to the sequence listing part.

[21345] GAM1374 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1374 target RNA, herein designated GAM TARGET RNA. GAM1374 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21346] GAM1374 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1374 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1374 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1374 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1374 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21347] The complementary binding of GAM1374 RNA, herein designated GAM RNA, to target binding sites on GAM1374 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1374 target RNA, herein designated GAM TARGET RNA, into GAM1374 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21348] It is appreciated that GAM1374 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1374 target genes. The mRNA of each one of this plurality of GAM1374 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1374 RNA, herein designated GAM RNA, and which when bound by GAM1374 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1374 target proteins.

[21349] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1374 gene, herein designated GAM GENE, on one or more GAM1374 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21350] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1374 correlate with, and may be deduced from, the identity of the target genes which GAM1374 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21351] Nucleotide sequences of the GAM1374 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1374 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1374 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1374 are further described hereinbelow with reference to Table Table1.

[21352] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1374 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21353] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1375 (GAM1375) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21354] GAM1375 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1375 was detected is described hereinabove with reference to Figs. 2-8.

[21355] GAM1375 gene, herein designated GAM GENE, and GAM1375 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21356] GAM1375 gene, herein designated GAM GENE, encodes a GAM1375 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1375 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1375 precursor RNA is designated SEQ ID:1348, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1348 is located at position 1643555 rela-

tive to contig NT_005832.12, on chromosome 3.

[21357] GAM1375 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21358] An enzyme complex designated DICER COMPLEX, dices the GAM1375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1375 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 96%) nucleotide sequence of GAM1375 RNA is designated SEQ ID:3024, and is provided hereinbelow with reference to the sequence listing part.

[21359] GAM1375 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1375 target RNA, herein designated GAM TARGET RNA. GAM1375 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21360] GAM1375 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1375 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1375 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1375 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1375 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21361] The complementary binding of GAM1375 RNA, herein designated GAM RNA, to target binding sites on GAM1375 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1375 target RNA, herein designated GAM TARGET RNA, into GAM1375 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21362] It is appreciated that GAM1375 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1375 target genes. The mRNA of each one of this plurality of GAM1375 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1375 RNA, herein designated GAM RNA, and which when bound by GAM1375 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1375

target proteins.

[21363] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1375 gene, herein designated GAM GENE, on one or more GAM1375 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21364] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1375 correlate with, and may be deduced from, the identity of the target genes which GAM1375 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21365] Nucleotide sequences of the GAM1375 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1375 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1375 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1375 are further described hereinbelow with reference to Table Table1.

[21366] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1375 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21367] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1376 (GAM1376) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21368] GAM1376 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1376 was detected is described hereinabove with reference to Figs. 2-8.

[21369] GAM1376 gene, herein designated GAM GENE, and

GAM1376 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21370] GAM1376 gene, herein designated GAM GENE, encodes a GAM1376 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1376 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1376 precursor RNA is designated SEQ ID:1349, and is provided hereinbelow with reference to the sequence listing part.

[21371] GAM1376 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98696, which mouse homolog is detected in mouse EST accession AW476255.1.

[21372] GAM1376 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21373] An enzyme complex designated DICER COMPLEX, dices the GAM1376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1376 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1376 RNA is designated SEQ ID:3025, and is provided hereinbelow with reference to the sequence listing part.

[21374] GAM1376 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1376 target RNA, herein designated GAM TARGET RNA. GAM1376 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21375] GAM1376 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1376 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1376 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1376 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1376 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21376] The complementary binding of GAM1376 RNA, herein designated GAM RNA, to target binding sites on GAM1376

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1376 target RNA, herein designated GAM TARGET RNA, into GAM1376 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21377] It is appreciated that GAM1376 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1376 target genes. The mRNA of each one of this plurality of GAM1376 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1376 RNA, herein designated GAM RNA, and which when bound by GAM1376 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1376 target proteins.

[21378] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1376 gene, herein designated GAM GENE, on one or more GAM1376 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21379] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1376 correlate with, and may be deduced from, the identity of the target genes which GAM1376 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21380] Nucleotide sequences of the GAM1376 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1376 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1376 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1376 are further described hereinbelow with reference to Table Table1.

[21381] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1376 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21382] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1377 (GAM1377) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21383] GAM1377 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1377 was detected is described hereinabove with reference to Figs. 2-8.

[21384] GAM1377 gene, herein designated GAM GENE, and GAM1377 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21385] GAM1377 gene, herein designated GAM GENE, encodes a GAM1377 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1377 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1377 precursor RNA is designated SEQ ID:1350, and is provided hereinbelow with reference to the sequence listing part.

[21386] GAM1377 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21387] An enzyme complex designated DICER COMPLEX, dices the GAM1377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1377 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1377 RNA is designated SEQ ID:3026, and

is provided hereinbelow with reference to the sequence listing part.

[21388] GAM1377 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1377 target RNA, herein designated GAM TARGET RNA. GAM1377 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21389] GAM1377 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1377 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1377 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1377 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1377 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21390] The complementary binding of GAM1377 RNA, herein designated GAM RNA, to target binding sites on GAM1377 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1377 target RNA, herein designated GAM TARGET RNA, into GAM1377 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21391] It is appreciated that GAM1377 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1377 target genes. The mRNA of each one of this plurality of GAM1377 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1377 RNA, herein designated GAM RNA, and which when bound by

GAM1377 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1377 target proteins.

[21392] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1377 gene, herein designated GAM GENE, on one or more GAM1377 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21393] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1377 correlate with, and may be deduced from, the identity of the target genes which GAM1377 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[21394] Nucleotide sequences of the GAM1377 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1377 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1377 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1377 are further described hereinbelow with reference to Table Table1.

[21395] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1377 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21396] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1378 (GAM1378) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21397] GAM1378 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1378 was detected is described hereinabove

with reference to Figs. 2-8.

[21398] GAM1378 gene, herein designated GAM GENE, and GAM1378 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21399] GAM1378 gene, herein designated GAM GENE, encodes a GAM1378 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1378 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1378 precursor RNA is designated SEQ ID:1351, and is provided hereinbelow with reference to the sequence listing part.

[21400] GAM1378 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21401] An enzyme complex designated DICER COMPLEX, dices the GAM1378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1378 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1378 RNA is designated SEQ ID:3027, and is provided hereinbelow with reference to the sequence listing part.

[21402] GAM1378 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1378 target RNA, herein designated GAM TARGET RNA. GAM1378 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21403] GAM1378 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1378 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1378 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1378 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1378 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21404] The complementary binding of GAM1378 RNA, herein designated GAM RNA, to target binding sites on GAM1378 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1378 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1378 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21405] It is appreciated that GAM1378 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1378 target genes. The mRNA of each one of this plurality of GAM1378 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1378 RNA, herein designated GAM RNA, and which when bound by GAM1378 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1378 target proteins.

[21406] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1378 gene, herein designated GAM GENE, on one or more GAM1378 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21407] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1378 correlate with, and may be deduced from, the identity of the target genes which GAM1378 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21408] Nucleotide sequences of the GAM1378 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1378 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1378 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1378 are further described hereinbelow with reference to Table Table1.

[21409] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1378 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[21410] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1379 (GAM1379) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21411] GAM1379 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1379 was detected is described hereinabove with reference to Figs. 2-8.

[21412] GAM1379 gene, herein designated GAM GENE, and GAM1379 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21413] GAM1379 gene, herein designated GAM GENE, encodes a GAM1379 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1379 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1379 precursor RNA is designated SEQ ID:1352, and is provided hereinbelow with reference to the sequence listing part.

[21414] GAM1379 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21415] An enzyme complex designated DICER COMPLEX, dices the GAM1379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1379 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1379 RNA is designated SEQ ID:3028, and is provided hereinbelow with reference to the sequence listing part.

[21416] GAM1379 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1379 target RNA, herein designated GAM TARGET RNA. GAM1379 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21417] GAM1379 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1379 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1379 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1379 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1379 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21418] The complementary binding of GAM1379 RNA, herein designated GAM RNA, to target binding sites on GAM1379 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1379 target RNA, herein designated GAM TARGET RNA, into GAM1379 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21419] It is appreciated that GAM1379 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1379 target genes. The mRNA of each one of this plurality of GAM1379 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1379 RNA, herein designated GAM RNA, and which when bound by GAM1379 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1379 target proteins.

[21420] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1379 gene, herein designated GAM GENE, on one or more GAM1379 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21421] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1379 correlate with, and may be deduced from, the identity of the target genes which GAM1379 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21422] Nucleotide sequences of the GAM1379 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1379 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1379 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1379 are further described hereinbelow with reference to Table Table1.

[21423] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1379 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21424] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1380 (GAM1380) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21425] GAM1380 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1380 was detected is described hereinabove with reference to Figs. 2-8.

[21426] GAM1380 gene, herein designated GAM GENE, and GAM1380 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21427] GAM1380 gene, herein designated GAM GENE, encodes a GAM1380 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1380 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1380 precursor RNA is designated SEQ ID:1353, and is provided hereinbelow with reference to the sequence listing part.

[21428] GAM1380 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21429] An enzyme complex designated DICER COMPLEX, dices

the GAM1380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1380 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1380 RNA is designated SEQ ID:3029, and is provided hereinbelow with reference to the sequence listing part.

[21430] GAM1380 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1380 target RNA, herein designated GAM TARGET RNA. GAM1380 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21431] GAM1380 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1380 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1380 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1380 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1380 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21432] The complementary binding of GAM1380 RNA, herein designated GAM RNA, to target binding sites on GAM1380 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1380 target RNA, herein designated GAM TARGET RNA, into GAM1380 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21433] It is appreciated that GAM1380 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1380 target genes. The mRNA of each one of this plurality of GAM1380 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1380 RNA, herein designated GAM RNA, and which when bound by GAM1380 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1380 target proteins.

[21434] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1380 gene, herein designated GAM GENE, on one or more GAM1380 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21435] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1380 correlate with, and may be deduced from, the identity of the target genes which GAM1380 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21436] Nucleotide sequences of the GAM1380 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1380 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1380 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1380 are further described hereinbelow with reference to Table Table1.

[21437] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1380 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21438] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1381 (GAM1381) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21439] GAM1381 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1381 was detected is described hereinabove with reference to Figs. 2-8.

[21440] GAM1381 gene, herein designated GAM GENE, and GAM1381 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21441] GAM1381 gene, herein designated GAM GENE, encodes a GAM1381 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1381 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1381 precursor RNA is designated SEQ ID:1354, and is provided hereinbelow with reference to the sequence listing part.

[21442] GAM1381 has a highly conserved, expressed mouse ho-

molog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99262, which mouse homolog is detected in mouse EST accession BI871906.1.

[21443] GAM1381 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21444] An enzyme complex designated DICER COMPLEX, dices the GAM1381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1381 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1381 RNA is designated SEQ ID:3030, and is provided hereinbelow with reference to the sequence listing part.

[21445] GAM1381 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1381 target RNA, herein designated GAM TARGET RNA. GAM1381 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21446] GAM1381 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1381 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1381 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1381 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1381 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21447] The complementary binding of GAM1381 RNA, herein designated GAM RNA, to target binding sites on GAM1381 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1381 target RNA, herein designated GAM TARGET RNA, into GAM1381 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21448] It is appreciated that GAM1381 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1381 target genes. The mRNA of each one of this plurality of GAM1381 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1381 RNA,

herein designated GAM RNA, and which when bound by GAM1381 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1381 target proteins.

[21449] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1381 gene, herein designated GAM GENE, on one or more GAM1381 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21450] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1381 correlate with, and may be deduced from, the identity of the target genes which

GAM1381 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21451] Nucleotide sequences of the GAM1381 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1381 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1381 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1381 are further described hereinbelow with reference to Table Table1.

[21452] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1381 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21453] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1382 (GAM1382) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21454] GAM1382 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1382 was detected is described hereinabove with reference to Figs. 2-8.

[21455] GAM1382 gene, herein designated GAM GENE, and GAM1382 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21456] GAM1382 gene, herein designated GAM GENE, encodes a GAM1382 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1382 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1382 precursor RNA is designated SEQ ID:1355, and is provided hereinbelow with reference to the sequence listing part.

[21457] GAM1382 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[21458] An enzyme complex designated DICER COMPLEX, dices the GAM1382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1382 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1382 RNA is designated SEQ ID:3031, and is provided hereinbelow with reference to the sequence listing part.

[21459] GAM1382 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1382 target RNA, herein designated GAM TARGET RNA. GAM1382 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21460] GAM1382 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1382 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1382 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1382 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1382 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21461] The complementary binding of GAM1382 RNA, herein designated GAM RNA, to target binding sites on GAM1382 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1382 target RNA, herein designated GAM TARGET RNA, into GAM1382 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21462] It is appreciated that GAM1382 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1382 target genes. The mRNA of each one of this plurality of GAM1382 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1382 RNA, herein designated GAM RNA, and which when bound by GAM1382 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1382 target proteins.

[21463] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1382 gene, herein designated GAM GENE, on one or more GAM1382 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21464] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1382 correlate with, and may be deduced from, the identity of the target genes which GAM1382 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21465] Nucleotide sequences of the GAM1382 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1382 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1382 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1382 are further described hereinbelow with reference to Table Table1.

[21466] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1382 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21467] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1383 (GAM1383) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21468] GAM1383 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1383 was detected is described hereinabove with reference to Figs. 2-8.

[21469] GAM1383 gene, herein designated GAM GENE, and GAM1383 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21470] GAM1383 gene, herein designated GAM GENE, encodes a GAM1383 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1383 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1383 precursor RNA is designated SEQ ID:1356, and is provided hereinbelow with

reference to the sequence listing part.

[21471] GAM1383 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21472] An enzyme complex designated DICER COMPLEX, dices the GAM1383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1383 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1383 RNA is designated SEQ ID:3032, and is provided hereinbelow with reference to the sequence listing part.

[21473] GAM1383 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1383 target RNA, herein designated GAM TARGET RNA. GAM1383 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21474] GAM1383 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1383 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1383 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1383 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1383 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21475] The complementary binding of GAM1383 RNA, herein designated GAM RNA, to target binding sites on GAM1383 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1383 target RNA, herein designated GAM TARGET RNA, into GAM1383 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21476] It is appreciated that GAM1383 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1383 target genes. The mRNA of each one of this plurality of GAM1383 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1383 RNA, herein designated GAM RNA, and which when bound by GAM1383 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1383

target proteins.

[21477] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1383 gene, herein designated GAM GENE, on one or more GAM1383 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21478] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1383 correlate with, and may be deduced from, the identity of the target genes which GAM1383 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21479] Nucleotide sequences of the GAM1383 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1383 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1383 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1383 are further described hereinbelow with reference to Table Table1.

[21480] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1383 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21481] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1384 (GAM1384) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21482] GAM1384 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1384 was detected is described hereinabove with reference to Figs. 2-8.

[21483] GAM1384 gene, herein designated GAM GENE, and

GAM1384 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21484] GAM1384 gene, herein designated GAM GENE, encodes a GAM1384 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1384 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1384 precursor RNA is designated SEQ ID:1357, and is provided hereinbelow with reference to the sequence listing part.

[21485] GAM1384 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21486] An enzyme complex designated DICER COMPLEX, dices the GAM1384 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1384 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1384 RNA is designated SEQ ID:3033, and is provided hereinbelow with reference to the sequence listing part.

[21487] GAM1384 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1384 target RNA, herein designated GAM TARGET RNA. GAM1384 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21488] GAM1384 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1384 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1384

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1384 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1384 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21489] The complementary binding of GAM1384 RNA, herein designated GAM RNA, to target binding sites on GAM1384 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1384 target RNA, herein designated GAM TARGET RNA, into GAM1384 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[21490] It is appreciated that GAM1384 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1384 target genes. The mRNA of each one of this plurality of GAM1384 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1384 RNA, herein designated GAM RNA, and which when bound by GAM1384 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1384 target proteins.

[21491] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1384 gene, herein designated GAM GENE, on one or more GAM1384 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21492] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1384 correlate with, and may be deduced from, the identity of the target genes which GAM1384 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21493] Nucleotide sequences of the GAM1384 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1384 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1384 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1384 are further described hereinbelow with reference to Table Table1.

[21494] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1384 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21495] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1385 (GAM1385) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21496] GAM1385 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1385 was detected is described hereinabove with reference to Figs. 2-8.

[21497] GAM1385 gene, herein designated GAM GENE, and GAM1385 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21498] GAM1385 gene, herein designated GAM GENE, encodes a GAM1385 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1385 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1385 precursor RNA is designated SEQ ID:1358, and is provided hereinbelow with reference to the sequence listing part.

[21499] GAM1385 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1385 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21500] An enzyme complex designated DICER COMPLEX, dices the GAM1385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1385 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1385 RNA is designated SEQ ID:3034, and is provided hereinbelow with reference to the sequence listing part.

[21501] GAM1385 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1385 target RNA, herein designated GAM TARGET

RNA. GAM1385 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21502] GAM1385 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1385 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1385 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1385 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1385 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21503] The complementary binding of GAM1385 RNA, herein designated GAM RNA, to target binding sites on GAM1385 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1385 target RNA, herein designated GAM TARGET RNA, into GAM1385 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21504] It is appreciated that GAM1385 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1385 target genes. The mRNA of each one of this plurality of GAM1385 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1385 RNA, herein designated GAM RNA, and which when bound by GAM1385 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1385 target proteins.

[21505] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1385 gene, herein designated GAM GENE, on one or more GAM1385 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21506] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1385 correlate with, and may be deduced from, the identity of the target genes which GAM1385 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21507] Nucleotide sequences of the GAM1385 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1385 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1385 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1385 are further described hereinbelow with reference to Table Table1.

[21508] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1385 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21509] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1386 (GAM1386) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21510] GAM1386 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1386 was detected is described hereinabove with reference to Figs. 2-8.

[21511] GAM1386 gene, herein designated GAM GENE, and GAM1386 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21512] GAM1386 gene, herein designated GAM GENE, encodes a

GAM1386 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1386 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1386 precursor RNA is designated SEQ ID:1359, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1359 is located at position 264518 relative to contig NT_029419.8, on chromosome 12.

[21513] GAM1386 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21514] An enzyme complex designated DICER COMPLEX, dices the GAM1386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1386 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1386 RNA is designated SEQ ID:3035, and is provided hereinbelow with reference to the sequence listing part.

[21515] GAM1386 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1386 target RNA, herein designated GAM TARGET RNA. GAM1386 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21516] GAM1386 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1386 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1386 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1386 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1386 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21517] The complementary binding of GAM1386 RNA, herein designated GAM RNA, to target binding sites on GAM1386 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1386 target RNA, herein designated GAM TARGET RNA, into GAM1386 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21518] It is appreciated that GAM1386 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1386 target genes. The mRNA of each one of this plurality of GAM1386 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1386 RNA, herein designated GAM RNA, and which when bound by GAM1386 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1386 target proteins.

[21519] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1386 gene, herein designated GAM GENE, on one or more GAM1386 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21520] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1386 correlate with, and may be deduced from, the identity of the target genes which GAM1386 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21521] Nucleotide sequences of the GAM1386 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1386 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1386 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1386 are further described hereinbelow with reference to Table Table1.

[21522] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1386 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21523] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1387 (GAM1387) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21524] GAM1387 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1387 was detected is described hereinabove with reference to Figs. 2-8.

[21525] GAM1387 gene, herein designated GAM GENE, and GAM1387 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21526] GAM1387 gene, herein designated GAM GENE, encodes a GAM1387 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1387 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1387 precursor RNA is designated SEQ ID:1360, and is provided hereinbelow with reference to the sequence listing part.

[21527] GAM1387 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1387 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21528] An enzyme complex designated DICER COMPLEX, dices the GAM1387 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1387 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1387 RNA is designated SEQ ID:3036, and is provided hereinbelow with reference to the sequence listing part.

[21529] GAM1387 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1387 target RNA, herein designated GAM TARGET RNA. GAM1387 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21530] GAM1387 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1387 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1387 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1387 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1387 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21531] The complementary binding of GAM1387 RNA, herein designated GAM RNA, to target binding sites on GAM1387 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1387 target RNA, herein designated GAM TARGET RNA, into GAM1387 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21532] It is appreciated that GAM1387 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1387 target genes. The mRNA of each one of this plurality of GAM1387 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1387 RNA, herein designated GAM RNA, and which when bound by GAM1387 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1387 target proteins.

[21533] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1387 gene, herein designated GAM GENE, on one or more GAM1387 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21534] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1387 correlate with, and may be deduced from, the identity of the target genes which GAM1387 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21535] Nucleotide sequences of the GAM1387 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1387 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1387 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1387 are further described hereinbelow with reference to Table Table1.

[21536] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1387 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21537] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1388 (GAM1388) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21538] GAM1388 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1388 was detected is described hereinabove with reference to Figs. 2-8.

[21539] GAM1388 gene, herein designated GAM GENE, and GAM1388 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21540] GAM1388 gene, herein designated GAM GENE, encodes a GAM1388 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1388 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1388 precursor RNA is designated SEQ ID:1361, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1361 is located at position 2987896 relative to contig NT_006713.11, on chromosome 5.

[21541] GAM1388 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21542] An enzyme complex designated DICER COMPLEX, dices the GAM1388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1388 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1388 RNA is designated SEQ ID:3037, and is provided hereinbelow with reference to the sequence listing part.

[21543] GAM1388 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1388 target RNA, herein designated GAM TARGET RNA. GAM1388 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21544] GAM1388 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1388 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1388 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1388 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1388 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21545] The complementary binding of GAM1388 RNA, herein designated GAM RNA, to target binding sites on GAM1388 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1388 target RNA, herein designated GAM TARGET RNA, into GAM1388 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21546] It is appreciated that GAM1388 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1388 target genes. The mRNA of each one of this plurality of GAM1388 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1388 RNA, herein designated GAM RNA, and which when bound by GAM1388 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1388 target proteins.

[21547] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1388 gene, herein designated GAM GENE, on one or more GAM1388 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21548] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1388 correlate with, and may be deduced from, the identity of the target genes which GAM1388 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21549] Nucleotide sequences of the GAM1388 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1388 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1388 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1388 are further described hereinbelow with reference to Table Table1.

[21550] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1388 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21551] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1389 (GAM1389) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21552] GAM1389 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1389 was detected is described hereinabove with reference to Figs. 2-8.

[21553] GAM1389 gene, herein designated GAM GENE, and GAM1389 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21554] GAM1389 gene, herein designated GAM GENE, encodes a GAM1389 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1389 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1389 precursor RNA is designated SEQ ID:1362, and is provided hereinbelow with reference to the sequence listing part.

[21555] GAM1389 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21556] An enzyme complex designated DICER COMPLEX, dices the GAM1389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1389 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1389 RNA is designated SEQ ID:3038, and is provided hereinbelow with reference to the sequence listing part.

[21557] GAM1389 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1389 target RNA, herein designated GAM TARGET RNA. GAM1389 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21558] GAM1389 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1389 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1389 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1389 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1389 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[21559] The complementary binding of GAM1389 RNA, herein designated GAM RNA, to target binding sites on GAM1389 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1389 target RNA, herein designated GAM TARGET RNA, into GAM1389 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21560] It is appreciated that GAM1389 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1389 target genes. The mRNA of each one of this plurality of GAM1389 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1389 RNA, herein designated GAM RNA, and which when bound by GAM1389 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1389 target proteins.

[21561] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1389 gene, herein designated GAM GENE, on one or

more GAM1389 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21562] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1389 correlate with, and may be deduced from, the identity of the target genes which GAM1389 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21563] Nucleotide sequences of the GAM1389 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1389 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1389 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1389 are further de-

scribed hereinbelow with reference to Table Table1.

[21564] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1389 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21565] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1390 (GAM1390) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21566] GAM1390 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1390 was detected is described hereinabove with reference to Figs. 2-8.

[21567] GAM1390 gene, herein designated GAM GENE, and GAM1390 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21568] GAM1390 gene, herein designated GAM GENE, encodes a GAM1390 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1390 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1390 precursor RNA is designated SEQ ID:1363, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1363 is located at position 1309377 relative to contig NT_033944.3, on chromosome 6.

[21569] GAM1390 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21570] An enzyme complex designated DICER COMPLEX, dices the GAM1390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1390 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1390 RNA is designated SEQ ID:3039, and is provided hereinbelow with reference to the sequence listing part.

[21571] GAM1390 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1390 target RNA, herein designated GAM TARGET RNA. GAM1390 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21572] GAM1390 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1390 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1390 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1390 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1390 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21573] The complementary binding of GAM1390 RNA, herein designated GAM RNA, to target binding sites on GAM1390 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1390 target RNA, herein designated GAM TARGET RNA, into GAM1390 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21574] It is appreciated that GAM1390 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1390 target genes. The mRNA of each one of this plurality of GAM1390 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1390 RNA, herein designated GAM RNA, and which when bound by GAM1390 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1390 target proteins.

[21575] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1390 gene, herein designated GAM GENE, on one or more GAM1390 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[21576] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1390 correlate with, and may be deduced from, the identity of the target genes which GAM1390 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21577] Nucleotide sequences of the GAM1390 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1390 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1390 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1390 are further described hereinbelow with reference to Table Table1.

[21578] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1390 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21579] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1391 (GAM1391) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[21580] GAM1391 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1391 was detected is described hereinabove with reference to Figs. 2-8.

[21581] GAM1391 gene, herein designated GAM GENE, and GAM1391 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21582] GAM1391 gene, herein designated GAM GENE, encodes a GAM1391 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1391 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1391 precursor RNA is designated SEQ ID:1364, and is provided hereinbelow with reference to the sequence listing part.

[21583] GAM1391 has 7 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[21584] SEQ ID:99235 detected in mouse EST Accession BE369926.1.

[21585] SEQ ID:99236 detected in mouse EST Accession BE371634.1.

[21586] SEQ ID:99237 detected in mouse EST Accession BF162728.1.

[21587] SEQ ID:99238 detected in mouse EST Accession BE572790.1.

[21588] SEQ ID:99239 detected in mouse EST Accession BG964017.1.

[21589] SEQ ID:99240 detected in mouse EST Accession BE291495.1.

[21590] SEQ ID:98424 detected in mouse EST Accession BF450182.1.

[21591] GAM1391 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[21592] An enzyme complex designated DICER COMPLEX, dices the GAM1391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1391 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1391 RNA is designated SEQ ID:3040, and is provided hereinbelow with reference to the sequence listing part.

[21593] GAM1391 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1391 target RNA, herein designated GAM TARGET RNA. GAM1391 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21594] GAM1391 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1391 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1391 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1391 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1391 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21595] The complementary binding of GAM1391 RNA, herein designated GAM RNA, to target binding sites on GAM1391 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1391 target RNA, herein designated GAM TARGET RNA, into GAM1391 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21596] It is appreciated that GAM1391 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1391 target genes. The mRNA of each one of this plurality of GAM1391 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1391 RNA, herein designated GAM RNA, and which when bound by GAM1391 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1391 target proteins.

[21597] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1391 gene, herein designated GAM GENE, on one or more GAM1391 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21598] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1391 correlate with, and may be deduced from, the identity of the target genes which GAM1391 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21599] Nucleotide sequences of the GAM1391 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1391 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1391 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1391 are further described hereinbelow with reference to Table Table1.

[21600] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1391 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21601] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1392 (GAM1392) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21602] GAM1392 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1392 was detected is described hereinabove with reference to Figs. 2-8.

[21603] GAM1392 gene, herein designated GAM GENE, and GAM1392 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21604] GAM1392 gene, herein designated GAM GENE, encodes a GAM1392 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1392 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1392 precursor RNA is designated SEQ ID:1365, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1365 is located at position 2248618 relative to contig NT_029419.8, on chromosome 12.

[21605] GAM1392 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21606] An enzyme complex designated DICER COMPLEX, dices the GAM1392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1392 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1392 RNA is designated SEQ ID:3041, and

is provided hereinbelow with reference to the sequence listing part.

[21607] GAM1392 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1392 target RNA, herein designated GAM TARGET RNA. GAM1392 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21608] GAM1392 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1392 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1392 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1392 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1392 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21609] The complementary binding of GAM1392 RNA, herein designated GAM RNA, to target binding sites on GAM1392 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1392 target RNA, herein designated GAM TARGET RNA, into GAM1392 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21610] It is appreciated that GAM1392 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1392 target genes. The mRNA of each one of this plurality of GAM1392 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1392 RNA, herein designated GAM RNA, and which when bound by

GAM1392 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1392 target proteins.

[21611] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1392 gene, herein designated GAM GENE, on one or more GAM1392 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21612] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1392 correlate with, and may be deduced from, the identity of the target genes which GAM1392 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[21613] Nucleotide sequences of the GAM1392 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1392 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1392 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1392 are further described hereinbelow with reference to Table Table1.

[21614] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1392 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21615] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1393 (GAM1393) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21616] GAM1393 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1393 was detected is described hereinabove

with reference to Figs. 2-8.

[21617] GAM1393 gene, herein designated GAM GENE, and GAM1393 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21618] GAM1393 gene, herein designated GAM GENE, encodes a GAM1393 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1393 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1393 precursor RNA is designated SEQ ID:1366, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1366 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[21619] GAM1393 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21620] An enzyme complex designated DICER COMPLEX, dices the GAM1393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1393 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1393 RNA is designated SEQ ID:3042, and is provided hereinbelow with reference to the sequence listing part.

[21621] GAM1393 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1393 target RNA, herein designated GAM TARGET RNA. GAM1393 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21622] GAM1393 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1393 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1393 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1393 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1393 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21623] The complementary binding of GAM1393 RNA, herein designated GAM RNA, to target binding sites on GAM1393 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1393 target RNA, herein designated GAM TARGET RNA, into GAM1393 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21624] It is appreciated that GAM1393 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1393 target genes. The mRNA of each one of this plurality of GAM1393 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1393 RNA, herein designated GAM RNA, and which when bound by GAM1393 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1393 target proteins.

[21625] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1393 gene, herein designated GAM GENE, on one or more GAM1393 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21626] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1393 correlate with, and may be deduced from, the identity of the target genes which GAM1393 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21627] Nucleotide sequences of the GAM1393 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1393 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1393 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1393 are further described hereinbelow with reference to Table Table1.

[21628] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1393 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21629] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1394 (GAM1394) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21630] GAM1394 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1394 was detected is described hereinabove with reference to Figs. 2-8.

[21631] GAM1394 gene, herein designated GAM GENE, and GAM1394 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21632] GAM1394 gene, herein designated GAM GENE, encodes a GAM1394 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1394 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1394 precursor RNA is

designated SEQ ID:1367, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1367 is located at position 3102351 relative to contig NT_011109.13, on chromosome 19.

[21633] GAM1394 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21634] An enzyme complex designated DICER COMPLEX, dices the GAM1394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1394 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1394 RNA is designated SEQ ID:3043, and is provided hereinbelow with reference to the sequence listing part.

[21635] GAM1394 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1394 target RNA, herein designated GAM TARGET RNA. GAM1394 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21636] GAM1394 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1394 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1394 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1394 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1394 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21637] The complementary binding of GAM1394 RNA, herein designated GAM RNA, to target binding sites on GAM1394 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1394 target RNA, herein designated GAM TARGET RNA, into GAM1394 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21638] It is appreciated that GAM1394 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1394 target genes. The mRNA of each one of this plurality of GAM1394 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1394 RNA,

herein designated GAM RNA, and which when bound by GAM1394 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1394 target proteins.

[21639] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1394 gene, herein designated GAM GENE, on one or more GAM1394 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21640] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1394 correlate with, and may be deduced from, the identity of the target genes which

GAM1394 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21641] Nucleotide sequences of the GAM1394 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1394 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1394 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1394 are further described hereinbelow with reference to Table Table1.

[21642] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1394 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21643] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1395 (GAM1395) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21644] GAM1395 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1395 was detected is described hereinabove with reference to Figs. 2-8.

[21645] GAM1395 gene, herein designated GAM GENE, and GAM1395 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21646] GAM1395 gene, herein designated GAM GENE, encodes a GAM1395 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1395 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1395 precursor RNA is designated SEQ ID:1368, and is provided hereinbelow with reference to the sequence listing part.

[21647] GAM1395 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[21648] An enzyme complex designated DICER COMPLEX, dices the GAM1395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1395 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1395 RNA is designated SEQ ID:3044, and is provided hereinbelow with reference to the sequence listing part.

[21649] GAM1395 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1395 target RNA, herein designated GAM TARGET RNA. GAM1395 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21650] GAM1395 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1395 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1395 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1395 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1395 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21651] The complementary binding of GAM1395 RNA, herein designated GAM RNA, to target binding sites on GAM1395 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1395 target RNA, herein designated GAM TARGET RNA, into GAM1395 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21652] It is appreciated that GAM1395 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1395 target genes. The mRNA of each one of this plurality of GAM1395 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1395 RNA, herein designated GAM RNA, and which when bound by GAM1395 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1395 target proteins.

[21653] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1395 gene, herein designated GAM GENE, on one or more GAM1395 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21654] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1395 correlate with, and may be deduced from, the identity of the target genes which GAM1395 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21655] Nucleotide sequences of the GAM1395 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1395 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1395 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1395 are further described hereinbelow with reference to Table Table1.

[21656] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1395 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21657] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1396 (GAM1396) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21658] GAM1396 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1396 was detected is described hereinabove with reference to Figs. 2-8.

[21659] GAM1396 gene, herein designated GAM GENE, and GAM1396 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21660] GAM1396 gene, herein designated GAM GENE, encodes a GAM1396 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1396 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1396 precursor RNA is designated SEQ ID:1369, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1369 is located at position 1083375 relative to contig NT_025702.10, on chromosome 5.

[21661] GAM1396 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21662] An enzyme complex designated DICER COMPLEX, dices the GAM1396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1396 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1396 RNA is designated SEQ ID:3045, and

is provided hereinbelow with reference to the sequence listing part.

[21663] GAM1396 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1396 target RNA, herein designated GAM TARGET RNA. GAM1396 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21664] GAM1396 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1396 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1396 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1396 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1396 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21665] The complementary binding of GAM1396 RNA, herein designated GAM RNA, to target binding sites on GAM1396 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1396 target RNA, herein designated GAM TARGET RNA, into GAM1396 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21666] It is appreciated that GAM1396 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1396 target genes. The mRNA of each one of this plurality of GAM1396 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1396 RNA, herein designated GAM RNA, and which when bound by

GAM1396 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1396 target proteins.

[21667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1396 gene, herein designated GAM GENE, on one or more GAM1396 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21668] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1396 correlate with, and may be deduced from, the identity of the target genes which GAM1396 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[21669] Nucleotide sequences of the GAM1396 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1396 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1396 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1396 are further described hereinbelow with reference to Table Table1.

[21670] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1396 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21671] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1397 (GAM1397) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21672] GAM1397 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1397 was detected is described hereinabove

with reference to Figs. 2-8.

[21673] GAM1397 gene, herein designated GAM GENE, and GAM1397 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21674] GAM1397 gene, herein designated GAM GENE, encodes a GAM1397 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1397 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1397 precursor RNA is designated SEQ ID:1370, and is provided hereinbelow with reference to the sequence listing part.

[21675] GAM1397 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21676] An enzyme complex designated DICER COMPLEX, dices the GAM1397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1397 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1397 RNA is designated SEQ ID:3046, and is provided hereinbelow with reference to the sequence listing part.

[21677] GAM1397 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1397 target RNA, herein designated GAM TARGET RNA. GAM1397 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21678] GAM1397 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1397 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1397 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1397 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1397 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21679] The complementary binding of GAM1397 RNA, herein designated GAM RNA, to target binding sites on GAM1397 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1397 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1397 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21680] It is appreciated that GAM1397 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1397 target genes. The mRNA of each one of this plurality of GAM1397 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1397 RNA, herein designated GAM RNA, and which when bound by GAM1397 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1397 target proteins.

[21681] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1397 gene, herein designated GAM GENE, on one or more GAM1397 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21682] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1397 correlate with, and may be deduced from, the identity of the target genes which GAM1397 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21683] Nucleotide sequences of the GAM1397 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1397 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1397 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1397 are further described hereinbelow with reference to Table Table1.

[21684] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1397 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[21685] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1398 (GAM1398) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21686] GAM1398 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1398 was detected is described hereinabove with reference to Figs. 2-8.

[21687] GAM1398 gene, herein designated GAM GENE, and GAM1398 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21688] GAM1398 gene, herein designated GAM GENE, encodes a GAM1398 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1398 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1398 precursor RNA is designated SEQ ID:1371, and is provided hereinbelow with reference to the sequence listing part.

[21689] GAM1398 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21690] An enzyme complex designated DICER COMPLEX, dices the GAM1398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1398 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1398 RNA is designated SEQ ID:3047, and is provided hereinbelow with reference to the sequence listing part.

[21691] GAM1398 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1398 target RNA, herein designated GAM TARGET RNA. GAM1398 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21692] GAM1398 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1398 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1398 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1398 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1398 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21693] The complementary binding of GAM1398 RNA, herein designated GAM RNA, to target binding sites on GAM1398 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1398 target RNA, herein designated GAM TARGET RNA, into GAM1398 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21694] It is appreciated that GAM1398 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1398 target genes. The mRNA of each one of this plurality of GAM1398 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1398 RNA, herein designated GAM RNA, and which when bound by GAM1398 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1398 target proteins.

[21695] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1398 gene, herein designated GAM GENE, on one or more GAM1398 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21696] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1398 correlate with, and may be deduced from, the identity of the target genes which GAM1398 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21697] Nucleotide sequences of the GAM1398 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1398 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1398 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1398 are further described hereinbelow with reference to Table Table1.

[21698] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1398 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21699] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1399 (GAM1399) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21700] GAM1399 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1399 was detected is described hereinabove with reference to Figs. 2-8.

[21701] GAM1399 gene, herein designated GAM GENE, and GAM1399 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[21702] GAM1399 gene, herein designated GAM GENE, encodes a GAM1399 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1399 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1399 precursor RNA is designated SEQ ID:1372, and is provided hereinbelow with reference to the sequence listing part.

[21703] GAM1399 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21704] An enzyme complex designated DICER COMPLEX, dices the GAM1399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1399 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1399 RNA is designated SEQ ID:3048, and is provided hereinbelow with reference to the sequence listing part.

[21705] GAM1399 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1399 target RNA, herein designated GAM TARGET RNA. GAM1399 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21706] GAM1399 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1399 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1399 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1399 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1399 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21707] The complementary binding of GAM1399 RNA, herein designated GAM RNA, to target binding sites on GAM1399 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1399 target RNA, herein designated GAM TARGET RNA, into GAM1399 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21708] It is appreciated that GAM1399 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1399 target genes. The mRNA of each one of this plurality of GAM1399 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1399 RNA, herein designated GAM RNA, and which when bound by GAM1399 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1399 target proteins.

[21709] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1399 gene, herein designated GAM GENE, on one or more GAM1399 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21710] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1399 correlate with, and may be deduced from, the identity of the target genes which GAM1399 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21711] Nucleotide sequences of the GAM1399 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1399 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1399 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1399 are further described hereinbelow with reference to Table Table1.

[21712] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1399 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21713] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1400 (GAM1400) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21714] GAM1400 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1400 was detected is described hereinabove with reference to Figs. 2-8.

[21715] GAM1400 gene, herein designated GAM GENE, and GAM1400 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21716] GAM1400 gene, herein designated GAM GENE, encodes a GAM1400 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1400 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1400 precursor RNA is designated SEQ ID:1373, and is provided hereinbelow with reference to the sequence listing part.

[21717] GAM1400 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1400 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21718] An enzyme complex designated DICER COMPLEX, dices the GAM1400 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1400 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1400 RNA is designated SEQ ID:3049, and is provided hereinbelow with reference to the sequence listing part.

[21719] GAM1400 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1400 target RNA, herein designated GAM TARGET RNA. GAM1400 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21720] GAM1400 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1400 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1400 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1400 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1400 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21721] The complementary binding of GAM1400 RNA, herein designated GAM RNA, to target binding sites on GAM1400 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1400 target RNA, herein designated GAM TARGET RNA, into GAM1400 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21722] It is appreciated that GAM1400 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1400 target genes. The mRNA of each one of this plurality of GAM1400 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1400 RNA, herein designated GAM RNA, and which when bound by GAM1400 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1400 target proteins.

[21723] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1400 gene, herein designated GAM GENE, on one or more GAM1400 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21724] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1400 correlate with, and may be deduced from, the identity of the target genes which GAM1400 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21725] Nucleotide sequences of the GAM1400 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1400 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1400 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1400 are further described hereinbelow with reference to Table Table1.

[21726] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1400 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21727] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1401 (GAM1401) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21728] GAM1401 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1401 was detected is described hereinabove with reference to Figs. 2-8.

[21729] GAM1401 gene, herein designated GAM GENE, and GAM1401 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21730] GAM1401 gene, herein designated GAM GENE, encodes a GAM1401 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1401 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1401 precursor RNA is designated SEQ ID:1374, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1374 is located at position 8872441 relative to contig NT_005375.11, on chromosome 2.

[21731] GAM1401 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21732] An enzyme complex designated DICER COMPLEX, dices the GAM1401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1401 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1401 RNA is designated SEQ ID:3050, and is provided hereinbelow with reference to the sequence listing part.

[21733] GAM1401 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1401 target RNA, herein designated GAM TARGET RNA. GAM1401 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21734] GAM1401 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1401 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1401 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1401 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1401 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21735] The complementary binding of GAM1401 RNA, herein designated GAM RNA, to target binding sites on GAM1401 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1401 target RNA, herein designated GAM TARGET RNA, into GAM1401 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21736] It is appreciated that GAM1401 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1401 target genes. The mRNA of each one of this plurality of GAM1401 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1401 RNA, herein designated GAM RNA, and which when bound by GAM1401 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1401 target proteins.

[21737] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1401 gene, herein designated GAM GENE, on one or more GAM1401 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21738] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1401 correlate with, and may be deduced from, the identity of the target genes which GAM1401 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21739] Nucleotide sequences of the GAM1401 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1401 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1401 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1401 are further described hereinbelow with reference to Table Table1.

[21740] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1401 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21741] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1402 (GAM1402) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21742] GAM1402 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1402 was detected is described hereinabove with reference to Figs. 2-8.

[21743] GAM1402 gene, herein designated GAM GENE, and GAM1402 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21744] GAM1402 gene, herein designated GAM GENE, encodes a GAM1402 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1402 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1402 precursor RNA is designated SEQ ID:1375, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1375 is located at position 8872441 relative to contig NT_005375.11, on chromosome 2.

[21745] GAM1402 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1402 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21746] An enzyme complex designated DICER COMPLEX, dices the GAM1402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1402 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1402 RNA is designated SEQ ID:3051, and is provided hereinbelow with reference to the sequence listing part.

[21747] GAM1402 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1402 target RNA, herein designated GAM TARGET

RNA. GAM1402 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21748] GAM1402 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1402 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1402 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1402 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1402 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21749] The complementary binding of GAM1402 RNA, herein designated GAM RNA, to target binding sites on GAM1402 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1402 target RNA, herein designated GAM TARGET RNA, into GAM1402 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21750] It is appreciated that GAM1402 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1402 target genes. The mRNA of each one of this plurality of GAM1402 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1402 RNA, herein designated GAM RNA, and which when bound by GAM1402 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1402 target proteins.

[21751] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1402 gene, herein designated GAM GENE, on one or more GAM1402 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21752] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1402 correlate with, and may be deduced from, the identity of the target genes which GAM1402 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21753] Nucleotide sequences of the GAM1402 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1402 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1402 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1402 are further described hereinbelow with reference to Table Table1.

[21754] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1402 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21755] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1403 (GAM1403) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21756] GAM1403 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1403 was detected is described hereinabove with reference to Figs. 2-8.

[21757] GAM1403 gene, herein designated GAM GENE, and GAM1403 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21758] GAM1403 gene, herein designated GAM GENE, encodes a

GAM1403 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1403 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1403 precursor RNA is designated SEQ ID:1376, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1376 is located at position 20712080 relative to contig NT_024524.11, on chromosome 13.

[21759] GAM1403 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21760] An enzyme complex designated DICER COMPLEX, dices the GAM1403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1403 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1403 RNA is designated SEQ ID:3052, and is provided hereinbelow with reference to the sequence listing part.

[21761] GAM1403 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1403 target RNA, herein designated GAM TARGET RNA. GAM1403 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21762] GAM1403 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1403 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1403 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1403 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1403 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21763] The complementary binding of GAM1403 RNA, herein designated GAM RNA, to target binding sites on GAM1403 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1403 target RNA, herein designated GAM TARGET RNA, into GAM1403 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21764] It is appreciated that GAM1403 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1403 target genes. The mRNA of each one of this plurality of GAM1403 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1403 RNA, herein designated GAM RNA, and which when bound by GAM1403 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1403 target proteins.

[21765] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1403 gene, herein designated GAM GENE, on one or more GAM1403 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21766] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1403 correlate with, and may be deduced from, the identity of the target genes which GAM1403 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21767] Nucleotide sequences of the GAM1403 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1403 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1403 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1403 are further described hereinbelow with reference to Table Table1.

[21768] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1403 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21769] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1404 (GAM1404) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21770] GAM1404 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1404 was detected is described hereinabove with reference to Figs. 2-8.

[21771] GAM1404 gene, herein designated GAM GENE, and GAM1404 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21772] GAM1404 gene, herein designated GAM GENE, encodes a GAM1404 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1404 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1404 precursor RNA is designated SEQ ID:1377, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1377 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[21773] GAM1404 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21774] An enzyme complex designated DICER COMPLEX, dices the GAM1404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1404 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1404 RNA is designated SEQ ID:3053, and is provided hereinbelow with reference to the sequence listing part.

[21775] GAM1404 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1404 target RNA, herein designated GAM TARGET RNA. GAM1404 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21776] GAM1404 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1404 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1404 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1404 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1404 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21777] The complementary binding of GAM1404 RNA, herein designated GAM RNA, to target binding sites on GAM1404 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1404 target RNA, herein designated GAM TARGET RNA, into GAM1404 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21778] It is appreciated that GAM1404 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1404 target genes. The mRNA of each one of this plurality of GAM1404 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1404 RNA, herein designated GAM RNA, and which when bound by GAM1404 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1404 target proteins.

[21779] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1404 gene, herein designated GAM GENE, on one or more GAM1404 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21780] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1404 correlate with, and may be deduced from, the identity of the target genes which GAM1404 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21781] Nucleotide sequences of the GAM1404 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1404 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1404 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1404 are further described hereinbelow with reference to Table Table1.

[21782] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1404 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21783] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1405 (GAM1405) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21784] GAM1405 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1405 was detected is described hereinabove with reference to Figs. 2-8.

[21785] GAM1405 gene, herein designated GAM GENE, and GAM1405 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21786] GAM1405 gene, herein designated GAM GENE, encodes a GAM1405 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1405 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1405 precursor RNA is designated SEQ ID:1378, and is provided hereinbelow with reference to the sequence listing part.

[21787] GAM1405 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21788] An enzyme complex designated DICER COMPLEX, dices the GAM1405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1405 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1405 RNA is designated SEQ ID:3054, and is provided hereinbelow with reference to the sequence listing part.

[21789] GAM1405 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1405 target RNA, herein designated GAM TARGET RNA. GAM1405 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21790] GAM1405 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1405 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1405 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1405 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1405 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21791] The complementary binding of GAM1405 RNA, herein designated GAM RNA, to target binding sites on GAM1405 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1405 target RNA, herein designated GAM TARGET RNA, into GAM1405 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21792] It is appreciated that GAM1405 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1405 target genes. The mRNA of each one of this plurality of GAM1405 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1405 RNA, herein designated GAM RNA, and which when bound by GAM1405 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1405 target proteins.

[21793] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1405 gene, herein designated GAM GENE, on one or more GAM1405 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21794] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1405 correlate with, and may be deduced from, the identity of the target genes which GAM1405 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21795] Nucleotide sequences of the GAM1405 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1405 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1405 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1405 are further described hereinbelow with reference to Table Table1.

[21796] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1405 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21797] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1406 (GAM1406) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21798] GAM1406 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1406 was detected is described hereinabove with reference to Figs. 2-8.

[21799] GAM1406 gene, herein designated GAM GENE, and GAM1406 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21800] GAM1406 gene, herein designated GAM GENE, encodes a GAM1406 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1406 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1406 precursor RNA is designated SEQ ID:1379, and is provided hereinbelow with reference to the sequence listing part.

[21801] GAM1406 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21802] An enzyme complex designated DICER COMPLEX, dices the GAM1406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1406 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1406 RNA is designated SEQ ID:3055, and is provided hereinbelow with reference to the sequence listing part.

[21803] GAM1406 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1406 target RNA, herein designated GAM TARGET RNA. GAM1406 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21804] GAM1406 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1406 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1406 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1406 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1406 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[21805] The complementary binding of GAM1406 RNA, herein designated GAM RNA, to target binding sites on GAM1406 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1406 target RNA, herein designated GAM TARGET RNA, into GAM1406 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21806] It is appreciated that GAM1406 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1406 target genes. The mRNA of each one of this plurality of GAM1406 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1406 RNA, herein designated GAM RNA, and which when bound by GAM1406 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1406 target proteins.

[21807] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1406 gene, herein designated GAM GENE, on one or

more GAM1406 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21808] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1406 correlate with, and may be deduced from, the identity of the target genes which GAM1406 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21809] Nucleotide sequences of the GAM1406 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1406 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1406 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1406 are further de-

scribed hereinbelow with reference to Table Table1.

[21810] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1406 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21811] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1407 (GAM1407) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21812] GAM1407 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1407 was detected is described hereinabove with reference to Figs. 2-8.

[21813] GAM1407 gene, herein designated GAM GENE, and GAM1407 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21814] GAM1407 gene, herein designated GAM GENE, encodes a GAM1407 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1407 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1407 precursor RNA is designated SEQ ID:1380, and is provided hereinbelow with reference to the sequence listing part.

[21815] GAM1407 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21816] An enzyme complex designated DICER COMPLEX, dices the GAM1407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1407 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1407 RNA is designated SEQ ID:3056, and is provided hereinbelow with reference to the sequence listing part.

[21817] GAM1407 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1407 target RNA, herein designated GAM TARGET RNA. GAM1407 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21818] GAM1407 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1407 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1407 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1407 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1407 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21819] The complementary binding of GAM1407 RNA, herein designated GAM RNA, to target binding sites on GAM1407 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1407 target RNA, herein designated GAM TARGET RNA, into GAM1407 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21820] It is appreciated that GAM1407 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1407 target genes. The mRNA of each one of this plurality of GAM1407 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1407 RNA, herein designated GAM RNA, and which when bound by GAM1407 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1407 target proteins.

[21821] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1407 gene, herein designated GAM GENE, on one or more GAM1407 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21822] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1407 correlate with, and may be deduced from, the identity of the target genes which GAM1407 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21823] Nucleotide sequences of the GAM1407 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1407 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1407 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1407 are further described hereinbelow with reference to Table Table1.

[21824] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1407 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21825] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1408 (GAM1408) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21826] GAM1408 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1408 was detected is described hereinabove with reference to Figs. 2-8.

[21827] GAM1408 gene, herein designated GAM GENE, and GAM1408 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21828] GAM1408 gene, herein designated GAM GENE, encodes a GAM1408 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1408 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1408 precursor RNA is designated SEQ ID:1381, and is provided hereinbelow with reference to the sequence listing part.

[21829] GAM1408 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21830] An enzyme complex designated DICER COMPLEX, dices the GAM1408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1408 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1408 RNA is designated SEQ ID:3057, and is provided hereinbelow with reference to the sequence listing part.

[21831] GAM1408 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1408 target RNA, herein designated GAM TARGET RNA. GAM1408 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21832] GAM1408 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1408 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1408 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1408 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1408 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21833] The complementary binding of GAM1408 RNA, herein designated GAM RNA, to target binding sites on GAM1408

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1408 target RNA, herein designated GAM TARGET RNA, into GAM1408 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21834] It is appreciated that GAM1408 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1408 target genes. The mRNA of each one of this plurality of GAM1408 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1408 RNA, herein designated GAM RNA, and which when bound by GAM1408 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1408 target proteins.

[21835] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1408 gene, herein designated GAM GENE, on one or more GAM1408 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21836] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1408 correlate with, and may be deduced from, the identity of the target genes which GAM1408 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21837] Nucleotide sequences of the GAM1408 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1408 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1408 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1408 are further described hereinbelow with reference to Table Table1.

[21838] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1408 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21839] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1409 (GAM1409) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21840] GAM1409 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1409 was detected is described hereinabove with reference to Figs. 2-8.

[21841] GAM1409 gene, herein designated GAM GENE, and GAM1409 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21842] GAM1409 gene, herein designated GAM GENE, encodes a GAM1409 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1409 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1409 precursor RNA is designated SEQ ID:1382, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1382 is located at position 142055 relative to contig NT_019609.9, on chromosome 16.

[21843] GAM1409 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21844] An enzyme complex designated DICER COMPLEX, dices the GAM1409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1409 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1409 RNA is designated SEQ ID:3058, and is provided hereinbelow with reference to the sequence listing part.

[21845] GAM1409 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1409 target RNA, herein designated GAM TARGET RNA. GAM1409 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21846] GAM1409 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1409 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1409 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1409 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1409 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21847] The complementary binding of GAM1409 RNA, herein designated GAM RNA, to target binding sites on GAM1409 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1409 target RNA, herein designated GAM TARGET RNA, into GAM1409 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21848] It is appreciated that GAM1409 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1409 target genes. The mRNA of each one of this plurality of GAM1409 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1409 RNA, herein designated GAM RNA, and which when bound by GAM1409 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1409 target proteins.

[21849] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1409 gene, herein designated GAM GENE, on one or more GAM1409 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21850] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1409 correlate with, and may

be deduced from, the identity of the target genes which GAM1409 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21851] Nucleotide sequences of the GAM1409 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1409 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1409 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1409 are further described hereinbelow with reference to Table Table1.

[21852] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1409 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21853] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1410 (GAM1410) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21854] GAM1410 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1410 was detected is described hereinabove with reference to Figs. 2-8.

[21855] GAM1410 gene, herein designated GAM GENE, and GAM1410 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21856] GAM1410 gene, herein designated GAM GENE, encodes a GAM1410 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1410 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1410 precursor RNA is designated SEQ ID:1383, and is provided hereinbelow with reference to the sequence listing part.

[21857] GAM1410 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[21858] SEQ ID:98751 detected in mouse EST Accession BI965972.1.

[21859] SEQ ID:98752 detected in mouse EST Accession

AI326210.1.

[21860] SEQ ID:98753 detected in mouse EST Accession BI965652.1.

[21861] GAM1410 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21862] An enzyme complex designated DICER COMPLEX, dices the GAM1410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1410 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1410 RNA is designated SEQ ID:3059, and

is provided hereinbelow with reference to the sequence listing part.

[21863] GAM1410 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1410 target RNA, herein designated GAM TARGET RNA. GAM1410 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21864] GAM1410 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1410 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1410 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1410 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1410 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21865] The complementary binding of GAM1410 RNA, herein designated GAM RNA, to target binding sites on GAM1410 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1410 target RNA, herein designated GAM TARGET RNA, into GAM1410 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21866] It is appreciated that GAM1410 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1410 target genes. The mRNA of each one of this plurality of GAM1410 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1410 RNA, herein designated GAM RNA, and which when bound by

GAM1410 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1410 target proteins.

[21867] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1410 gene, herein designated GAM GENE, on one or more GAM1410 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21868] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1410 correlate with, and may be deduced from, the identity of the target genes which GAM1410 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[21869] Nucleotide sequences of the GAM1410 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1410 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1410 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1410 are further described hereinbelow with reference to Table Table1.

[21870] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1410 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21871] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1411 (GAM1411) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21872] GAM1411 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1411 was detected is described hereinabove

with reference to Figs. 2-8.

[21873] GAM1411 gene, herein designated GAM GENE, and GAM1411 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21874] GAM1411 gene, herein designated GAM GENE, encodes a GAM1411 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1411 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1411 precursor RNA is designated SEQ ID:1384, and is provided hereinbelow with reference to the sequence listing part.

[21875] GAM1411 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[21876] SEQ ID:99241 detected in mouse EST Accession BI965972.1.

[21877] SEQ ID:99242 detected in mouse EST Accession BI965652.1.

[21878] SEQ ID:99243 detected in mouse EST Accession

AI326210.1.

[21879] GAM1411 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21880] An enzyme complex designated DICER COMPLEX, dices the GAM1411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1411 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1411 RNA is designated SEQ ID:3060, and is provided hereinbelow with reference to the sequence listing part.

[21881] GAM1411 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1411 target RNA, herein designated GAM TARGET RNA. GAM1411 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21882] GAM1411 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1411 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1411 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1411 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1411 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21883] The complementary binding of GAM1411 RNA, herein designated GAM RNA, to target binding sites on GAM1411 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1411 target RNA, herein designated GAM TARGET RNA, into GAM1411 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21884] It is appreciated that GAM1411 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1411 target genes. The mRNA of each one of this plurality of GAM1411 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1411 RNA, herein designated GAM RNA, and which when bound by GAM1411 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1411

target proteins.

[21885] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1411 gene, herein designated GAM GENE, on one or more GAM1411 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21886] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1411 correlate with, and may be deduced from, the identity of the target genes which GAM1411 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21887] Nucleotide sequences of the GAM1411 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1411 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1411 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1411 are further described hereinbelow with reference to Table Table1.

[21888] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1411 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21889] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1412 (GAM1412) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21890] GAM1412 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1412 was detected is described hereinabove with reference to Figs. 2-8.

[21891] GAM1412 gene, herein designated GAM GENE, and

GAM1412 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21892] GAM1412 gene, herein designated GAM GENE, encodes a GAM1412 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1412 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1412 precursor RNA is designated SEQ ID:1385, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1385 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[21893] GAM1412 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21894] An enzyme complex designated DICER COMPLEX, dices the GAM1412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1412 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1412 RNA is designated SEQ ID:3061, and is provided hereinbelow with reference to the sequence listing part.

[21895] GAM1412 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1412 target RNA, herein designated GAM TARGET RNA. GAM1412 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21896] GAM1412 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1412 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1412 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1412 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1412 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21897] The complementary binding of GAM1412 RNA, herein designated GAM RNA, to target binding sites on GAM1412 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1412 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1412 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21898] It is appreciated that GAM1412 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1412 target genes. The mRNA of each one of this plurality of GAM1412 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1412 RNA, herein designated GAM RNA, and which when bound by GAM1412 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1412 target proteins.

[21899] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1412 gene, herein designated GAM GENE, on one or more GAM1412 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21900] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1412 correlate with, and may be deduced from, the identity of the target genes which GAM1412 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21901] Nucleotide sequences of the GAM1412 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1412 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1412 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1412 are further described hereinbelow with reference to Table Table1.

[21902] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1412 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[21903] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1413 (GAM1413) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21904] GAM1413 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1413 was detected is described hereinabove with reference to Figs. 2-8.

[21905] GAM1413 gene, herein designated GAM GENE, and GAM1413 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21906] GAM1413 gene, herein designated GAM GENE, encodes a GAM1413 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1413 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1413 precursor RNA is designated SEQ ID:1386, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1386 is located at position 4851356 relative to contig NT_022517.13, on chromosome 3.

[21907] GAM1413 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21908] An enzyme complex designated DICER COMPLEX, dices the GAM1413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1413 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1413 RNA is designated SEQ ID:3062, and is provided hereinbelow with reference to the sequence

listing part.

[21909] GAM1413 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1413 target RNA, herein designated GAM TARGET RNA. GAM1413 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21910] GAM1413 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1413 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1413 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1413 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1413 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21911] The complementary binding of GAM1413 RNA, herein designated GAM RNA, to target binding sites on GAM1413 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1413 target RNA, herein designated GAM TARGET RNA, into GAM1413 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21912] It is appreciated that GAM1413 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1413 target genes. The mRNA of each one of this plurality of GAM1413 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1413 RNA, herein designated GAM RNA, and which when bound by GAM1413 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1413 target proteins.

[21913] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1413 gene, herein designated GAM GENE, on one or more GAM1413 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21914] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1413 correlate with, and may be deduced from, the identity of the target genes which GAM1413 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21915] Nucleotide sequences of the GAM1413 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1413 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1413 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1413 are further described hereinbelow with reference to Table Table1.

[21916] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1413 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21917] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1414 (GAM1414) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21918] GAM1414 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1414 was detected is described hereinabove with reference to Figs. 2-8.

[21919] GAM1414 gene, herein designated GAM GENE, and GAM1414 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21920] GAM1414 gene, herein designated GAM GENE, encodes a GAM1414 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1414 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1414 precursor RNA is designated SEQ ID:1387, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1387 is located at position 15686145 relative to contig NT_033899.3, on chromosome 11.

[21921] GAM1414 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[21922] An enzyme complex designated DICER COMPLEX, dices the GAM1414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1414 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1414 RNA is designated SEQ ID:3063, and is provided hereinbelow with reference to the sequence listing part.

[21923] GAM1414 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1414 target RNA, herein designated GAM TARGET RNA. GAM1414 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21924] GAM1414 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1414 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1414 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1414 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1414 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21925] The complementary binding of GAM1414 RNA, herein designated GAM RNA, to target binding sites on GAM1414 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1414 target RNA, herein designated GAM TARGET RNA, into GAM1414 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21926] It is appreciated that GAM1414 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1414 target genes. The mRNA of each one of this plurality of GAM1414 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1414 RNA, herein designated GAM RNA, and which when bound by GAM1414 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1414 target proteins.

[21927] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1414 gene, herein designated GAM GENE, on one or more GAM1414 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21928] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1414 correlate with, and may be deduced from, the identity of the target genes which GAM1414 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21929] Nucleotide sequences of the GAM1414 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1414 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1414 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1414 are further described hereinbelow with reference to Table Table1.

[21930] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1414 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21931] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1415 (GAM1415) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21932] GAM1415 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1415 was detected is described hereinabove with reference to Figs. 2-8.

[21933] GAM1415 gene, herein designated GAM GENE, and GAM1415 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21934] GAM1415 gene, herein designated GAM GENE, encodes a GAM1415 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1415 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1415 precursor RNA is designated SEQ ID:1388, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1388 is located at position 4851366 relative to contig NT_022517.13, on chromosome 3.

[21935] GAM1415 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21936] An enzyme complex designated DICER COMPLEX, dices the GAM1415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1415 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1415 RNA is designated SEQ ID:3064, and

is provided hereinbelow with reference to the sequence listing part.

[21937] GAM1415 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1415 target RNA, herein designated GAM TARGET RNA. GAM1415 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21938] GAM1415 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1415 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1415 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1415 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1415 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21939] The complementary binding of GAM1415 RNA, herein designated GAM RNA, to target binding sites on GAM1415 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1415 target RNA, herein designated GAM TARGET RNA, into GAM1415 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21940] It is appreciated that GAM1415 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1415 target genes. The mRNA of each one of this plurality of GAM1415 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1415 RNA, herein designated GAM RNA, and which when bound by

GAM1415 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1415 target proteins.

[21941] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1415 gene, herein designated GAM GENE, on one or more GAM1415 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21942] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1415 correlate with, and may be deduced from, the identity of the target genes which GAM1415 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[21943] Nucleotide sequences of the GAM1415 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1415 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1415 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1415 are further described hereinbelow with reference to Table Table1.

[21944] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1415 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21945] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1416 (GAM1416) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21946] GAM1416 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1416 was detected is described hereinabove

with reference to Figs. 2-8.

[21947] GAM1416 gene, herein designated GAM GENE, and GAM1416 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21948] GAM1416 gene, herein designated GAM GENE, encodes a GAM1416 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1416 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1416 precursor RNA is designated SEQ ID:1389, and is provided hereinbelow with reference to the sequence listing part.

[21949] GAM1416 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21950] An enzyme complex designated DICER COMPLEX, dices the GAM1416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1416 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1416 RNA is designated SEQ ID:3065, and is provided hereinbelow with reference to the sequence listing part.

[21951] GAM1416 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1416 target RNA, herein designated GAM TARGET RNA. GAM1416 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21952] GAM1416 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1416 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1416 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1416 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1416 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21953] The complementary binding of GAM1416 RNA, herein designated GAM RNA, to target binding sites on GAM1416 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1416 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1416 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21954] It is appreciated that GAM1416 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1416 target genes. The mRNA of each one of this plurality of GAM1416 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1416 RNA, herein designated GAM RNA, and which when bound by GAM1416 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1416 target proteins.

[21955] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1416 gene, herein designated GAM GENE, on one or more GAM1416 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21956] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1416 correlate with, and may be deduced from, the identity of the target genes which GAM1416 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21957] Nucleotide sequences of the GAM1416 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1416 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1416 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1416 are further described hereinbelow with reference to Table Table1.

[21958] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1416 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[21959] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1417 (GAM1417) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21960] GAM1417 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1417 was detected is described hereinabove with reference to Figs. 2-8.

[21961] GAM1417 gene, herein designated GAM GENE, and GAM1417 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21962] GAM1417 gene, herein designated GAM GENE, encodes a GAM1417 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1417 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1417 precursor RNA is designated SEQ ID:1390, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1390 is located at position 6312082 relative to contig NT_033899.3, on chromosome 11.

[21963] GAM1417 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21964] An enzyme complex designated DICER COMPLEX, dices the GAM1417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1417 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1417 RNA is designated SEQ ID:3066, and is provided hereinbelow with reference to the sequence

listing part.

[21965] GAM1417 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1417 target RNA, herein designated GAM TARGET RNA. GAM1417 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21966] GAM1417 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1417 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1417 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1417 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1417 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21967] The complementary binding of GAM1417 RNA, herein designated GAM RNA, to target binding sites on GAM1417 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1417 target RNA, herein designated GAM TARGET RNA, into GAM1417 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21968] It is appreciated that GAM1417 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1417 target genes. The mRNA of each one of this plurality of GAM1417 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1417 RNA, herein designated GAM RNA, and which when bound by GAM1417 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1417 target proteins.

[21969] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1417 gene, herein designated GAM GENE, on one or more GAM1417 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21970] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1417 correlate with, and may be deduced from, the identity of the target genes which GAM1417 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21971] Nucleotide sequences of the GAM1417 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1417 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1417 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1417 are further described hereinbelow with reference to Table Table1.

[21972] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1417 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21973] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1418 (GAM1418) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21974] GAM1418 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1418 was detected is described hereinabove with reference to Figs. 2-8.

[21975] GAM1418 gene, herein designated GAM GENE, and GAM1418 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21976] GAM1418 gene, herein designated GAM GENE, encodes a GAM1418 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1418 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1418 precursor RNA is designated SEQ ID:1391, and is provided hereinbelow with reference to the sequence listing part.

[21977] GAM1418 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21978] An enzyme complex designated DICER COMPLEX, dices

the GAM1418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1418 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1418 RNA is designated SEQ ID:3067, and is provided hereinbelow with reference to the sequence listing part.

[21979] GAM1418 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1418 target RNA, herein designated GAM TARGET RNA. GAM1418 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21980] GAM1418 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1418 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1418 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1418 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1418 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21981] The complementary binding of GAM1418 RNA, herein designated GAM RNA, to target binding sites on GAM1418 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1418 target RNA, herein designated GAM TARGET RNA, into GAM1418 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21982] It is appreciated that GAM1418 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1418 target genes. The mRNA of each one of this plurality of GAM1418 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1418 RNA, herein designated GAM RNA, and which when bound by GAM1418 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1418 target proteins.

[21983] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1418 gene, herein designated GAM GENE, on one or more GAM1418 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21984] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1418 correlate with, and may be deduced from, the identity of the target genes which GAM1418 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21985] Nucleotide sequences of the GAM1418 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1418 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1418 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1418 are further described hereinbelow with reference to Table Table1.

[21986] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1418 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[21987] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1419 (GAM1419) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[21988] GAM1419 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1419 was detected is described hereinabove with reference to Figs. 2-8.

[21989] GAM1419 gene, herein designated GAM GENE, and GAM1419 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[21990] GAM1419 gene, herein designated GAM GENE, encodes a GAM1419 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1419 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1419 precursor RNA is designated SEQ ID:1392, and is provided hereinbelow with reference to the sequence listing part.

[21991] GAM1419 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[21992] An enzyme complex designated DICER COMPLEX, dices the GAM1419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1419 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1419 RNA is designated SEQ ID:3068, and is provided hereinbelow with reference to the sequence listing part.

[21993] GAM1419 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1419 target RNA, herein designated GAM TARGET RNA. GAM1419 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[21994] GAM1419 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1419 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1419 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1419 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1419 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[21995] The complementary binding of GAM1419 RNA, herein designated GAM RNA, to target binding sites on GAM1419 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1419 target RNA, herein designated GAM TARGET RNA, into GAM1419 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[21996] It is appreciated that GAM1419 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1419 target genes. The mRNA of each one of this plurality of GAM1419 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1419 RNA, herein designated GAM RNA, and which when bound by GAM1419 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1419 target proteins.

[21997] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1419 gene, herein designated GAM GENE, on one or more GAM1419 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[21998] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1419 correlate with, and may be deduced from, the identity of the target genes which GAM1419 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[21999] Nucleotide sequences of the GAM1419 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1419 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1419 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1419 are further described hereinbelow with reference to Table Table1.

[22000] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1419 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22001] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1420 (GAM1420) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22002] GAM1420 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1420 was detected is described hereinabove with reference to Figs. 2-8.

[22003] GAM1420 gene, herein designated GAM GENE, and GAM1420 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22004] GAM1420 gene, herein designated GAM GENE, encodes a GAM1420 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1420 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1420 precursor RNA is designated SEQ ID:1393, and is provided hereinbelow with reference to the sequence listing part.

[22005] GAM1420 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22006] An enzyme complex designated DICER COMPLEX, dices the GAM1420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1420 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1420 RNA is designated SEQ ID:3069, and is provided hereinbelow with reference to the sequence listing part.

[22007] GAM1420 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1420 target RNA, herein designated GAM TARGET RNA. GAM1420 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22008] GAM1420 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1420 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1420 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1420 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1420 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22009] The complementary binding of GAM1420 RNA, herein designated GAM RNA, to target binding sites on GAM1420 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1420 target RNA, herein designated GAM TARGET RNA, into GAM1420 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22010] It is appreciated that GAM1420 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1420 target genes. The mRNA of each one of this plurality of GAM1420 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1420 RNA, herein designated GAM RNA, and which when bound by GAM1420 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1420 target proteins.

[22011] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1420 gene, herein designated GAM GENE, on one or more GAM1420 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22012] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1420 correlate with, and may be deduced from, the identity of the target genes which GAM1420 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22013] Nucleotide sequences of the GAM1420 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1420 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1420 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1420 are further described hereinbelow with reference to Table Table1.

[22014] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1420 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22015] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1421 (GAM1421) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22016] GAM1421 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1421 was detected is described hereinabove with reference to Figs. 2-8.

[22017] GAM1421 gene, herein designated GAM GENE, and GAM1421 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22018] GAM1421 gene, herein designated GAM GENE, encodes a GAM1421 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1421 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1421 precursor RNA is designated SEQ ID:1394, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1394 is located at position 3102342 relative to contig NT_011109.13, on chromosome 19.

[22019] GAM1421 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1421 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22020] An enzyme complex designated DICER COMPLEX, dices the GAM1421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1421 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1421 RNA is designated SEQ ID:3070, and is provided hereinbelow with reference to the sequence listing part.

[22021] GAM1421 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1421 target RNA, herein designated GAM TARGET

RNA. GAM1421 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22022] GAM1421 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1421 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1421 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1421 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1421 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22023] The complementary binding of GAM1421 RNA, herein designated GAM RNA, to target binding sites on GAM1421 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1421 target RNA, herein designated GAM TARGET RNA, into GAM1421 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22024] It is appreciated that GAM1421 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1421 target genes. The mRNA of each one of this plurality of GAM1421 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1421 RNA, herein designated GAM RNA, and which when bound by GAM1421 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1421 target proteins.

[22025] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1421 gene, herein designated GAM GENE, on one or more GAM1421 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22026] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1421 correlate with, and may be deduced from, the identity of the target genes which GAM1421 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22027] Nucleotide sequences of the GAM1421 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1421 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1421 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1421 are further described hereinbelow with reference to Table Table1.

[22028] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1421 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22029] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1422 (GAM1422) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22030] GAM1422 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1422 was detected is described hereinabove with reference to Figs. 2-8.

[22031] GAM1422 gene, herein designated GAM GENE, and GAM1422 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22032] GAM1422 gene, herein designated GAM GENE, encodes a

GAM1422 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1422 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1422 precursor RNA is designated SEQ ID:1395, and is provided hereinbelow with reference to the sequence listing part.

[22033] GAM1422 has 52 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[22034] SEQ ID:98444 detected in mouse EST Accession BG067621.1.

[22035] SEQ ID:98445 detected in mouse EST Accession BF123424.1.

[22036] SEQ ID:98446 detected in mouse EST Accession BG795846.1.

[22037] SEQ ID:98447 detected in mouse EST Accession AL022870.1.

[22038] SEQ ID:98448 detected in mouse EST Accession BI899486.1.

[22039] SEQ ID:98449 detected in mouse EST Accession AL022949.1.

[22040] SEQ ID:98450 detected in mouse EST Accession AU021041.1.

[22041] SEQ ID:98451 detected in mouse EST Accession BG068727.1.

[22042] SEQ ID:98452 detected in mouse EST Accession BG069712.1.

[22043] SEQ ID:98453 detected in mouse EST Accession AU035733.1.

[22044] SEQ ID:98454 detected in mouse EST Accession BG076798.1.

[22045] SEQ ID:98455 detected in mouse EST Accession BF457531.1.

[22046] SEQ ID:100154 detected in mouse EST Accession BG082707.1.

[22047] SEQ ID:100155 detected in mouse EST Accession AL022651.1.

[22048] SEQ ID:98432 detected in mouse EST Accession BI899545.1.

[22049] SEQ ID:98433 detected in mouse EST Accession AL024309.1.

[22050] SEQ ID:98434 detected in mouse EST Accession

AL361653.1.

[22051] SEQ ID:98435 detected in mouse EST Accession AL024140.1.

[22052] SEQ ID:98436 detected in mouse EST Accession BI899798.1.

[22053] SEQ ID:98437 detected in mouse EST Accession C87199.1.

[22054] SEQ ID:98438 detected in mouse EST Accession BB698195.1.

[22055] SEQ ID:98439 detected in mouse EST Accession AL022890.1.

[22056] SEQ ID:98440 detected in mouse EST Accession BG080760.1.

[22057] SEQ ID:98441 detected in mouse EST Accession BI899549.1.

[22058] SEQ ID:98442 detected in mouse EST Accession BG081752.1.

[22059] SEQ ID:98443 detected in mouse EST Accession BB293160.2.

[22060] SEQ ID:98825 detected in mouse EST Accession BI899545.1.

[22061] SEQ ID:98826 detected in mouse EST Accession AL024309.1.

[22062] SEQ ID:98827 detected in mouse EST Accession AL361653.1.

[22063] SEQ ID:98828 detected in mouse EST Accession BI899486.1.

[22064] SEQ ID:98829 detected in mouse EST Accession BG076798.1.

[22065] SEQ ID:98830 detected in mouse EST Accession AU021041.1.

[22066] SEQ ID:98831 detected in mouse EST Accession BG080760.1.

[22067] SEQ ID:98832 detected in mouse EST Accession BI899549.1.

[22068] SEQ ID:98833 detected in mouse EST Accession BG081752.1.

[22069] SEQ ID:98834 detected in mouse EST Accession BB293160.2.

[22070] SEQ ID:98835 detected in mouse EST Accession BF123424.1.

[22071] SEQ ID:98836 detected in mouse EST Accession AL024140.1.

[22072] SEQ ID:98837 detected in mouse EST Accession BI899798.1.

[22073] SEQ ID:98838 detected in mouse EST Accession

C87199.1.

[22074] SEQ ID:98839 detected in mouse EST Accession BB698195.1.

[22075] SEQ ID:98840 detected in mouse EST Accession AL022890.1.

[22076] SEQ ID:98841 detected in mouse EST Accession BG082707.1.

[22077] SEQ ID:98842 detected in mouse EST Accession AL022949.1.

[22078] SEQ ID:98843 detected in mouse EST Accession BG068727.1.

[22079] SEQ ID:98844 detected in mouse EST Accession BF457531.1.

[22080] SEQ ID:98845 detected in mouse EST Accession BG069712.1.

[22081] SEQ ID:98846 detected in mouse EST Accession BG067621.1.

[22082] SEQ ID:98847 detected in mouse EST Accession AU035733.1.

[22083] SEQ ID:98848 detected in mouse EST Accession AL022651.1.

[22084] SEQ ID:98849 detected in mouse EST Accession AL022870.1.

[22085] SEQ ID:98850 detected in mouse EST Accession BG795846.1.

[22086] GAM1422 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22087] An enzyme complex designated DICER COMPLEX, dices the GAM1422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1422 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1422 RNA is designated SEQ ID:3071, and is provided hereinbelow with reference to the sequence

listing part.

[22088] GAM1422 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1422 target RNA, herein designated GAM TARGET RNA. GAM1422 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22089] GAM1422 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1422 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1422 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1422 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1422 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22090] The complementary binding of GAM1422 RNA, herein designated GAM RNA, to target binding sites on GAM1422 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1422 target RNA, herein designated GAM TARGET RNA, into GAM1422 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22091] It is appreciated that GAM1422 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1422 target genes. The mRNA of each one of this plurality of GAM1422 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1422 RNA, herein designated GAM RNA, and which when bound by GAM1422 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1422 target proteins.

[22092] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1422 gene, herein designated GAM GENE, on one or more GAM1422 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22093] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1422 correlate with, and may be deduced from, the identity of the target genes which GAM1422 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22094] Nucleotide sequences of the GAM1422 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1422 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1422 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1422 are further described hereinbelow with reference to Table Table1.

[22095] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1422 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22096] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1423 (GAM1423) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22097] GAM1423 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1423 was detected is described hereinabove with reference to Figs. 2-8.

[22098] GAM1423 gene, herein designated GAM GENE, and GAM1423 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22099] GAM1423 gene, herein designated GAM GENE, encodes a GAM1423 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1423 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1423 precursor RNA is designated SEQ ID:1396, and is provided hereinbelow with reference to the sequence listing part.

[22100] GAM1423 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22101] An enzyme complex designated DICER COMPLEX, dices

the GAM1423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1423 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1423 RNA is designated SEQ ID:3072, and is provided hereinbelow with reference to the sequence listing part.

[22102] GAM1423 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1423 target RNA, herein designated GAM TARGET RNA. GAM1423 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22103] GAM1423 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1423 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1423 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1423 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1423 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22104] The complementary binding of GAM1423 RNA, herein designated GAM RNA, to target binding sites on GAM1423 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1423 target RNA, herein designated GAM TARGET RNA, into GAM1423 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22105] It is appreciated that GAM1423 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1423 target genes. The mRNA of each one of this plurality of GAM1423 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1423 RNA, herein designated GAM RNA, and which when bound by GAM1423 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1423 target proteins.

[22106] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1423 gene, herein designated GAM GENE, on one or more GAM1423 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22107] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1423 correlate with, and may be deduced from, the identity of the target genes which GAM1423 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22108] Nucleotide sequences of the GAM1423 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1423 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1423 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1423 are further described hereinbelow with reference to Table Table1.

[22109] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1423 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22110] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1424 (GAM1424) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22111] GAM1424 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1424 was detected is described hereinabove with reference to Figs. 2-8.

[22112] GAM1424 gene, herein designated GAM GENE, and GAM1424 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22113] GAM1424 gene, herein designated GAM GENE, encodes a GAM1424 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1424 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1424 precursor RNA is designated SEQ ID:1397, and is provided hereinbelow with reference to the sequence listing part.

[22114] GAM1424 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22115] An enzyme complex designated DICER COMPLEX, dices the GAM1424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1424 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1424 RNA is designated SEQ ID:3073, and is provided hereinbelow with reference to the sequence listing part.

[22116] GAM1424 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1424 target RNA, herein designated GAM TARGET RNA. GAM1424 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22117] GAM1424 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1424 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1424 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1424 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1424 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22118] The complementary binding of GAM1424 RNA, herein designated GAM RNA, to target binding sites on GAM1424 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1424 target RNA, herein designated GAM TARGET RNA, into GAM1424 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22119] It is appreciated that GAM1424 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1424 target genes. The mRNA of each one of this plurality of GAM1424 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1424 RNA, herein designated GAM RNA, and which when bound by GAM1424 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1424 target proteins.

[22120] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1424 gene, herein designated GAM GENE, on one or more GAM1424 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22121] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1424 correlate with, and may be deduced from, the identity of the target genes which GAM1424 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22122] Nucleotide sequences of the GAM1424 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1424 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1424 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1424 are further described hereinbelow with reference to Table Table1.

[22123] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1424 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22124] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1425 (GAM1425) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22125] GAM1425 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1425 was detected is described hereinabove with reference to Figs. 2-8.

[22126] GAM1425 gene, herein designated GAM GENE, and GAM1425 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22127] GAM1425 gene, herein designated GAM GENE, encodes a GAM1425 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1425 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1425 precursor RNA is designated SEQ ID:1398, and is provided hereinbelow with reference to the sequence listing part.

[22128] GAM1425 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22129] An enzyme complex designated DICER COMPLEX, dices the GAM1425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1425 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1425 RNA is designated SEQ ID:3074, and is provided hereinbelow with reference to the sequence listing part.

[22130] GAM1425 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1425 target RNA, herein designated GAM TARGET RNA. GAM1425 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22131] GAM1425 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1425 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1425 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1425 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1425 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22132] The complementary binding of GAM1425 RNA, herein designated GAM RNA, to target binding sites on GAM1425 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1425 target RNA, herein designated GAM TARGET RNA, into GAM1425 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22133] It is appreciated that GAM1425 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1425 target genes. The mRNA of each one of this plurality of GAM1425 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1425 RNA, herein designated GAM RNA, and which when bound by GAM1425 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1425 target proteins.

[22134] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1425 gene, herein designated GAM GENE, on one or more GAM1425 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22135] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1425 correlate with, and may be deduced from, the identity of the target genes which GAM1425 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22136] Nucleotide sequences of the GAM1425 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1425 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1425 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1425 are further described hereinbelow with reference to Table Table1.

[22137] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1425 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22138] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1426 (GAM1426) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22139] GAM1426 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1426 was detected is described hereinabove with reference to Figs. 2-8.

[22140] GAM1426 gene, herein designated GAM GENE, and GAM1426 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22141] GAM1426 gene, herein designated GAM GENE, encodes a GAM1426 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1426 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1426 precursor RNA is designated SEQ ID:1399, and is provided hereinbelow with reference to the sequence listing part.

[22142] GAM1426 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22143] An enzyme complex designated DICER COMPLEX, dices the GAM1426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1426 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1426 RNA is designated SEQ ID:3075, and is provided hereinbelow with reference to the sequence listing part.

[22144] GAM1426 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1426 target RNA, herein designated GAM TARGET RNA. GAM1426 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22145] GAM1426 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1426 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1426 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1426 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1426 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[22146] The complementary binding of GAM1426 RNA, herein designated GAM RNA, to target binding sites on GAM1426 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1426 target RNA, herein designated GAM TARGET RNA, into GAM1426 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22147] It is appreciated that GAM1426 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1426 target genes. The mRNA of each one of this plurality of GAM1426 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1426 RNA, herein designated GAM RNA, and which when bound by GAM1426 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1426 target proteins.

[22148] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1426 gene, herein designated GAM GENE, on one or

more GAM1426 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22149] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1426 correlate with, and may be deduced from, the identity of the target genes which GAM1426 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22150] Nucleotide sequences of the GAM1426 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1426 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1426 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1426 are further de-

scribed hereinbelow with reference to Table Table1.

[22151] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1426 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22152] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1427 (GAM1427) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22153] GAM1427 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1427 was detected is described hereinabove with reference to Figs. 2-8.

[22154] GAM1427 gene, herein designated GAM GENE, and GAM1427 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22155] GAM1427 gene, herein designated GAM GENE, encodes a GAM1427 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1427 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1427 precursor RNA is designated SEQ ID:1400, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1400 is located at position 237307 relative to contig NT_024812.8, on chromosome 16.

[22156] GAM1427 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22157] An enzyme complex designated DICER COMPLEX, dices the GAM1427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1427 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1427 RNA is designated SEQ ID:3076, and is provided hereinbelow with reference to the sequence listing part.

[22158] GAM1427 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1427 target RNA, herein designated GAM TARGET RNA. GAM1427 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22159] GAM1427 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1427 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1427 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1427 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1427 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22160] The complementary binding of GAM1427 RNA, herein designated GAM RNA, to target binding sites on GAM1427 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1427 target RNA, herein designated GAM TARGET RNA, into GAM1427 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22161] It is appreciated that GAM1427 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1427 target genes. The mRNA of each one of this plurality of GAM1427 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1427 RNA, herein designated GAM RNA, and which when bound by GAM1427 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1427 target proteins.

[22162] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1427 gene, herein designated GAM GENE, on one or more GAM1427 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[22163] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1427 correlate with, and may be deduced from, the identity of the target genes which GAM1427 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22164] Nucleotide sequences of the GAM1427 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1427 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1427 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1427 are further described hereinbelow with reference to Table Table1.

[22165] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1427 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22166] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1428 (GAM1428) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[22167] GAM1428 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1428 was detected is described hereinabove with reference to Figs. 2-8.

[22168] GAM1428 gene, herein designated GAM GENE, and GAM1428 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22169] GAM1428 gene, herein designated GAM GENE, encodes a GAM1428 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1428 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1428 precursor RNA is designated SEQ ID:1401, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1401 is located at position 1809181 relative to contig NT_023451.11, on chromosome 6.

[22170] GAM1428 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1428 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22171] An enzyme complex designated DICER COMPLEX, dices the GAM1428 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1428 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1428 RNA is designated SEQ ID:3077, and is provided hereinbelow with reference to the sequence listing part.

[22172] GAM1428 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1428 target RNA, herein designated GAM TARGET RNA. GAM1428 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22173] GAM1428 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1428 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1428 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1428 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1428 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22174] The complementary binding of GAM1428 RNA, herein designated GAM RNA, to target binding sites on GAM1428 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1428 target RNA, herein designated GAM TARGET RNA, into GAM1428 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22175] It is appreciated that GAM1428 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1428 target genes. The mRNA of each one of this plurality of GAM1428 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1428 RNA, herein designated GAM RNA, and which when bound by GAM1428 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1428 target proteins.

[22176] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1428 gene, herein designated GAM GENE, on one or more GAM1428 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22177] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1428 correlate with, and may be deduced from, the identity of the target genes which GAM1428 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22178] Nucleotide sequences of the GAM1428 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1428 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1428 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1428 are further described hereinbelow with reference to Table Table1.

[22179] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1428 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22180] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1429 (GAM1429) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22181] GAM1429 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1429 was detected is described hereinabove with reference to Figs. 2-8.

[22182] GAM1429 gene, herein designated GAM GENE, and GAM1429 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22183] GAM1429 gene, herein designated GAM GENE, encodes a GAM1429 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1429 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1429 precursor RNA is designated SEQ ID:1402, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1402 is located at position 22523324 relative to contig NT_011362.7, on chromosome 20.

[22184] GAM1429 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22185] An enzyme complex designated DICER COMPLEX, dices the GAM1429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1429 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1429 RNA is designated SEQ ID:3078, and is provided hereinbelow with reference to the sequence listing part.

[22186] GAM1429 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1429 target RNA, herein designated GAM TARGET RNA. GAM1429 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22187] GAM1429 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1429 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1429 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1429 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1429 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22188] The complementary binding of GAM1429 RNA, herein designated GAM RNA, to target binding sites on GAM1429 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1429 target RNA, herein designated GAM TARGET RNA, into GAM1429 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22189] It is appreciated that GAM1429 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1429 target genes. The mRNA of each one of this plurality of GAM1429 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1429 RNA, herein designated GAM RNA, and which when bound by GAM1429 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1429 target proteins.

[22190] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1429 gene, herein designated GAM GENE, on one or more GAM1429 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22191] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1429 correlate with, and may be deduced from, the identity of the target genes which GAM1429 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22192] Nucleotide sequences of the GAM1429 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1429 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1429 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1429 are further described hereinbelow with reference to Table Table1.

[22193] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1429 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22194] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1430 (GAM1430) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22195] GAM1430 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1430 was detected is described hereinabove with reference to Figs. 2-8.

[22196] GAM1430 gene, herein designated GAM GENE, and GAM1430 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22197] GAM1430 gene, herein designated GAM GENE, encodes a GAM1430 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1430 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1430 precursor RNA is designated SEQ ID:1403, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1403 is located at position 2045039 relative to contig NT_005962.13, on chromosome 3.

[22198] GAM1430 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1430 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22199] An enzyme complex designated DICER COMPLEX, dices the GAM1430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1430 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1430 RNA is designated SEQ ID:3079, and is provided hereinbelow with reference to the sequence listing part.

[22200] GAM1430 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1430 target RNA, herein designated GAM TARGET

RNA. GAM1430 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22201] GAM1430 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1430 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1430 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1430 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1430 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22202] The complementary binding of GAM1430 RNA, herein designated GAM RNA, to target binding sites on GAM1430 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1430 target RNA, herein designated GAM TARGET RNA, into GAM1430 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22203] It is appreciated that GAM1430 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1430 target genes. The mRNA of each one of this plurality of GAM1430 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1430 RNA, herein designated GAM RNA, and which when bound by GAM1430 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1430 target proteins.

[22204] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1430 gene, herein designated GAM GENE, on one or more GAM1430 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22205] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1430 correlate with, and may be deduced from, the identity of the target genes which GAM1430 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22206] Nucleotide sequences of the GAM1430 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1430 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1430 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1430 are further described hereinbelow with reference to Table Table1.

[22207] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1430 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22208] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1431 (GAM1431) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22209] GAM1431 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1431 was detected is described hereinabove with reference to Figs. 2-8.

[22210] GAM1431 gene, herein designated GAM GENE, and GAM1431 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22211] GAM1431 gene, herein designated GAM GENE, encodes a

GAM1431 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1431 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1431 precursor RNA is designated SEQ ID:1404, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1404 is located at position 174362 relative to contig NT_007819.11, on chromosome 7.

[22212] GAM1431 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22213] An enzyme complex designated DICER COMPLEX, dices the GAM1431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1431 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1431 RNA is designated SEQ ID:3080, and is provided hereinbelow with reference to the sequence listing part.

[22214] GAM1431 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1431 target RNA, herein designated GAM TARGET RNA. GAM1431 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22215] GAM1431 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1431 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1431 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1431 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1431 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22216] The complementary binding of GAM1431 RNA, herein designated GAM RNA, to target binding sites on GAM1431 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1431 target RNA, herein designated GAM TARGET RNA, into GAM1431 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22217] It is appreciated that GAM1431 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1431 target genes. The mRNA of each one of this plurality of GAM1431 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1431 RNA, herein designated GAM RNA, and which when bound by GAM1431 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1431 target proteins.

[22218] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1431 gene, herein designated GAM GENE, on one or more GAM1431 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22219] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1431 correlate with, and may be deduced from, the identity of the target genes which GAM1431 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22220] Nucleotide sequences of the GAM1431 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1431 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1431 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1431 are further described hereinbelow with reference to Table Table1.

[22221] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1431 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22222] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1432 (GAM1432) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22223] GAM1432 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1432 was detected is described hereinabove with reference to Figs. 2-8.

[22224] GAM1432 gene, herein designated GAM GENE, and GAM1432 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22225] GAM1432 gene, herein designated GAM GENE, encodes a GAM1432 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1432 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1432 precursor RNA is designated SEQ ID:1405, and is provided hereinbelow with reference to the sequence listing part.

[22226] GAM1432 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1432 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22227] An enzyme complex designated DICER COMPLEX, dices the GAM1432 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1432 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1432 RNA is designated SEQ ID:3081, and is provided hereinbelow with reference to the sequence listing part.

[22228] GAM1432 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1432 target RNA, herein designated GAM TARGET RNA. GAM1432 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22229] GAM1432 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1432 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1432 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1432 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1432 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22230] The complementary binding of GAM1432 RNA, herein designated GAM RNA, to target binding sites on GAM1432 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1432 target RNA, herein designated GAM TARGET RNA, into GAM1432 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22231] It is appreciated that GAM1432 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1432 target genes. The mRNA of each one of this plurality of GAM1432 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1432 RNA, herein designated GAM RNA, and which when bound by GAM1432 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1432 target proteins.

[22232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1432 gene, herein designated GAM GENE, on one or more GAM1432 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22233] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1432 correlate with, and may be deduced from, the identity of the target genes which GAM1432 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22234] Nucleotide sequences of the GAM1432 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1432 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1432 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1432 are further described hereinbelow with reference to Table Table1.

[22235] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1432 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22236] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1433 (GAM1433) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22237] GAM1433 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1433 was detected is described hereinabove with reference to Figs. 2-8.

[22238] GAM1433 gene, herein designated GAM GENE, and GAM1433 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22239] GAM1433 gene, herein designated GAM GENE, encodes a GAM1433 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1433 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1433 precursor RNA is designated SEQ ID:1406, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1406 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[22240] GAM1433 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22241] An enzyme complex designated DICER COMPLEX, dices the GAM1433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1433 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1433 RNA is designated SEQ ID:3082, and is provided hereinbelow with reference to the sequence listing part.

[22242] GAM1433 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1433 target RNA, herein designated GAM TARGET RNA. GAM1433 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22243] GAM1433 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1433 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1433 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1433 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1433 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22244] The complementary binding of GAM1433 RNA, herein designated GAM RNA, to target binding sites on GAM1433 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1433 target RNA, herein designated GAM TARGET RNA, into GAM1433 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22245] It is appreciated that GAM1433 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1433 target genes. The mRNA of each one of this plurality of GAM1433 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1433 RNA, herein designated GAM RNA, and which when bound by GAM1433 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1433 target proteins.

[22246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1433 gene, herein designated GAM GENE, on one or more GAM1433 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22247] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1433 correlate with, and may be deduced from, the identity of the target genes which GAM1433 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22248] Nucleotide sequences of the GAM1433 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1433 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1433 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1433 are further described hereinbelow with reference to Table Table1.

[22249] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1433 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22250] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1434 (GAM1434) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22251] GAM1434 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1434 was detected is described hereinabove with reference to Figs. 2-8.

[22252] GAM1434 gene, herein designated GAM GENE, and GAM1434 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22253] GAM1434 gene, herein designated GAM GENE, encodes a GAM1434 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1434 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1434 precursor RNA is designated SEQ ID:1407, and is provided hereinbelow with reference to the sequence listing part.

[22254] GAM1434 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22255] An enzyme complex designated DICER COMPLEX, dices the GAM1434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1434 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1434 RNA is designated SEQ ID:3083, and is provided hereinbelow with reference to the sequence listing part.

[22256] GAM1434 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1434 target RNA, herein designated GAM TARGET RNA. GAM1434 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22257] GAM1434 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1434 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1434 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1434 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1434 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[22258] The complementary binding of GAM1434 RNA, herein designated GAM RNA, to target binding sites on GAM1434 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1434 target RNA, herein designated GAM TARGET RNA, into GAM1434 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22259] It is appreciated that GAM1434 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1434 target genes. The mRNA of each one of this plurality of GAM1434 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1434 RNA, herein designated GAM RNA, and which when bound by GAM1434 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1434 target proteins.

[22260] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1434 gene, herein designated GAM GENE, on one or

more GAM1434 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22261] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1434 correlate with, and may be deduced from, the identity of the target genes which GAM1434 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22262] Nucleotide sequences of the GAM1434 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1434 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1434 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1434 are further de-

scribed hereinbelow with reference to Table Table1.

[22263] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1434 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22264] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1435 (GAM1435) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22265] GAM1435 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1435 was detected is described hereinabove with reference to Figs. 2-8.

[22266] GAM1435 gene, herein designated GAM GENE, and GAM1435 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22267] GAM1435 gene, herein designated GAM GENE, encodes a GAM1435 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1435 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1435 precursor RNA is designated SEQ ID:1408, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1408 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[22268] GAM1435 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[22269] SEQ ID:100198 detected in mouse EST Accession AA671455.1.

[22270] SEQ ID:100199 detected in mouse EST Accession BE943987.1.

[22271] SEQ ID:100200 detected in mouse EST Accession BE691413.1.

[22272] SEQ ID:100201 detected in mouse EST Accession BG808025.1.

[22273] SEQ ID:100202 detected in mouse EST Accession BG808010.1.

[22274] SEQ ID:100203 detected in mouse EST Accession BG807850.1.

[22275] SEQ ID:100204 detected in mouse EST Accession BG805970.1.

[22276] SEQ ID:100205 detected in mouse EST Accession AW208601.1.

[22277] SEQ ID:100206 detected in mouse EST Accession BB610842.1.

[22278] SEQ ID:100207 detected in mouse EST Accession BB609859.1.

[22279] SEQ ID:100208 detected in mouse EST Accession AW824753.1.

[22280] SEQ ID:100209 detected in mouse EST Accession AA144533.1.

[22281] SEQ ID:100210 detected in mouse EST Accession BE691447.1.

[22282] SEQ ID:100211 detected in mouse EST Accession BG145596.1.

[22283] SEQ ID:100212 detected in mouse EST Accession BE692802.1.

[22284] GAM1435 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1435 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22285] An enzyme complex designated DICER COMPLEX, dices the GAM1435 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1435 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1435 RNA is designated SEQ ID:3084, and is provided hereinbelow with reference to the sequence listing part.

[22286] GAM1435 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1435 target RNA, herein designated GAM TARGET RNA. GAM1435 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22287] GAM1435 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1435 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1435 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1435 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1435 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22288] The complementary binding of GAM1435 RNA, herein designated GAM RNA, to target binding sites on GAM1435 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1435 target RNA, herein designated GAM TARGET RNA, into GAM1435 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22289] It is appreciated that GAM1435 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1435 target genes. The mRNA of each one of this plurality of GAM1435 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1435 RNA, herein designated GAM RNA, and which when bound by GAM1435 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1435 target proteins.

[22290] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1435 gene, herein designated GAM GENE, on one or more GAM1435 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22291] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1435 correlate with, and may be deduced from, the identity of the target genes which GAM1435 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22292] Nucleotide sequences of the GAM1435 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1435 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1435 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1435 are further described hereinbelow with reference to Table Table1.

[22293] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1435 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22294] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1436 (GAM1436) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22295] GAM1436 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1436 was detected is described hereinabove with reference to Figs. 2-8.

[22296] GAM1436 gene, herein designated GAM GENE, and GAM1436 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22297] GAM1436 gene, herein designated GAM GENE, encodes a GAM1436 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1436 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1436 precursor RNA is designated SEQ ID:1409, and is provided hereinbelow with reference to the sequence listing part.

[22298] GAM1436 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22299] An enzyme complex designated DICER COMPLEX, dices the GAM1436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1436 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1436 RNA is designated SEQ ID:3085, and is provided hereinbelow with reference to the sequence listing part.

[22300] GAM1436 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1436 target RNA, herein designated GAM TARGET RNA. GAM1436 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22301] GAM1436 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1436 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1436 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1436 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1436 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22302] The complementary binding of GAM1436 RNA, herein designated GAM RNA, to target binding sites on GAM1436 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1436 target RNA, herein designated GAM TARGET RNA, into GAM1436 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22303] It is appreciated that GAM1436 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1436 target genes. The mRNA of each one of this

plurality of GAM1436 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1436 RNA, herein designated GAM RNA, and which when bound by GAM1436 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1436 target proteins.

[22304] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1436 gene, herein designated GAM GENE, on one or more GAM1436 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22305] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1436 correlate with, and may be deduced from, the identity of the target genes which GAM1436 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22306] Nucleotide sequences of the GAM1436 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1436 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1436 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1436 are further described hereinbelow with reference to Table Table1.

[22307] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1436 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22308] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1437 (GAM1437) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[22309] GAM1437 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1437 was detected is described hereinabove with reference to Figs. 2-8.

[22310] GAM1437 gene, herein designated GAM GENE, and GAM1437 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22311] GAM1437 gene, herein designated GAM GENE, encodes a GAM1437 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1437 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1437 precursor RNA is designated SEQ ID:1410, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1410 is located at position 65229 relative to contig NT_024901.11, on chromosome 17.

[22312] GAM1437 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22313] An enzyme complex designated DICER COMPLEX, dices the GAM1437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1437 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1437 RNA is designated SEQ ID:3086, and is provided hereinbelow with reference to the sequence listing part.

[22314] GAM1437 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1437 target RNA, herein designated GAM TARGET RNA. GAM1437 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22315] GAM1437 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1437 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1437 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1437 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1437 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[22316] The complementary binding of GAM1437 RNA, herein designated GAM RNA, to target binding sites on GAM1437 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1437 target RNA, herein designated GAM TARGET RNA, into GAM1437 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22317] It is appreciated that GAM1437 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1437 target genes. The mRNA of each one of this plurality of GAM1437 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1437 RNA, herein designated GAM RNA, and which when bound by GAM1437 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1437 target proteins.

[22318] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1437 gene, herein designated GAM GENE, on one or

more GAM1437 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22319] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1437 correlate with, and may be deduced from, the identity of the target genes which GAM1437 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22320] Nucleotide sequences of the GAM1437 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1437 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1437 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1437 are further de-

scribed hereinbelow with reference to Table Table1.

[22321] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1437 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22322] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1438 (GAM1438) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22323] GAM1438 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1438 was detected is described hereinabove with reference to Figs. 2-8.

[22324] GAM1438 gene, herein designated GAM GENE, and GAM1438 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22325] GAM1438 gene, herein designated GAM GENE, encodes a GAM1438 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1438 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1438 precursor RNA is designated SEQ ID:1411, and is provided hereinbelow with reference to the sequence listing part.

[22326] GAM1438 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22327] An enzyme complex designated DICER COMPLEX, dices the GAM1438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1438 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1438 RNA is designated SEQ ID:3087, and is provided hereinbelow with reference to the sequence listing part.

[22328] GAM1438 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1438 target RNA, herein designated GAM TARGET RNA. GAM1438 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22329] GAM1438 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1438 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1438 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1438 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1438 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22330] The complementary binding of GAM1438 RNA, herein designated GAM RNA, to target binding sites on GAM1438 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1438 target RNA, herein designated GAM TARGET RNA, into GAM1438 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22331] It is appreciated that GAM1438 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1438 target genes. The mRNA of each one of this plurality of GAM1438 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1438 RNA, herein designated GAM RNA, and which when bound by GAM1438 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1438 target proteins.

[22332] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1438 gene, herein designated GAM GENE, on one or more GAM1438 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22333] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1438 correlate with, and may be deduced from, the identity of the target genes which GAM1438 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22334] Nucleotide sequences of the GAM1438 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1438 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1438 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1438 are further described hereinbelow with reference to Table Table1.

[22335] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1438 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22336] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1439 (GAM1439) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22337] GAM1439 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1439 was detected is described hereinabove with reference to Figs. 2-8.

[22338] GAM1439 gene, herein designated GAM GENE, and GAM1439 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22339] GAM1439 gene, herein designated GAM GENE, encodes a GAM1439 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1439 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1439 precursor RNA is designated SEQ ID:1412, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1412 is located at position 40742576 relative to contig NT_026437.9, on chromosome 14.

[22340] GAM1439 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22341] An enzyme complex designated DICER COMPLEX, dices the GAM1439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1439 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1439 RNA is designated SEQ ID:3088, and is provided hereinbelow with reference to the sequence listing part.

[22342] GAM1439 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1439 target RNA, herein designated GAM TARGET RNA. GAM1439 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22343] GAM1439 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1439 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1439 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1439 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1439 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22344] The complementary binding of GAM1439 RNA, herein designated GAM RNA, to target binding sites on GAM1439 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1439 target RNA, herein designated GAM TARGET RNA, into GAM1439 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22345] It is appreciated that GAM1439 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1439 target genes. The mRNA of each one of this plurality of GAM1439 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1439 RNA, herein designated GAM RNA, and which when bound by GAM1439 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1439 target proteins.

[22346] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1439 gene, herein designated GAM GENE, on one or more GAM1439 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22347] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1439 correlate with, and may be deduced from, the identity of the target genes which GAM1439 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22348] Nucleotide sequences of the GAM1439 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1439 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1439 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1439 are further described hereinbelow with reference to Table Table1.

[22349] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1439 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22350] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1440 (GAM1440) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22351] GAM1440 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1440 was detected is described hereinabove with reference to Figs. 2-8.

[22352] GAM1440 gene, herein designated GAM GENE, and GAM1440 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22353] GAM1440 gene, herein designated GAM GENE, encodes a GAM1440 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1440 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1440 precursor RNA is designated SEQ ID:1413, and is provided hereinbelow with reference to the sequence listing part.

[22354] GAM1440 has 23 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[22355] SEQ ID:98958 detected in mouse EST Accession BI652678.1.

[22356] SEQ ID:98959 detected in mouse EST Accession BB621170.1.

[22357] SEQ ID:98960 detected in mouse EST Accession BI221824.1.

[22358] SEQ ID:98961 detected in mouse EST Accession BI112062.1.

[22359] SEQ ID:98962 detected in mouse EST Accession BG808761.1.

[22360] SEQ ID:98963 detected in mouse EST Accession AW913724.1.

[22361] SEQ ID:98964 detected in mouse EST Accession

BI103503.1.

[22362] SEQ ID:98965 detected in mouse EST Accession BI646101.1.

[22363] SEQ ID:98966 detected in mouse EST Accession BI904701.1.

[22364] SEQ ID:98967 detected in mouse EST Accession BI647166.1.

[22365] SEQ ID:98968 detected in mouse EST Accession BI656364.1.

[22366] SEQ ID:98969 detected in mouse EST Accession BI414193.1.

[22367] SEQ ID:98970 detected in mouse EST Accession AW320568.1.

[22368] SEQ ID:98971 detected in mouse EST Accession BE946230.1.

[22369] SEQ ID:98972 detected in mouse EST Accession BG245021.1.

[22370] SEQ ID:98973 detected in mouse EST Accession BF320339.1.

[22371] SEQ ID:98974 detected in mouse EST Accession BE854824.1.

[22372] SEQ ID:98975 detected in mouse EST Accession BI903612.1.

[22373] SEQ ID:98976 detected in mouse EST Accession BG922758.1.

[22374] SEQ ID:98977 detected in mouse EST Accession BI853226.1.

[22375] SEQ ID:98978 detected in mouse EST Accession BI736225.1.

[22376] SEQ ID:98979 detected in mouse EST Accession BI557876.1.

[22377] SEQ ID:98980 detected in mouse EST Accession BF784670.1.

[22378] GAM1440 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22379] An enzyme complex designated DICER COMPLEX, dices the GAM1440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1440 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1440 RNA is designated SEQ ID:3089, and is provided hereinbelow with reference to the sequence listing part.

[22380] GAM1440 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1440 target RNA, herein designated GAM TARGET RNA. GAM1440 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22381] GAM1440 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1440 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1440 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1440 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1440 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22382] The complementary binding of GAM1440 RNA, herein designated GAM RNA, to target binding sites on GAM1440 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1440 target RNA, herein designated GAM TARGET RNA, into GAM1440 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22383] It is appreciated that GAM1440 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1440 target genes. The mRNA of each one of this plurality of GAM1440 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1440 RNA, herein designated GAM RNA, and which when bound by GAM1440 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1440 target proteins.

[22384] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1440 gene, herein designated GAM GENE, on one or more GAM1440 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22385] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1440 correlate with, and may be deduced from, the identity of the target genes which GAM1440 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22386] Nucleotide sequences of the GAM1440 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1440 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1440 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1440 are further described hereinbelow with reference to Table Table1.

[22387] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1440 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22388] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1441 (GAM1441) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22389] GAM1441 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1441 was detected is described hereinabove with reference to Figs. 2-8.

[22390] GAM1441 gene, herein designated GAM GENE, and GAM1441 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22391] GAM1441 gene, herein designated GAM GENE, encodes a GAM1441 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1441 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1441 precursor RNA is designated SEQ ID:1414, and is provided hereinbelow with reference to the sequence listing part.

[22392] GAM1441 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1441 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22393] An enzyme complex designated DICER COMPLEX, dices the GAM1441 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1441 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1441 RNA is designated SEQ ID:3090, and is provided hereinbelow with reference to the sequence listing part.

[22394] GAM1441 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1441 target RNA, herein designated GAM TARGET RNA. GAM1441 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22395] GAM1441 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1441 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1441 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1441 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1441 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22396] The complementary binding of GAM1441 RNA, herein designated GAM RNA, to target binding sites on GAM1441 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1441 target RNA, herein designated GAM TARGET RNA, into GAM1441 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22397] It is appreciated that GAM1441 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1441 target genes. The mRNA of each one of this plurality of GAM1441 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1441 RNA, herein designated GAM RNA, and which when bound by GAM1441 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1441 target proteins.

[22398] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1441 gene, herein designated GAM GENE, on one or more GAM1441 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22399] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1441 correlate with, and may be deduced from, the identity of the target genes which GAM1441 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22400] Nucleotide sequences of the GAM1441 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1441 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1441 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1441 are further described hereinbelow with reference to Table Table1.

[22401] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1441 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22402] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1442 (GAM1442) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22403] GAM1442 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1442 was detected is described hereinabove with reference to Figs. 2-8.

[22404] GAM1442 gene, herein designated GAM GENE, and GAM1442 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22405] GAM1442 gene, herein designated GAM GENE, encodes a GAM1442 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1442 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1442 precursor RNA is designated SEQ ID:1415, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1415 is located at position 6294463 relative to contig NT_024981.11, on chromosome 18.

[22406] GAM1442 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22407] An enzyme complex designated DICER COMPLEX, dices the GAM1442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1442 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1442 RNA is designated SEQ ID:3091, and is provided hereinbelow with reference to the sequence listing part.

[22408] GAM1442 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1442 target RNA, herein designated GAM TARGET RNA. GAM1442 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22409] GAM1442 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1442 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1442 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1442 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1442 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22410] The complementary binding of GAM1442 RNA, herein designated GAM RNA, to target binding sites on GAM1442 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1442 target RNA, herein designated GAM TARGET RNA, into GAM1442 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22411] It is appreciated that GAM1442 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1442 target genes. The mRNA of each one of this plurality of GAM1442 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1442 RNA, herein designated GAM RNA, and which when bound by GAM1442 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1442 target proteins.

[22412] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1442 gene, herein designated GAM GENE, on one or more GAM1442 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22413] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1442 correlate with, and may be deduced from, the identity of the target genes which GAM1442 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22414] Nucleotide sequences of the GAM1442 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1442 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1442 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1442 are further described hereinbelow with reference to Table Table1.

[22415] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1442 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22416] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1443 (GAM1443) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22417] GAM1443 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1443 was detected is described hereinabove with reference to Figs. 2-8.

[22418] GAM1443 gene, herein designated GAM GENE, and GAM1443 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22419] GAM1443 gene, herein designated GAM GENE, encodes a GAM1443 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1443 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1443 precursor RNA is designated SEQ ID:1416, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1416 is located at position 6294458 relative to contig NT_024981.11, on chromosome 18.

[22420] GAM1443 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1443 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22421] An enzyme complex designated DICER COMPLEX, dices the GAM1443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1443 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1443 RNA is designated SEQ ID:3092, and is provided hereinbelow with reference to the sequence listing part.

[22422] GAM1443 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1443 target RNA, herein designated GAM TARGET

RNA. GAM1443 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22423] GAM1443 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1443 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1443 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1443 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1443 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22424] The complementary binding of GAM1443 RNA, herein designated GAM RNA, to target binding sites on GAM1443 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1443 target RNA, herein designated GAM TARGET RNA, into GAM1443 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22425] It is appreciated that GAM1443 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1443 target genes. The mRNA of each one of this plurality of GAM1443 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1443 RNA, herein designated GAM RNA, and which when bound by GAM1443 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1443 target proteins.

[22426] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1443 gene, herein designated GAM GENE, on one or more GAM1443 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22427] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1443 correlate with, and may be deduced from, the identity of the target genes which GAM1443 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22428] Nucleotide sequences of the GAM1443 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1443 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1443 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1443 are further described hereinbelow with reference to Table Table1.

[22429] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1443 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22430] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1444 (GAM1444) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22431] GAM1444 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1444 was detected is described hereinabove with reference to Figs. 2-8.

[22432] GAM1444 gene, herein designated GAM GENE, and GAM1444 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22433] GAM1444 gene, herein designated GAM GENE, encodes a

GAM1444 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1444 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1444 precursor RNA is designated SEQ ID:1417, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1417 is located at position 1171154 relative to contig NT_022567.9, on chromosome 3.

[22434] GAM1444 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22435] An enzyme complex designated DICER COMPLEX, dices the GAM1444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1444 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1444 RNA is designated SEQ ID:3093, and is provided hereinbelow with reference to the sequence listing part.

[22436] GAM1444 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1444 target RNA, herein designated GAM TARGET RNA. GAM1444 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22437] GAM1444 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1444 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1444 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1444 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1444 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22438] The complementary binding of GAM1444 RNA, herein designated GAM RNA, to target binding sites on GAM1444 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1444 target RNA, herein designated GAM TARGET RNA, into GAM1444 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22439] It is appreciated that GAM1444 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1444 target genes. The mRNA of each one of this plurality of GAM1444 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1444 RNA, herein designated GAM RNA, and which when bound by GAM1444 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1444 target proteins.

[22440] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1444 gene, herein designated GAM GENE, on one or more GAM1444 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22441] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1444 correlate with, and may be deduced from, the identity of the target genes which GAM1444 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22442] Nucleotide sequences of the GAM1444 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1444 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1444 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1444 are further described hereinbelow with reference to Table Table1.

[22443] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1444 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22444] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1445 (GAM1445) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22445] GAM1445 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1445 was detected is described hereinabove with reference to Figs. 2-8.

[22446] GAM1445 gene, herein designated GAM GENE, and GAM1445 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22447] GAM1445 gene, herein designated GAM GENE, encodes a GAM1445 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1445 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1445 precursor RNA is designated SEQ ID:1418, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1418 is located at position 2554140 relative to contig NT_004852.13, on chromosome 1.

[22448] GAM1445 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22449] An enzyme complex designated DICER COMPLEX, dices the GAM1445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1445 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1445 RNA is designated SEQ ID:3094, and is provided hereinbelow with reference to the sequence listing part.

[22450] GAM1445 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1445 target RNA, herein designated GAM TARGET RNA. GAM1445 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22451] GAM1445 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1445 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1445 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1445 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1445 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22452] The complementary binding of GAM1445 RNA, herein designated GAM RNA, to target binding sites on GAM1445 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1445 target RNA, herein designated GAM TARGET RNA, into GAM1445 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22453] It is appreciated that GAM1445 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1445 target genes. The mRNA of each one of this plurality of GAM1445 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1445 RNA, herein designated GAM RNA, and which when bound by GAM1445 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1445 target proteins.

[22454] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1445 gene, herein designated GAM GENE, on one or more GAM1445 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22455] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1445 correlate with, and may be deduced from, the identity of the target genes which GAM1445 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22456] Nucleotide sequences of the GAM1445 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1445 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1445 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1445 are further described hereinbelow with reference to Table Table1.

[22457] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1445 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22458] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1446 (GAM1446) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22459] GAM1446 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1446 was detected is described hereinabove with reference to Figs. 2-8.

[22460] GAM1446 gene, herein designated GAM GENE, and GAM1446 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22461] GAM1446 gene, herein designated GAM GENE, encodes a GAM1446 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1446 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1446 precursor RNA is designated SEQ ID:1419, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1419 is located at position 2719367 relative to contig NT_009237.13, on chromosome 11.

[22462] GAM1446 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22463] An enzyme complex designated DICER COMPLEX, dices the GAM1446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1446 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1446 RNA is designated SEQ ID:3095, and is provided hereinbelow with reference to the sequence listing part.

[22464] GAM1446 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1446 target RNA, herein designated GAM TARGET RNA. GAM1446 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22465] GAM1446 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1446 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1446 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1446 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1446 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22466] The complementary binding of GAM1446 RNA, herein designated GAM RNA, to target binding sites on GAM1446 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1446 target RNA, herein designated GAM TARGET RNA, into GAM1446 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22467] It is appreciated that GAM1446 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1446 target genes. The mRNA of each one of this

plurality of GAM1446 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1446 RNA, herein designated GAM RNA, and which when bound by GAM1446 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1446 target proteins.

[22468] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1446 gene, herein designated GAM GENE, on one or more GAM1446 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22469] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1446 correlate with, and may be deduced from, the identity of the target genes which GAM1446 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22470] Nucleotide sequences of the GAM1446 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1446 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1446 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1446 are further described hereinbelow with reference to Table Table1.

[22471] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1446 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22472] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1447 (GAM1447) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[22473] GAM1447 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1447 was detected is described hereinabove with reference to Figs. 2-8.

[22474] GAM1447 gene, herein designated GAM GENE, and GAM1447 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22475] GAM1447 gene, herein designated GAM GENE, encodes a GAM1447 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1447 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1447 precursor RNA is designated SEQ ID:1420, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1420 is located at position 4851359 relative to contig NT_022517.13, on chromosome 3.

[22476] GAM1447 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22477] An enzyme complex designated DICER COMPLEX, dices the GAM1447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1447 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1447 RNA is designated SEQ ID:3096, and is provided hereinbelow with reference to the sequence listing part.

[22478] GAM1447 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1447 target RNA, herein designated GAM TARGET RNA. GAM1447 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22479] GAM1447 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1447 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1447 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1447 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1447 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[22480] The complementary binding of GAM1447 RNA, herein designated GAM RNA, to target binding sites on GAM1447 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1447 target RNA, herein designated GAM TARGET RNA, into GAM1447 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22481] It is appreciated that GAM1447 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1447 target genes. The mRNA of each one of this plurality of GAM1447 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1447 RNA, herein designated GAM RNA, and which when bound by GAM1447 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1447 target proteins.

[22482] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1447 gene, herein designated GAM GENE, on one or

more GAM1447 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22483] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1447 correlate with, and may be deduced from, the identity of the target genes which GAM1447 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22484] Nucleotide sequences of the GAM1447 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1447 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1447 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1447 are further de-

scribed hereinbelow with reference to Table Table1.

[22485] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1447 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22486] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1448 (GAM1448) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22487] GAM1448 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1448 was detected is described hereinabove with reference to Figs. 2-8.

[22488] GAM1448 gene, herein designated GAM GENE, and GAM1448 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22489] GAM1448 gene, herein designated GAM GENE, encodes a GAM1448 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1448 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1448 precursor RNA is designated SEQ ID:1421, and is provided hereinbelow with reference to the sequence listing part.

[22490] GAM1448 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22491] An enzyme complex designated DICER COMPLEX, dices the GAM1448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1448 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1448 RNA is designated SEQ ID:3097, and is provided hereinbelow with reference to the sequence listing part.

[22492] GAM1448 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1448 target RNA, herein designated GAM TARGET RNA. GAM1448 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22493] GAM1448 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1448 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1448 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1448 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1448 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22494] The complementary binding of GAM1448 RNA, herein designated GAM RNA, to target binding sites on GAM1448 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1448 target RNA, herein designated GAM TARGET RNA, into GAM1448 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22495] It is appreciated that GAM1448 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1448 target genes. The mRNA of each one of this plurality of GAM1448 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1448 RNA, herein designated GAM RNA, and which when bound by GAM1448 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1448 target proteins.

[22496] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1448 gene, herein designated GAM GENE, on one or more GAM1448 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22497] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1448 correlate with, and may be deduced from, the identity of the target genes which GAM1448 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22498] Nucleotide sequences of the GAM1448 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1448 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1448 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1448 are further described hereinbelow with reference to Table Table1.

[22499] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1448 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22500] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1449 (GAM1449) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22501] GAM1449 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1449 was detected is described hereinabove with reference to Figs. 2-8.

[22502] GAM1449 gene, herein designated GAM GENE, and GAM1449 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22503] GAM1449 gene, herein designated GAM GENE, encodes a GAM1449 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1449 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1449 precursor RNA is designated SEQ ID:1422, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1422 is located at position 2907544 relative to contig NT_015805.11, on chromosome 2.

[22504] GAM1449 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22505] An enzyme complex designated DICER COMPLEX, dices the GAM1449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1449 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1449 RNA is designated SEQ ID:3098, and is provided hereinbelow with reference to the sequence listing part.

[22506] GAM1449 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1449 target RNA, herein designated GAM TARGET RNA. GAM1449 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22507] GAM1449 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1449 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1449 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1449 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1449 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22508] The complementary binding of GAM1449 RNA, herein designated GAM RNA, to target binding sites on GAM1449 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1449 target RNA, herein designated GAM TARGET RNA, into GAM1449 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22509] It is appreciated that GAM1449 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1449 target genes. The mRNA of each one of this plurality of GAM1449 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1449 RNA, herein designated GAM RNA, and which when bound by GAM1449 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1449 target proteins.

[22510] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1449 gene, herein designated GAM GENE, on one or more GAM1449 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22511] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1449 correlate with, and may be deduced from, the identity of the target genes which GAM1449 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22512] Nucleotide sequences of the GAM1449 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1449 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1449 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1449 are further described hereinbelow with reference to Table Table1.

[22513] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1449 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22514] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1450 (GAM1450) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22515] GAM1450 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1450 was detected is described hereinabove with reference to Figs. 2-8.

[22516] GAM1450 gene, herein designated GAM GENE, and GAM1450 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22517] GAM1450 gene, herein designated GAM GENE, encodes a GAM1450 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1450 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1450 precursor RNA is designated SEQ ID:1423, and is provided hereinbelow with reference to the sequence listing part.

[22518] GAM1450 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22519] An enzyme complex designated DICER COMPLEX, dices the GAM1450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1450 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1450 RNA is designated SEQ ID:3099, and is provided hereinbelow with reference to the sequence listing part.

[22520] GAM1450 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1450 target RNA, herein designated GAM TARGET RNA. GAM1450 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22521] GAM1450 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1450 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1450 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1450 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1450 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22522] The complementary binding of GAM1450 RNA, herein designated GAM RNA, to target binding sites on GAM1450 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1450 target RNA, herein designated GAM TARGET RNA, into GAM1450 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22523] It is appreciated that GAM1450 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1450 target genes. The mRNA of each one of this plurality of GAM1450 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1450 RNA, herein designated GAM RNA, and which when bound by GAM1450 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1450 target proteins.

[22524] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1450 gene, herein designated GAM GENE, on one or more GAM1450 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22525] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1450 correlate with, and may

be deduced from, the identity of the target genes which GAM1450 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22526] Nucleotide sequences of the GAM1450 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1450 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1450 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1450 are further described hereinbelow with reference to Table Table1.

[22527] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1450 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22528] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1451 (GAM1451) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22529] GAM1451 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1451 was detected is described hereinabove with reference to Figs. 2-8.

[22530] GAM1451 gene, herein designated GAM GENE, and GAM1451 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22531] GAM1451 gene, herein designated GAM GENE, encodes a GAM1451 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1451 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1451 precursor RNA is designated SEQ ID:1424, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1424 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[22532] GAM1451 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22533] An enzyme complex designated DICER COMPLEX, dices the GAM1451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1451 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1451 RNA is designated SEQ ID:3100, and is provided hereinbelow with reference to the sequence listing part.

[22534] GAM1451 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1451 target RNA, herein designated GAM TARGET RNA. GAM1451 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[22535] GAM1451 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1451 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1451 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1451 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1451 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22536] The complementary binding of GAM1451 RNA, herein

designated GAM RNA, to target binding sites on GAM1451 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1451 target RNA, herein designated GAM TARGET RNA, into GAM1451 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22537] It is appreciated that GAM1451 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1451 target genes. The mRNA of each one of this plurality of GAM1451 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1451 RNA, herein designated GAM RNA, and which when bound by GAM1451 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1451 target proteins.

[22538] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1451 gene, herein designated GAM GENE, on one or more GAM1451 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22539] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1451 correlate with, and may be deduced from, the identity of the target genes which GAM1451 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22540] Nucleotide sequences of the GAM1451 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1451 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1451 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1451 are further described hereinbelow with reference to Table Table1.

[22541] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1451 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22542] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1452 (GAM1452) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22543] GAM1452 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1452 was detected is described hereinabove with reference to Figs. 2-8.

[22544] GAM1452 gene, herein designated GAM GENE, and GAM1452 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22545] GAM1452 gene, herein designated GAM GENE, encodes a GAM1452 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1452 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1452 precursor RNA is designated SEQ ID:1425, and is provided hereinbelow with reference to the sequence listing part.

[22546] GAM1452 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22547] An enzyme complex designated DICER COMPLEX, dices the GAM1452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1452 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide se-

quence of GAM1452 RNA is designated SEQ ID:3101, and is provided hereinbelow with reference to the sequence listing part.

[22548] GAM1452 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1452 target RNA, herein designated GAM TARGET RNA. GAM1452 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22549] GAM1452 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1452 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1452 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1452 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1452 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22550] The complementary binding of GAM1452 RNA, herein designated GAM RNA, to target binding sites on GAM1452 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1452 target RNA, herein designated GAM TARGET RNA, into GAM1452 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22551] It is appreciated that GAM1452 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1452 target genes. The mRNA of each one of this plurality of GAM1452 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1452 RNA,

herein designated GAM RNA, and which when bound by GAM1452 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1452 target proteins.

[22552] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1452 gene, herein designated GAM GENE, on one or more GAM1452 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22553] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1452 correlate with, and may be deduced from, the identity of the target genes which

GAM1452 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22554] Nucleotide sequences of the GAM1452 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1452 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1452 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1452 are further described hereinbelow with reference to Table Table1.

[22555] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1452 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22556] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1453 (GAM1453) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22557] GAM1453 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1453 was detected is described hereinabove with reference to Figs. 2-8.

[22558] GAM1453 gene, herein designated GAM GENE, and GAM1453 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22559] GAM1453 gene, herein designated GAM GENE, encodes a GAM1453 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1453 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1453 precursor RNA is designated SEQ ID:1426, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1426 is located at position 2349689 relative to contig NT_021907.13, on chromosome 1.

[22560] GAM1453 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22561] An enzyme complex designated DICER COMPLEX, dices the GAM1453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1453 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1453 RNA is designated SEQ ID:3102, and is provided hereinbelow with reference to the sequence listing part.

[22562] GAM1453 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1453 target RNA, herein designated GAM TARGET RNA. GAM1453 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22563] GAM1453 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1453 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1453 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1453 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1453 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22564] The complementary binding of GAM1453 RNA, herein designated GAM RNA, to target binding sites on GAM1453

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1453 target RNA, herein designated GAM TARGET RNA, into GAM1453 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22565] It is appreciated that GAM1453 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1453 target genes. The mRNA of each one of this plurality of GAM1453 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1453 RNA, herein designated GAM RNA, and which when bound by GAM1453 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1453 target proteins.

[22566] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1453 gene, herein designated GAM GENE, on one or more GAM1453 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22567] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1453 correlate with, and may be deduced from, the identity of the target genes which GAM1453 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22568] Nucleotide sequences of the GAM1453 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1453 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1453 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1453 are further described hereinbelow with reference to Table Table1.

[22569] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1453 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22570] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1454 (GAM1454) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22571] GAM1454 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1454 was detected is described hereinabove with reference to Figs. 2-8.

[22572] GAM1454 gene, herein designated GAM GENE, and GAM1454 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22573] GAM1454 gene, herein designated GAM GENE, encodes a GAM1454 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1454 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1454 precursor RNA is designated SEQ ID:1427, and is provided hereinbelow with reference to the sequence listing part.

[22574] GAM1454 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22575] An enzyme complex designated DICER COMPLEX, dices the GAM1454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1454 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1454 RNA is designated SEQ ID:3103, and

is provided hereinbelow with reference to the sequence listing part.

[22576] GAM1454 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1454 target RNA, herein designated GAM TARGET RNA. GAM1454 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22577] GAM1454 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1454 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1454 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1454 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1454 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22578] The complementary binding of GAM1454 RNA, herein designated GAM RNA, to target binding sites on GAM1454 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1454 target RNA, herein designated GAM TARGET RNA, into GAM1454 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22579] It is appreciated that GAM1454 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1454 target genes. The mRNA of each one of this plurality of GAM1454 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1454 RNA, herein designated GAM RNA, and which when bound by

GAM1454 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1454 target proteins.

[22580] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1454 gene, herein designated GAM GENE, on one or more GAM1454 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22581] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1454 correlate with, and may be deduced from, the identity of the target genes which GAM1454 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[22582] Nucleotide sequences of the GAM1454 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1454 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1454 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1454 are further described hereinbelow with reference to Table Table1.

[22583] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1454 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22584] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1455 (GAM1455) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22585] GAM1455 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1455 was detected is described hereinabove

with reference to Figs. 2-8.

[22586] GAM1455 gene, herein designated GAM GENE, and GAM1455 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22587] GAM1455 gene, herein designated GAM GENE, encodes a GAM1455 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1455 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1455 precursor RNA is designated SEQ ID:1428, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1428 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[22588] GAM1455 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22589] An enzyme complex designated DICER COMPLEX, dices the GAM1455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1455 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1455 RNA is designated SEQ ID:3104, and is provided hereinbelow with reference to the sequence listing part.

[22590] GAM1455 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1455 target RNA, herein designated GAM TARGET RNA. GAM1455 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22591] GAM1455 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1455 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1455 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1455 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1455 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22592] The complementary binding of GAM1455 RNA, herein designated GAM RNA, to target binding sites on GAM1455 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1455 target RNA, herein designated GAM TARGET RNA, into GAM1455 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22593] It is appreciated that GAM1455 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1455 target genes. The mRNA of each one of this plurality of GAM1455 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1455 RNA, herein designated GAM RNA, and which when bound by GAM1455 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1455 target proteins.

[22594] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1455 gene, herein designated GAM GENE, on one or more GAM1455 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22595] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1455 correlate with, and may be deduced from, the identity of the target genes which GAM1455 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22596] Nucleotide sequences of the GAM1455 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1455 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1455 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1455 are further described hereinbelow with reference to Table Table1.

[22597] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1455 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22598] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1456 (GAM1456) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22599] GAM1456 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1456 was detected is described hereinabove with reference to Figs. 2-8.

[22600] GAM1456 gene, herein designated GAM GENE, and GAM1456 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22601] GAM1456 gene, herein designated GAM GENE, encodes a GAM1456 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1456 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1456 precursor RNA is

designated SEQ ID:1429, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1429 is located at position 5446699 relative to contig NT_022459.11, on chromosome 3.

[22602] GAM1456 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22603] An enzyme complex designated DICER COMPLEX, dices the GAM1456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1456 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1456 RNA is designated SEQ ID:3105, and is provided hereinbelow with reference to the sequence listing part.

[22604] GAM1456 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1456 target RNA, herein designated GAM TARGET RNA. GAM1456 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22605] GAM1456 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1456 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1456 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1456 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1456 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22606] The complementary binding of GAM1456 RNA, herein designated GAM RNA, to target binding sites on GAM1456 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1456 target RNA, herein designated GAM TARGET RNA, into GAM1456 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22607] It is appreciated that GAM1456 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1456 target genes. The mRNA of each one of this plurality of GAM1456 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1456 RNA,

herein designated GAM RNA, and which when bound by GAM1456 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1456 target proteins.

[22608] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1456 gene, herein designated GAM GENE, on one or more GAM1456 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22609] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1456 correlate with, and may be deduced from, the identity of the target genes which

GAM1456 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22610] Nucleotide sequences of the GAM1456 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1456 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1456 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1456 are further described hereinbelow with reference to Table Table1.

[22611] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1456 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22612] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1457 (GAM1457) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22613] GAM1457 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1457 was detected is described hereinabove with reference to Figs. 2-8.

[22614] GAM1457 gene, herein designated GAM GENE, and GAM1457 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22615] GAM1457 gene, herein designated GAM GENE, encodes a GAM1457 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1457 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1457 precursor RNA is designated SEQ ID:1430, and is provided hereinbelow with reference to the sequence listing part.

[22616] GAM1457 has 5 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[22617] SEQ ID:99199 detected in mouse EST Accession BI899720.1.

[22618] SEQ ID:99200 detected in mouse EST Accession BI899837.1.

[22619] SEQ ID:99201 detected in mouse EST Accession BI899410.1.

[22620] SEQ ID:99202 detected in mouse EST Accession BE655126.1.

[22621] SEQ ID:98223 detected in mouse EST Accession BI899719.1.

[22622] GAM1457 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22623] An enzyme complex designated DICER COMPLEX, dices the GAM1457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1457 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1457 RNA is designated SEQ ID:3106, and is provided hereinbelow with reference to the sequence listing part.

[22624] GAM1457 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1457 target RNA, herein designated GAM TARGET RNA. GAM1457 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22625] GAM1457 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1457 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1457 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1457 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1457 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22626] The complementary binding of GAM1457 RNA, herein designated GAM RNA, to target binding sites on GAM1457 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1457 target RNA, herein designated GAM TARGET RNA, into GAM1457 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22627] It is appreciated that GAM1457 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1457 target genes. The mRNA of each one of this plurality of GAM1457 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1457 RNA, herein designated GAM RNA, and which when bound by GAM1457 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1457 target proteins.

[22628] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1457 gene, herein designated GAM GENE, on one or more GAM1457 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22629] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1457 correlate with, and may be deduced from, the identity of the target genes which GAM1457 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22630] Nucleotide sequences of the GAM1457 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1457 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1457 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1457 are further described hereinbelow with reference to Table Table1.

[22631] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1457 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22632] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1458 (GAM1458) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22633] GAM1458 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1458 was detected is described hereinabove with reference to Figs. 2-8.

[22634] GAM1458 gene, herein designated GAM GENE, and GAM1458 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22635] GAM1458 gene, herein designated GAM GENE, encodes a GAM1458 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1458 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1458 precursor RNA is designated SEQ ID:1431, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1431 is located at position 12701528 relative to contig NT_011109.13, on chromosome 19.

[22636] GAM1458 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22637] An enzyme complex designated DICER COMPLEX, dices the GAM1458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1458 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1458 RNA is designated SEQ ID:3107, and is provided hereinbelow with reference to the sequence listing part.

[22638] GAM1458 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1458 target RNA, herein designated GAM TARGET RNA. GAM1458 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22639] GAM1458 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1458 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1458 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1458 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1458 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22640] The complementary binding of GAM1458 RNA, herein designated GAM RNA, to target binding sites on GAM1458 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1458 target RNA, herein designated GAM TARGET RNA, into GAM1458 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22641] It is appreciated that GAM1458 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1458 target genes. The mRNA of each one of this plurality of GAM1458 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1458 RNA, herein designated GAM RNA, and which when bound by GAM1458 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1458 target proteins.

[22642] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1458 gene, herein designated GAM GENE, on one or more GAM1458 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22643] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1458 correlate with, and may be deduced from, the identity of the target genes which GAM1458 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22644] Nucleotide sequences of the GAM1458 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1458 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1458 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1458 are further described hereinbelow with reference to Table Table1.

[22645] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1458 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22646] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1459 (GAM1459) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22647] GAM1459 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1459 was detected is described hereinabove with reference to Figs. 2-8.

[22648] GAM1459 gene, herein designated GAM GENE, and GAM1459 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22649] GAM1459 gene, herein designated GAM GENE, encodes a GAM1459 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1459 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1459 precursor RNA is designated SEQ ID:1432, and is provided hereinbelow with reference to the sequence listing part.

[22650] GAM1459 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22651] An enzyme complex designated DICER COMPLEX, dices the GAM1459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1459 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1459 RNA is designated SEQ ID:3108, and is provided hereinbelow with reference to the sequence listing part.

[22652] GAM1459 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1459 target RNA, herein designated GAM TARGET RNA. GAM1459 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22653] GAM1459 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1459 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1459 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1459 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1459 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22654] The complementary binding of GAM1459 RNA, herein designated GAM RNA, to target binding sites on GAM1459 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1459 target RNA, herein designated GAM TARGET RNA, into GAM1459 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22655] It is appreciated that GAM1459 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1459 target genes. The mRNA of each one of this plurality of GAM1459 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1459 RNA, herein designated GAM RNA, and which when bound by GAM1459 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1459 target proteins.

[22656] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1459 gene, herein designated GAM GENE, on one or more GAM1459 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22657] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1459 correlate with, and may

be deduced from, the identity of the target genes which GAM1459 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22658] Nucleotide sequences of the GAM1459 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1459 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1459 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1459 are further described hereinbelow with reference to Table Table1.

[22659] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1459 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22660] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1460 (GAM1460) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22661] GAM1460 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1460 was detected is described hereinabove with reference to Figs. 2-8.

[22662] GAM1460 gene, herein designated GAM GENE, and GAM1460 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22663] GAM1460 gene, herein designated GAM GENE, encodes a GAM1460 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1460 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1460 precursor RNA is designated SEQ ID:1433, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1433 is located at position 19848489 relative to contig NT_005403.11, on chromosome 2.

[22664] GAM1460 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22665] An enzyme complex designated DICER COMPLEX, dices the GAM1460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1460 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1460 RNA is designated SEQ ID:3109, and is provided hereinbelow with reference to the sequence listing part.

[22666] GAM1460 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1460 target RNA, herein designated GAM TARGET RNA. GAM1460 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[22667] GAM1460 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1460 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1460 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1460 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1460 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22668] The complementary binding of GAM1460 RNA, herein

designated GAM RNA, to target binding sites on GAM1460 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1460 target RNA, herein designated GAM TARGET RNA, into GAM1460 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22669] It is appreciated that GAM1460 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1460 target genes. The mRNA of each one of this plurality of GAM1460 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1460 RNA, herein designated GAM RNA, and which when bound by GAM1460 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1460 target proteins.

[22670] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1460 gene, herein designated GAM GENE, on one or more GAM1460 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22671] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1460 correlate with, and may be deduced from, the identity of the target genes which GAM1460 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22672] Nucleotide sequences of the GAM1460 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1460 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1460 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1460 are further described hereinbelow with reference to Table Table1.

[22673] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1460 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22674] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1461 (GAM1461) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22675] GAM1461 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1461 was detected is described hereinabove with reference to Figs. 2-8.

[22676] GAM1461 gene, herein designated GAM GENE, and GAM1461 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22677] GAM1461 gene, herein designated GAM GENE, encodes a GAM1461 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1461 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1461 precursor RNA is designated SEQ ID:1434, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1434 is located at position 6531656 relative to contig NT_010194.13, on chromosome 15.

[22678] GAM1461 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22679] An enzyme complex designated DICER COMPLEX, dices the GAM1461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1461 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1461 RNA is designated SEQ ID:3110, and is provided hereinbelow with reference to the sequence listing part.

[22680] GAM1461 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1461 target RNA, herein designated GAM TARGET RNA. GAM1461 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22681] GAM1461 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1461 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1461 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1461 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1461 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22682] The complementary binding of GAM1461 RNA, herein designated GAM RNA, to target binding sites on GAM1461 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1461 target RNA, herein designated GAM TARGET RNA, into GAM1461 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22683] It is appreciated that GAM1461 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1461 target genes. The mRNA of each one of this plurality of GAM1461 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1461 RNA, herein designated GAM RNA, and which when bound by GAM1461 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1461 target proteins.

[22684] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1461 gene, herein designated GAM GENE, on one or more GAM1461 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22685] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1461 correlate with, and may be deduced from, the identity of the target genes which GAM1461 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22686] Nucleotide sequences of the GAM1461 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1461 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1461 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1461 are further described hereinbelow with reference to Table Table1.

[22687] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1461 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22688] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1462 (GAM1462) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22689] GAM1462 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1462 was detected is described hereinabove with reference to Figs. 2-8.

[22690] GAM1462 gene, herein designated GAM GENE, and GAM1462 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22691] GAM1462 gene, herein designated GAM GENE, encodes a GAM1462 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1462 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1462 precursor RNA is designated SEQ ID:1435, and is provided hereinbelow with reference to the sequence listing part.

[22692] GAM1462 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98076, which mouse homolog is detected in mouse EST accession AW411769.1.

[22693] GAM1462 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1462 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22694] An enzyme complex designated DICER COMPLEX, dices the GAM1462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1462 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1462 RNA is designated SEQ ID:3111, and is provided hereinbelow with reference to the sequence listing part.

[22695] GAM1462 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1462 target RNA, herein designated GAM TARGET

RNA. GAM1462 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22696] GAM1462 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1462 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1462 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1462 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1462 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22697] The complementary binding of GAM1462 RNA, herein designated GAM RNA, to target binding sites on GAM1462 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1462 target RNA, herein designated GAM TARGET RNA, into GAM1462 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22698] It is appreciated that GAM1462 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1462 target genes. The mRNA of each one of this plurality of GAM1462 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1462 RNA, herein designated GAM RNA, and which when bound by GAM1462 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1462 target proteins.

[22699] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1462 gene, herein designated GAM GENE, on one or more GAM1462 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22700] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1462 correlate with, and may be deduced from, the identity of the target genes which GAM1462 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22701] Nucleotide sequences of the GAM1462 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1462 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1462 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1462 are further described hereinbelow with reference to Table Table1.

[22702] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1462 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22703] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1463 (GAM1463) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22704] GAM1463 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1463 was detected is described hereinabove with reference to Figs. 2-8.

[22705] GAM1463 gene, herein designated GAM GENE, and GAM1463 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22706] GAM1463 gene, herein designated GAM GENE, encodes a

GAM1463 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1463 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1463 precursor RNA is designated SEQ ID:1436, and is provided hereinbelow with reference to the sequence listing part.

[22707] GAM1463 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22708] An enzyme complex designated DICER COMPLEX, dices the GAM1463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1463 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1463 RNA is designated SEQ ID:3112, and is provided hereinbelow with reference to the sequence listing part.

[22709] GAM1463 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1463 target RNA, herein designated GAM TARGET RNA. GAM1463 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22710] GAM1463 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1463 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1463 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1463 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1463 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22711] The complementary binding of GAM1463 RNA, herein designated GAM RNA, to target binding sites on GAM1463 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1463 target RNA, herein designated GAM TARGET RNA, into GAM1463 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22712] It is appreciated that GAM1463 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1463 target genes. The mRNA of each one of this plurality of GAM1463 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1463 RNA, herein designated GAM RNA, and which when bound by GAM1463 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1463 target proteins.

[22713] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1463 gene, herein designated GAM GENE, on one or more GAM1463 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[22714] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1463 correlate with, and may be deduced from, the identity of the target genes which GAM1463 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22715] Nucleotide sequences of the GAM1463 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1463 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1463 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1463 are further described hereinbelow with reference to Table Table1.

[22716] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1463 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22717] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1464 (GAM1464) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[22718] GAM1464 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1464 was detected is described hereinabove with reference to Figs. 2-8.

[22719] GAM1464 gene, herein designated GAM GENE, and GAM1464 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22720] GAM1464 gene, herein designated GAM GENE, encodes a GAM1464 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1464 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1464 precursor RNA is designated SEQ ID:1437, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1437 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[22721] GAM1464 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences

of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[22722] SEQ ID:99607 detected in mouse EST Accession BB609859.1.

[22723] SEQ ID:99608 detected in mouse EST Accession AA144533.1.

[22724] SEQ ID:99609 detected in mouse EST Accession AA671455.1.

[22725] SEQ ID:99610 detected in mouse EST Accession BE943987.1.

[22726] SEQ ID:99611 detected in mouse EST Accession BG808025.1.

[22727] SEQ ID:99612 detected in mouse EST Accession BG808010.1.

[22728] SEQ ID:99618 detected in mouse EST Accession BB610842.1.

[22729] SEQ ID:99619 detected in mouse EST Accession AW824753.1.

[22730] SEQ ID:99620 detected in mouse EST Accession BE691413.1.

[22731] SEQ ID:99621 detected in mouse EST Accession BE691447.1.

[22732] SEQ ID:99622 detected in mouse EST Accession

BG145596.1.

[22733] SEQ ID:99623 detected in mouse EST Accession BE692802.1.

[22734] SEQ ID:99624 detected in mouse EST Accession AW208601.1.

[22735] SEQ ID:99640 detected in mouse EST Accession BG807850.1.

[22736] SEQ ID:99641 detected in mouse EST Accession BG805970.1.

[22737] GAM1464 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22738] An enzyme complex designated DICER COMPLEX, dices the GAM1464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1464 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1464 RNA is designated SEQ ID:3113, and is provided hereinbelow with reference to the sequence listing part.

[22739] GAM1464 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1464 target RNA, herein designated GAM TARGET RNA. GAM1464 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22740] GAM1464 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1464 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1464 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1464 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1464 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22741] The complementary binding of GAM1464 RNA, herein designated GAM RNA, to target binding sites on GAM1464 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1464 target RNA, herein designated GAM TARGET RNA, into GAM1464 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22742] It is appreciated that GAM1464 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1464 target genes. The mRNA of each one of this plurality of GAM1464 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1464 RNA, herein designated GAM RNA, and which when bound by GAM1464 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1464 target proteins.

[22743] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1464 gene, herein designated GAM GENE, on one or more GAM1464 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22744] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1464 correlate with, and may be deduced from, the identity of the target genes which GAM1464 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22745] Nucleotide sequences of the GAM1464 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1464 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1464 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1464 are further described hereinbelow with reference to Table Table1.

[22746] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1464 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22747] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1465 (GAM1465) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22748] GAM1465 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1465 was detected is described hereinabove with reference to Figs. 2-8.

[22749] GAM1465 gene, herein designated GAM GENE, and GAM1465 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22750] GAM1465 gene, herein designated GAM GENE, encodes a GAM1465 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1465 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1465 precursor RNA is designated SEQ ID:1438, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1438 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[22751] GAM1465 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1465 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22752] An enzyme complex designated DICER COMPLEX, dices the GAM1465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1465 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1465 RNA is designated SEQ ID:3114, and is provided hereinbelow with reference to the sequence listing part.

[22753] GAM1465 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1465 target RNA, herein designated GAM TARGET

RNA. GAM1465 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22754] GAM1465 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1465 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1465 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1465 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1465 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22755] The complementary binding of GAM1465 RNA, herein designated GAM RNA, to target binding sites on GAM1465 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1465 target RNA, herein designated GAM TARGET RNA, into GAM1465 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22756] It is appreciated that GAM1465 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1465 target genes. The mRNA of each one of this plurality of GAM1465 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1465 RNA, herein designated GAM RNA, and which when bound by GAM1465 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1465 target proteins.

[22757] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1465 gene, herein designated GAM GENE, on one or more GAM1465 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22758] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1465 correlate with, and may be deduced from, the identity of the target genes which GAM1465 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22759] Nucleotide sequences of the GAM1465 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1465 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1465 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1465 are further described hereinbelow with reference to Table Table1.

[22760] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1465 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22761] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1466 (GAM1466) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22762] GAM1466 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1466 was detected is described hereinabove with reference to Figs. 2-8.

[22763] GAM1466 gene, herein designated GAM GENE, and GAM1466 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22764] GAM1466 gene, herein designated GAM GENE, encodes a

GAM1466 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1466 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1466 precursor RNA is designated SEQ ID:1439, and is provided hereinbelow with reference to the sequence listing part.

[22765] GAM1466 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22766] An enzyme complex designated DICER COMPLEX, dices the GAM1466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1466 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1466 RNA is designated SEQ ID:3115, and is provided hereinbelow with reference to the sequence listing part.

[22767] GAM1466 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1466 target RNA, herein designated GAM TARGET RNA. GAM1466 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22768] GAM1466 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1466 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1466 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1466 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1466 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22769] The complementary binding of GAM1466 RNA, herein designated GAM RNA, to target binding sites on GAM1466 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1466 target RNA, herein designated GAM TARGET RNA, into GAM1466 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22770] It is appreciated that GAM1466 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1466 target genes. The mRNA of each one of this plurality of GAM1466 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1466 RNA, herein designated GAM RNA, and which when bound by GAM1466 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1466 target proteins.

[22771] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1466 gene, herein designated GAM GENE, on one or more GAM1466 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[22772] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1466 correlate with, and may be deduced from, the identity of the target genes which GAM1466 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22773] Nucleotide sequences of the GAM1466 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1466 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1466 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1466 are further described hereinbelow with reference to Table Table1.

[22774] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1466 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22775] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1467 (GAM1467) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[22776] GAM1467 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1467 was detected is described hereinabove with reference to Figs. 2-8.

[22777] GAM1467 gene, herein designated GAM GENE, and GAM1467 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22778] GAM1467 gene, herein designated GAM GENE, encodes a GAM1467 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1467 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1467 precursor RNA is designated SEQ ID:1440, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1440 is located at position 36924270 relative to contig NT_007592.11, on chromosome 6.

[22779] GAM1467 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1467 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22780] An enzyme complex designated DICER COMPLEX, dices the GAM1467 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1467 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1467 RNA is designated SEQ ID:3116, and is provided hereinbelow with reference to the sequence listing part.

[22781] GAM1467 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1467 target RNA, herein designated GAM TARGET RNA. GAM1467 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22782] GAM1467 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1467 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1467 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1467 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1467 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22783] The complementary binding of GAM1467 RNA, herein designated GAM RNA, to target binding sites on GAM1467 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1467 target RNA, herein designated GAM TARGET RNA, into GAM1467 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22784] It is appreciated that GAM1467 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1467 target genes. The mRNA of each one of this plurality of GAM1467 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1467 RNA, herein designated GAM RNA, and which when bound by GAM1467 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1467 target proteins.

[22785] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1467 gene, herein designated GAM GENE, on one or more GAM1467 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22786] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1467 correlate with, and may be deduced from, the identity of the target genes which GAM1467 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22787] Nucleotide sequences of the GAM1467 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1467 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1467 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1467 are further described hereinbelow with reference to Table Table1.

[22788] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1467 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22789] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1468 (GAM1468) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22790] GAM1468 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1468 was detected is described hereinabove with reference to Figs. 2-8.

[22791] GAM1468 gene, herein designated GAM GENE, and GAM1468 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22792] GAM1468 gene, herein designated GAM GENE, encodes a GAM1468 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1468 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1468 precursor RNA is designated SEQ ID:1441, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1441 is located at position 2484248 relative to contig NT_005058.11, on chromosome 2.

[22793] GAM1468 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22794] An enzyme complex designated DICER COMPLEX, dices the GAM1468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1468 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1468 RNA is designated SEQ ID:3117, and is provided hereinbelow with reference to the sequence listing part.

[22795] GAM1468 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1468 target RNA, herein designated GAM TARGET RNA. GAM1468 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22796] GAM1468 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1468 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1468 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1468 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1468 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22797] The complementary binding of GAM1468 RNA, herein designated GAM RNA, to target binding sites on GAM1468 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1468 target RNA, herein designated GAM TARGET RNA, into GAM1468 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22798] It is appreciated that GAM1468 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1468 target genes. The mRNA of each one of this plurality of GAM1468 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1468 RNA, herein designated GAM RNA, and which when bound by GAM1468 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1468 target proteins.

[22799] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1468 gene, herein designated GAM GENE, on one or more GAM1468 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22800] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1468 correlate with, and may be deduced from, the identity of the target genes which GAM1468 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22801] Nucleotide sequences of the GAM1468 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1468 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1468 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1468 are further described hereinbelow with reference to Table Table1.

[22802] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1468 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22803] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1469 (GAM1469) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22804] GAM1469 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1469 was detected is described hereinabove with reference to Figs. 2-8.

[22805] GAM1469 gene, herein designated GAM GENE, and GAM1469 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22806] GAM1469 gene, herein designated GAM GENE, encodes a GAM1469 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1469 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1469 precursor RNA is designated SEQ ID:1442, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1442 is located at position 1164089 relative to contig NT_024797.11, on chromosome 16.

[22807] GAM1469 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1469 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22808] An enzyme complex designated DICER COMPLEX, dices the GAM1469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1469 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1469 RNA is designated SEQ ID:3118, and is provided hereinbelow with reference to the sequence listing part.

[22809] GAM1469 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1469 target RNA, herein designated GAM TARGET

RNA. GAM1469 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22810] GAM1469 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1469 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1469 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1469 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1469 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22811] The complementary binding of GAM1469 RNA, herein designated GAM RNA, to target binding sites on GAM1469 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1469 target RNA, herein designated GAM TARGET RNA, into GAM1469 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22812] It is appreciated that GAM1469 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1469 target genes. The mRNA of each one of this plurality of GAM1469 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1469 RNA, herein designated GAM RNA, and which when bound by GAM1469 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1469 target proteins.

[22813] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1469 gene, herein designated GAM GENE, on one or more GAM1469 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22814] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1469 correlate with, and may be deduced from, the identity of the target genes which GAM1469 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22815] Nucleotide sequences of the GAM1469 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1469 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1469 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1469 are further described hereinbelow with reference to Table Table1.

[22816] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1469 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22817] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1470 (GAM1470) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22818] GAM1470 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1470 was detected is described hereinabove with reference to Figs. 2-8.

[22819] GAM1470 gene, herein designated GAM GENE, and GAM1470 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22820] GAM1470 gene, herein designated GAM GENE, encodes a

GAM1470 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1470 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1470 precursor RNA is designated SEQ ID:1443, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1443 is located at position 8160189 relative to contig NT_011196.11, on chromosome 19.

[22821] GAM1470 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22822] An enzyme complex designated DICER COMPLEX, dices the GAM1470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1470 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1470 RNA is designated SEQ ID:3119, and is provided hereinbelow with reference to the sequence listing part.

[22823] GAM1470 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1470 target RNA, herein designated GAM TARGET RNA. GAM1470 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22824] GAM1470 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1470 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1470 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1470 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1470 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22825] The complementary binding of GAM1470 RNA, herein designated GAM RNA, to target binding sites on GAM1470 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1470 target RNA, herein designated GAM TARGET RNA, into GAM1470 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22826] It is appreciated that GAM1470 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1470 target genes. The mRNA of each one of this plurality of GAM1470 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1470 RNA, herein designated GAM RNA, and which when bound by GAM1470 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1470 target proteins.

[22827] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1470 gene, herein designated GAM GENE, on one or more GAM1470 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22828] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1470 correlate with, and may be deduced from, the identity of the target genes which GAM1470 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22829] Nucleotide sequences of the GAM1470 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1470 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1470 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1470 are further described hereinbelow with reference to Table Table1.

[22830] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1470 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22831] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1471 (GAM1471) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22832] GAM1471 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1471 was detected is described hereinabove with reference to Figs. 2-8.

[22833] GAM1471 gene, herein designated GAM GENE, and GAM1471 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22834] GAM1471 gene, herein designated GAM GENE, encodes a GAM1471 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1471 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1471 precursor RNA is designated SEQ ID:1444, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1444 is located at position 3241962 relative to contig NT_004852.13, on chromosome 1.

[22835] GAM1471 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22836] An enzyme complex designated DICER COMPLEX, dices the GAM1471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1471 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1471 RNA is designated SEQ ID:3120, and is provided hereinbelow with reference to the sequence listing part.

[22837] GAM1471 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1471 target RNA, herein designated GAM TARGET RNA. GAM1471 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22838] GAM1471 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1471 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1471 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1471 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1471 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22839] The complementary binding of GAM1471 RNA, herein designated GAM RNA, to target binding sites on GAM1471 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1471 target RNA, herein designated GAM TARGET RNA, into GAM1471 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22840] It is appreciated that GAM1471 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1471 target genes. The mRNA of each one of this plurality of GAM1471 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1471 RNA, herein designated GAM RNA, and which when bound by GAM1471 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1471 target proteins.

[22841] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1471 gene, herein designated GAM GENE, on one or more GAM1471 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22842] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1471 correlate with, and may be deduced from, the identity of the target genes which GAM1471 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22843] Nucleotide sequences of the GAM1471 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1471 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1471 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1471 are further described hereinbelow with reference to Table Table1.

[22844] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1471 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22845] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1472 (GAM1472) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22846] GAM1472 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1472 was detected is described hereinabove with reference to Figs. 2-8.

[22847] GAM1472 gene, herein designated GAM GENE, and GAM1472 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22848] GAM1472 gene, herein designated GAM GENE, encodes a GAM1472 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1472 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1472 precursor RNA is designated SEQ ID:1445, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1445 is located at position 1907100 relative to contig NT_009770.13, on chromosome 12.

[22849] GAM1472 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22850] An enzyme complex designated DICER COMPLEX, dices the GAM1472 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1472 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1472 RNA is designated SEQ ID:3121, and is provided hereinbelow with reference to the sequence listing part.

[22851] GAM1472 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1472 target RNA, herein designated GAM TARGET RNA. GAM1472 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22852] GAM1472 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1472 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1472

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1472 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1472 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22853] The complementary binding of GAM1472 RNA, herein designated GAM RNA, to target binding sites on GAM1472 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1472 target RNA, herein designated GAM TARGET RNA, into GAM1472 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[22854] It is appreciated that GAM1472 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1472 target genes. The mRNA of each one of this plurality of GAM1472 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1472 RNA, herein designated GAM RNA, and which when bound by GAM1472 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1472 target proteins.

[22855] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1472 gene, herein designated GAM GENE, on one or more GAM1472 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22856] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1472 correlate with, and may be deduced from, the identity of the target genes which GAM1472 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22857] Nucleotide sequences of the GAM1472 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1472 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1472 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1472 are further described hereinbelow with reference to Table Table1.

[22858] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1472 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22859] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1473 (GAM1473) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22860] GAM1473 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1473 was detected is described hereinabove with reference to Figs. 2-8.

[22861] GAM1473 gene, herein designated GAM GENE, and GAM1473 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22862] GAM1473 gene, herein designated GAM GENE, encodes a GAM1473 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1473 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1473 precursor RNA is designated SEQ ID:1446, and is provided hereinbelow with reference to the sequence listing part.

[22863] GAM1473 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1473 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22864] An enzyme complex designated DICER COMPLEX, dices the GAM1473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1473 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1473 RNA is designated SEQ ID:3122, and is provided hereinbelow with reference to the sequence listing part.

[22865] GAM1473 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1473 target RNA, herein designated GAM TARGET

RNA. GAM1473 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22866] GAM1473 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1473 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1473 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1473 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1473 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22867] The complementary binding of GAM1473 RNA, herein designated GAM RNA, to target binding sites on GAM1473 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1473 target RNA, herein designated GAM TARGET RNA, into GAM1473 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22868] It is appreciated that GAM1473 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1473 target genes. The mRNA of each one of this plurality of GAM1473 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1473 RNA, herein designated GAM RNA, and which when bound by GAM1473 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1473 target proteins.

[22869] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1473 gene, herein designated GAM GENE, on one or more GAM1473 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22870] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1473 correlate with, and may be deduced from, the identity of the target genes which GAM1473 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22871] Nucleotide sequences of the GAM1473 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1473 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1473 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1473 are further described hereinbelow with reference to Table Table1.

[22872] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1473 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22873] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1474 (GAM1474) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22874] GAM1474 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1474 was detected is described hereinabove with reference to Figs. 2-8.

[22875] GAM1474 gene, herein designated GAM GENE, and GAM1474 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22876] GAM1474 gene, herein designated GAM GENE, encodes a

GAM1474 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1474 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1474 precursor RNA is designated SEQ ID:1447, and is provided hereinbelow with reference to the sequence listing part.

[22877] GAM1474 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22878] An enzyme complex designated DICER COMPLEX, dices the GAM1474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1474 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1474 RNA is designated SEQ ID:3123, and is provided hereinbelow with reference to the sequence listing part.

[22879] GAM1474 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1474 target RNA, herein designated GAM TARGET RNA. GAM1474 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22880] GAM1474 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1474 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1474 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1474 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1474 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22881] The complementary binding of GAM1474 RNA, herein designated GAM RNA, to target binding sites on GAM1474 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1474 target RNA, herein designated GAM TARGET RNA, into GAM1474 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22882] It is appreciated that GAM1474 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1474 target genes. The mRNA of each one of this plurality of GAM1474 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1474 RNA, herein designated GAM RNA, and which when bound by GAM1474 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1474 target proteins.

[22883] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1474 gene, herein designated GAM GENE, on one or more GAM1474 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[22884] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1474 correlate with, and may be deduced from, the identity of the target genes which GAM1474 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22885] Nucleotide sequences of the GAM1474 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1474 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1474 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1474 are further described hereinbelow with reference to Table Table1.

[22886] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1474 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22887] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1475 (GAM1475) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[22888] GAM1475 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1475 was detected is described hereinabove with reference to Figs. 2-8.

[22889] GAM1475 gene, herein designated GAM GENE, and GAM1475 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22890] GAM1475 gene, herein designated GAM GENE, encodes a GAM1475 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1475 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1475 precursor RNA is designated SEQ ID:1448, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1448 is located at position 1235058 relative to contig NT_009526.11, on chromosome 12.

[22891] GAM1475 has 3 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences

of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[22892] SEQ ID:100178 detected in mouse EST Accession AI326210.1.

[22893] SEQ ID:100179 detected in mouse EST Accession BI965652.1.

[22894] SEQ ID:100180 detected in mouse EST Accession BI965972.1.

[22895] GAM1475 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22896] An enzyme complex designated DICER COMPLEX, dices the GAM1475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1475 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1475 RNA is designated SEQ ID:3124, and is provided hereinbelow with reference to the sequence listing part.

[22897] GAM1475 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1475 target RNA, herein designated GAM TARGET RNA. GAM1475 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22898] GAM1475 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1475 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1475 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1475 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1475 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22899] The complementary binding of GAM1475 RNA, herein designated GAM RNA, to target binding sites on GAM1475 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1475 target RNA, herein designated GAM TARGET RNA, into GAM1475 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22900] It is appreciated that GAM1475 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1475 target genes. The mRNA of each one of this plurality of GAM1475 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1475 RNA, herein designated GAM RNA, and which when bound by GAM1475 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1475 target proteins.

[22901] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1475 gene, herein designated GAM GENE, on one or more GAM1475 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[22902] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1475 correlate with, and may be deduced from, the identity of the target genes which GAM1475 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22903] Nucleotide sequences of the GAM1475 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1475 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1475 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1475 are further described hereinbelow with reference to Table Table1.

[22904] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1475 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22905] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1476 (GAM1476) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[22906] GAM1476 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1476 was detected is described hereinabove with reference to Figs. 2-8.

[22907] GAM1476 gene, herein designated GAM GENE, and GAM1476 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22908] GAM1476 gene, herein designated GAM GENE, encodes a GAM1476 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1476 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1476 precursor RNA is designated SEQ ID:1449, and is provided hereinbelow with reference to the sequence listing part.

[22909] GAM1476 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22910] An enzyme complex designated DICER COMPLEX, dices the GAM1476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1476 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1476 RNA is designated SEQ ID:3125, and is provided hereinbelow with reference to the sequence listing part.

[22911] GAM1476 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1476 target RNA, herein designated GAM TARGET RNA. GAM1476 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22912] GAM1476 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1476 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1476 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1476 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1476 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22913] The complementary binding of GAM1476 RNA, herein designated GAM RNA, to target binding sites on GAM1476 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1476 target RNA, herein designated GAM TARGET RNA, into GAM1476 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22914] It is appreciated that GAM1476 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1476 target genes. The mRNA of each one of this plurality of GAM1476 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1476 RNA, herein designated GAM RNA, and which when bound by GAM1476 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1476 target proteins.

[22915] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1476 gene, herein designated GAM GENE, on one or more GAM1476 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22916] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1476 correlate with, and may be deduced from, the identity of the target genes which GAM1476 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22917] Nucleotide sequences of the GAM1476 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1476 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1476 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1476 are further described hereinbelow with reference to Table Table1.

[22918] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1476 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22919] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1477 (GAM1477) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22920] GAM1477 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1477 was detected is described hereinabove with reference to Figs. 2-8.

[22921] GAM1477 gene, herein designated GAM GENE, and GAM1477 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22922] GAM1477 gene, herein designated GAM GENE, encodes a GAM1477 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1477 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1477 precursor RNA is designated SEQ ID:1450, and is provided hereinbelow with reference to the sequence listing part.

[22923] GAM1477 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22924] An enzyme complex designated DICER COMPLEX, dices the GAM1477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1477 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1477 RNA is designated SEQ ID:3126, and is provided hereinbelow with reference to the sequence listing part.

[22925] GAM1477 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1477 target RNA, herein designated GAM TARGET RNA. GAM1477 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22926] GAM1477 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1477 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1477 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1477 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1477 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22927] The complementary binding of GAM1477 RNA, herein designated GAM RNA, to target binding sites on GAM1477 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1477 target RNA, herein designated GAM TARGET RNA, into GAM1477 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22928] It is appreciated that GAM1477 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1477 target genes. The mRNA of each one of this plurality of GAM1477 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1477 RNA, herein designated GAM RNA, and which when bound by GAM1477 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1477 target proteins.

[22929] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1477 gene, herein designated GAM GENE, on one or more GAM1477 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22930] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1477 correlate with, and may

be deduced from, the identity of the target genes which GAM1477 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22931] Nucleotide sequences of the GAM1477 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1477 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1477 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1477 are further described hereinbelow with reference to Table Table1.

[22932] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1477 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22933] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1478 (GAM1478) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22934] GAM1478 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1478 was detected is described hereinabove with reference to Figs. 2-8.

[22935] GAM1478 gene, herein designated GAM GENE, and GAM1478 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22936] GAM1478 gene, herein designated GAM GENE, encodes a GAM1478 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1478 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1478 precursor RNA is designated SEQ ID:1451, and is provided hereinbelow with reference to the sequence listing part.

[22937] GAM1478 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22938] An enzyme complex designated DICER COMPLEX, dices the GAM1478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1478 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1478 RNA is designated SEQ ID:3127, and is provided hereinbelow with reference to the sequence listing part.

[22939] GAM1478 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1478 target RNA, herein designated GAM TARGET RNA. GAM1478 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22940] GAM1478 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1478 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1478 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1478 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1478 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22941] The complementary binding of GAM1478 RNA, herein designated GAM RNA, to target binding sites on GAM1478 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1478 target RNA, herein designated GAM TARGET RNA, into GAM1478 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22942] It is appreciated that GAM1478 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1478 target genes. The mRNA of each one of this plurality of GAM1478 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1478 RNA, herein designated GAM RNA, and which when bound by GAM1478 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1478 target proteins.

[22943] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1478 gene, herein designated GAM GENE, on one or more GAM1478 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22944] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1478 correlate with, and may be deduced from, the identity of the target genes which GAM1478 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22945] Nucleotide sequences of the GAM1478 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1478 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1478 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1478 are further described hereinbelow with reference to Table Table1.

[22946] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1478 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22947] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1479 (GAM1479) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22948] GAM1479 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1479 was detected is described hereinabove with reference to Figs. 2-8.

[22949] GAM1479 gene, herein designated GAM GENE, and GAM1479 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22950] GAM1479 gene, herein designated GAM GENE, encodes a GAM1479 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1479 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1479 precursor RNA is

designated SEQ ID:1452, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1452 is located at position 1135927 relative to contig NT_029289.7, on chromosome 5.

[22951] GAM1479 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22952] An enzyme complex designated DICER COMPLEX, dices the GAM1479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1479 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1479 RNA is designated SEQ ID:3128, and is provided hereinbelow with reference to the sequence listing part.

[22953] GAM1479 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1479 target RNA, herein designated GAM TARGET RNA. GAM1479 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22954] GAM1479 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1479 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1479 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1479 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1479 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22955] The complementary binding of GAM1479 RNA, herein designated GAM RNA, to target binding sites on GAM1479 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1479 target RNA, herein designated GAM TARGET RNA, into GAM1479 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22956] It is appreciated that GAM1479 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1479 target genes. The mRNA of each one of this plurality of GAM1479 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1479 RNA,

herein designated GAM RNA, and which when bound by GAM1479 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1479 target proteins.

[22957] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1479 gene, herein designated GAM GENE, on one or more GAM1479 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22958] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1479 correlate with, and may be deduced from, the identity of the target genes which

GAM1479 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22959] Nucleotide sequences of the GAM1479 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1479 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1479 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1479 are further described hereinbelow with reference to Table Table1.

[22960] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1479 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22961] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1480 (GAM1480) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22962] GAM1480 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1480 was detected is described hereinabove with reference to Figs. 2-8.

[22963] GAM1480 gene, herein designated GAM GENE, and GAM1480 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22964] GAM1480 gene, herein designated GAM GENE, encodes a GAM1480 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1480 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1480 precursor RNA is designated SEQ ID:1453, and is provided hereinbelow with reference to the sequence listing part.

[22965] GAM1480 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[22966] An enzyme complex designated DICER COMPLEX, dices the GAM1480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1480 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1480 RNA is designated SEQ ID:3129, and is provided hereinbelow with reference to the sequence listing part.

[22967] GAM1480 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1480 target RNA, herein designated GAM TARGET RNA. GAM1480 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22968] GAM1480 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1480 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1480 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1480 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1480 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22969] The complementary binding of GAM1480 RNA, herein designated GAM RNA, to target binding sites on GAM1480 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1480 target RNA, herein designated GAM TARGET RNA, into GAM1480 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22970] It is appreciated that GAM1480 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1480 target genes. The mRNA of each one of this plurality of GAM1480 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1480 RNA, herein designated GAM RNA, and which when bound by GAM1480 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1480 target proteins.

[22971] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1480 gene, herein designated GAM GENE, on one or more GAM1480 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22972] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1480 correlate with, and may be deduced from, the identity of the target genes which GAM1480 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[22973] Nucleotide sequences of the GAM1480 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1480 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1480 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1480 are further described hereinbelow with reference to Table Table1.

[22974] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1480 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22975] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1481 (GAM1481) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22976] GAM1481 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1481 was detected is described hereinabove with reference to Figs. 2-8.

[22977] GAM1481 gene, herein designated GAM GENE, and GAM1481 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22978] GAM1481 gene, herein designated GAM GENE, encodes a GAM1481 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1481 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1481 precursor RNA is designated SEQ ID:1454, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1454 is located at position 3263798 relative to contig NT_028392.4, on chromosome 20.

[22979] GAM1481 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22980] An enzyme complex designated DICER COMPLEX, dices the GAM1481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1481 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1481 RNA is designated SEQ ID:3130, and

is provided hereinbelow with reference to the sequence listing part.

[22981] GAM1481 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1481 target RNA, herein designated GAM TARGET RNA. GAM1481 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22982] GAM1481 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1481 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1481 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1481 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1481 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22983] The complementary binding of GAM1481 RNA, herein designated GAM RNA, to target binding sites on GAM1481 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1481 target RNA, herein designated GAM TARGET RNA, into GAM1481 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22984] It is appreciated that GAM1481 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1481 target genes. The mRNA of each one of this plurality of GAM1481 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1481 RNA, herein designated GAM RNA, and which when bound by

GAM1481 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1481 target proteins.

[22985] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1481 gene, herein designated GAM GENE, on one or more GAM1481 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[22986] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1481 correlate with, and may be deduced from, the identity of the target genes which GAM1481 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[22987] Nucleotide sequences of the GAM1481 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1481 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1481 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1481 are further described hereinbelow with reference to Table Table1.

[22988] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1481 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[22989] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1482 (GAM1482) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[22990] GAM1482 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1482 was detected is described hereinabove

with reference to Figs. 2-8.

[22991] GAM1482 gene, herein designated GAM GENE, and GAM1482 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[22992] GAM1482 gene, herein designated GAM GENE, encodes a GAM1482 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1482 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1482 precursor RNA is designated SEQ ID:1455, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1455 is located at position 174355 relative to contig NT_007819.11, on chromosome 7.

[22993] GAM1482 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[22994] An enzyme complex designated DICER COMPLEX, dices the GAM1482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1482 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1482 RNA is designated SEQ ID:3131, and is provided hereinbelow with reference to the sequence listing part.

[22995] GAM1482 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1482 target RNA, herein designated GAM TARGET RNA. GAM1482 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[22996] GAM1482 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1482 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1482 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1482 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1482 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[22997] The complementary binding of GAM1482 RNA, herein designated GAM RNA, to target binding sites on GAM1482 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1482 target RNA, herein designated GAM TARGET RNA, into GAM1482 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[22998] It is appreciated that GAM1482 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1482 target genes. The mRNA of each one of this plurality of GAM1482 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1482 RNA, herein designated GAM RNA, and which when bound by GAM1482 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1482 target proteins.

[22999] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1482 gene, herein designated GAM GENE, on one or more GAM1482 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23000] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1482 correlate with, and may be deduced from, the identity of the target genes which GAM1482 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23001] Nucleotide sequences of the GAM1482 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1482 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1482 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1482 are further described hereinbelow with reference to Table Table1.

[23002] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1482 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23003] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1483 (GAM1483) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23004] GAM1483 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1483 was detected is described hereinabove with reference to Figs. 2-8.

[23005] GAM1483 gene, herein designated GAM GENE, and GAM1483 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23006] GAM1483 gene, herein designated GAM GENE, encodes a GAM1483 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1483 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1483 precursor RNA is

designated SEQ ID:1456, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1456 is located at position 2907490 relative to contig NT_015805.11, on chromosome 2.

[23007] GAM1483 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23008] An enzyme complex designated DICER COMPLEX, dices the GAM1483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1483 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1483 RNA is designated SEQ ID:3132, and is provided hereinbelow with reference to the sequence listing part.

[23009] GAM1483 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1483 target RNA, herein designated GAM TARGET RNA. GAM1483 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23010] GAM1483 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1483 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1483 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1483 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1483 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23011] The complementary binding of GAM1483 RNA, herein designated GAM RNA, to target binding sites on GAM1483 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1483 target RNA, herein designated GAM TARGET RNA, into GAM1483 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23012] It is appreciated that GAM1483 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1483 target genes. The mRNA of each one of this plurality of GAM1483 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1483 RNA,

herein designated GAM RNA, and which when bound by GAM1483 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1483 target proteins.

[23013] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1483 gene, herein designated GAM GENE, on one or more GAM1483 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23014] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1483 correlate with, and may be deduced from, the identity of the target genes which

GAM1483 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23015] Nucleotide sequences of the GAM1483 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1483 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1483 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1483 are further described hereinbelow with reference to Table Table1.

[23016] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1483 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23017] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1484 (GAM1484) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23018] GAM1484 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1484 was detected is described hereinabove with reference to Figs. 2-8.

[23019] GAM1484 gene, herein designated GAM GENE, and GAM1484 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23020] GAM1484 gene, herein designated GAM GENE, encodes a GAM1484 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1484 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1484 precursor RNA is designated SEQ ID:1457, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1457 is located at position 280476 relative to contig NT_007758.8, on chromosome 7.

[23021] GAM1484 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23022] An enzyme complex designated DICER COMPLEX, dices the GAM1484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1484 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1484 RNA is designated SEQ ID:3133, and is provided hereinbelow with reference to the sequence listing part.

[23023] GAM1484 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1484 target RNA, herein designated GAM TARGET RNA. GAM1484 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23024] GAM1484 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1484 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1484 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1484 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1484 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23025] The complementary binding of GAM1484 RNA, herein designated GAM RNA, to target binding sites on GAM1484

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1484 target RNA, herein designated GAM TARGET RNA, into GAM1484 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23026] It is appreciated that GAM1484 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1484 target genes. The mRNA of each one of this plurality of GAM1484 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1484 RNA, herein designated GAM RNA, and which when bound by GAM1484 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1484 target proteins.

[23027] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1484 gene, herein designated GAM GENE, on one or more GAM1484 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23028] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1484 correlate with, and may be deduced from, the identity of the target genes which GAM1484 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23029] Nucleotide sequences of the GAM1484 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1484 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1484 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1484 are further described hereinbelow with reference to Table Table1.

[23030] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1484 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23031] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1485 (GAM1485) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23032] GAM1485 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1485 was detected is described hereinabove with reference to Figs. 2-8.

[23033] GAM1485 gene, herein designated GAM GENE, and GAM1485 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23034] GAM1485 gene, herein designated GAM GENE, encodes a GAM1485 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1485 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1485 precursor RNA is designated SEQ ID:1458, and is provided hereinbelow with reference to the sequence listing part.

[23035] GAM1485 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23036] An enzyme complex designated DICER COMPLEX, dices the GAM1485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1485 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1485 RNA is designated SEQ ID:3134, and

is provided hereinbelow with reference to the sequence listing part.

[23037] GAM1485 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1485 target RNA, herein designated GAM TARGET RNA. GAM1485 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23038] GAM1485 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1485 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1485 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1485 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1485 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23039] The complementary binding of GAM1485 RNA, herein designated GAM RNA, to target binding sites on GAM1485 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1485 target RNA, herein designated GAM TARGET RNA, into GAM1485 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23040] It is appreciated that GAM1485 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1485 target genes. The mRNA of each one of this plurality of GAM1485 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1485 RNA, herein designated GAM RNA, and which when bound by

GAM1485 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1485 target proteins.

[23041] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1485 gene, herein designated GAM GENE, on one or more GAM1485 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23042] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1485 correlate with, and may be deduced from, the identity of the target genes which GAM1485 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[23043] Nucleotide sequences of the GAM1485 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1485 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1485 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1485 are further described hereinbelow with reference to Table Table1.

[23044] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1485 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23045] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1486 (GAM1486) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23046] GAM1486 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1486 was detected is described hereinabove

with reference to Figs. 2-8.

[23047] GAM1486 gene, herein designated GAM GENE, and GAM1486 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23048] GAM1486 gene, herein designated GAM GENE, encodes a GAM1486 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1486 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1486 precursor RNA is designated SEQ ID:1459, and is provided hereinbelow with reference to the sequence listing part.

[23049] GAM1486 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23050] An enzyme complex designated DICER COMPLEX, dices the GAM1486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1486 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1486 RNA is designated SEQ ID:3135, and is provided hereinbelow with reference to the sequence listing part.

[23051] GAM1486 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1486 target RNA, herein designated GAM TARGET RNA. GAM1486 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23052] GAM1486 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1486 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1486 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1486 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1486 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23053] The complementary binding of GAM1486 RNA, herein designated GAM RNA, to target binding sites on GAM1486 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1486 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1486 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23054] It is appreciated that GAM1486 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1486 target genes. The mRNA of each one of this plurality of GAM1486 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1486 RNA, herein designated GAM RNA, and which when bound by GAM1486 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1486 target proteins.

[23055] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1486 gene, herein designated GAM GENE, on one or more GAM1486 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23056] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1486 correlate with, and may be deduced from, the identity of the target genes which GAM1486 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23057] Nucleotide sequences of the GAM1486 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1486 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1486 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1486 are further described hereinbelow with reference to Table Table1.

[23058] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1486 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[23059] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1487 (GAM1487) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23060] GAM1487 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1487 was detected is described hereinabove with reference to Figs. 2-8.

[23061] GAM1487 gene, herein designated GAM GENE, and GAM1487 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23062] GAM1487 gene, herein designated GAM GENE, encodes a GAM1487 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1487 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1487 precursor RNA is designated SEQ ID:1460, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1460 is located at position 3343909 relative to contig NT_032977.3, on chromosome 1.

[23063] GAM1487 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23064] An enzyme complex designated DICER COMPLEX, dices the GAM1487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1487 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1487 RNA is designated SEQ ID:3136, and is provided hereinbelow with reference to the sequence

listing part.

[23065] GAM1487 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1487 target RNA, herein designated GAM TARGET RNA. GAM1487 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23066] GAM1487 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1487 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1487 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1487 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1487 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23067] The complementary binding of GAM1487 RNA, herein designated GAM RNA, to target binding sites on GAM1487 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1487 target RNA, herein designated GAM TARGET RNA, into GAM1487 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23068] It is appreciated that GAM1487 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1487 target genes. The mRNA of each one of this plurality of GAM1487 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1487 RNA, herein designated GAM RNA, and which when bound by GAM1487 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1487 target proteins.

[23069] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1487 gene, herein designated GAM GENE, on one or more GAM1487 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23070] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1487 correlate with, and may be deduced from, the identity of the target genes which GAM1487 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23071] Nucleotide sequences of the GAM1487 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1487 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1487 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1487 are further described hereinbelow with reference to Table Table1.

[23072] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1487 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23073] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1488 (GAM1488) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23074] GAM1488 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1488 was detected is described hereinabove with reference to Figs. 2-8.

[23075] GAM1488 gene, herein designated GAM GENE, and GAM1488 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23076] GAM1488 gene, herein designated GAM GENE, encodes a GAM1488 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1488 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1488 precursor RNA is designated SEQ ID:1461, and is provided hereinbelow with reference to the sequence listing part.

[23077] GAM1488 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23078] An enzyme complex designated DICER COMPLEX, dices

the GAM1488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1488 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 96%) nucleotide sequence of GAM1488 RNA is designated SEQ ID:3137, and is provided hereinbelow with reference to the sequence listing part.

[23079] GAM1488 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1488 target RNA, herein designated GAM TARGET RNA. GAM1488 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23080] GAM1488 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1488 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1488 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1488 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1488 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23081] The complementary binding of GAM1488 RNA, herein designated GAM RNA, to target binding sites on GAM1488 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1488 target RNA, herein designated GAM TARGET RNA, into GAM1488 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23082] It is appreciated that GAM1488 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1488 target genes. The mRNA of each one of this plurality of GAM1488 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1488 RNA, herein designated GAM RNA, and which when bound by GAM1488 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1488 target proteins.

[23083] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1488 gene, herein designated GAM GENE, on one or more GAM1488 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23084] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1488 correlate with, and may be deduced from, the identity of the target genes which GAM1488 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23085] Nucleotide sequences of the GAM1488 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1488 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1488 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1488 are further described hereinbelow with reference to Table Table1.

[23086] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1488 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23087] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1489 (GAM1489) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23088] GAM1489 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1489 was detected is described hereinabove with reference to Figs. 2-8.

[23089] GAM1489 gene, herein designated GAM GENE, and GAM1489 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23090] GAM1489 gene, herein designated GAM GENE, encodes a GAM1489 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1489 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1489 precursor RNA is designated SEQ ID:1462, and is provided hereinbelow with reference to the sequence listing part.

[23091] GAM1489 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23092] An enzyme complex designated DICER COMPLEX, dices the GAM1489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1489 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1489 RNA is designated SEQ ID:3138, and is provided hereinbelow with reference to the sequence listing part.

[23093] GAM1489 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1489 target RNA, herein designated GAM TARGET RNA. GAM1489 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23094] GAM1489 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1489 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1489 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1489 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1489 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23095] The complementary binding of GAM1489 RNA, herein designated GAM RNA, to target binding sites on GAM1489 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1489 target RNA, herein designated GAM TARGET RNA, into GAM1489 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23096] It is appreciated that GAM1489 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1489 target genes. The mRNA of each one of this plurality of GAM1489 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1489 RNA, herein designated GAM RNA, and which when bound by GAM1489 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1489 target proteins.

[23097] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1489 gene, herein designated GAM GENE, on one or more GAM1489 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23098] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1489 correlate with, and may be deduced from, the identity of the target genes which GAM1489 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23099] Nucleotide sequences of the GAM1489 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1489 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1489 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1489 are further described hereinbelow with reference to Table Table1.

[23100] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1489 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23101] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1490 (GAM1490) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23102] GAM1490 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1490 was detected is described hereinabove with reference to Figs. 2-8.

[23103] GAM1490 gene, herein designated GAM GENE, and GAM1490 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23104] GAM1490 gene, herein designated GAM GENE, encodes a GAM1490 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1490 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1490 precursor RNA is designated SEQ ID:1463, and is provided hereinbelow with reference to the sequence listing part.

[23105] GAM1490 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23106] An enzyme complex designated DICER COMPLEX, dices the GAM1490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1490 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1490 RNA is designated SEQ ID:3139, and is provided hereinbelow with reference to the sequence listing part.

[23107] GAM1490 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1490 target RNA, herein designated GAM TARGET RNA. GAM1490 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23108] GAM1490 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1490 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1490 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1490 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1490 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23109] The complementary binding of GAM1490 RNA, herein designated GAM RNA, to target binding sites on GAM1490 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1490 target RNA, herein designated GAM TARGET RNA, into GAM1490 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23110] It is appreciated that GAM1490 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1490 target genes. The mRNA of each one of this plurality of GAM1490 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1490 RNA, herein designated GAM RNA, and which when bound by GAM1490 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1490 target proteins.

[23111] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1490 gene, herein designated GAM GENE, on one or more GAM1490 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23112] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1490 correlate with, and may be deduced from, the identity of the target genes which GAM1490 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23113] Nucleotide sequences of the GAM1490 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1490 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1490 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1490 are further described hereinbelow with reference to Table Table1.

[23114] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1490 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23115] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1491 (GAM1491) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23116] GAM1491 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1491 was detected is described hereinabove with reference to Figs. 2-8.

[23117] GAM1491 gene, herein designated GAM GENE, and GAM1491 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23118] GAM1491 gene, herein designated GAM GENE, encodes a GAM1491 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1491 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1491 precursor RNA is designated SEQ ID:1464, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1464 is located at position 4851374 relative to contig NT_022517.13, on chromosome 3.

[23119] GAM1491 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1491 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23120] An enzyme complex designated DICER COMPLEX, dices the GAM1491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1491 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1491 RNA is designated SEQ ID:3140, and is provided hereinbelow with reference to the sequence listing part.

[23121] GAM1491 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1491 target RNA, herein designated GAM TARGET

RNA. GAM1491 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23122] GAM1491 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1491 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1491 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1491 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1491 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23123] The complementary binding of GAM1491 RNA, herein designated GAM RNA, to target binding sites on GAM1491 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1491 target RNA, herein designated GAM TARGET RNA, into GAM1491 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23124] It is appreciated that GAM1491 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1491 target genes. The mRNA of each one of this plurality of GAM1491 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1491 RNA, herein designated GAM RNA, and which when bound by GAM1491 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1491 target proteins.

[23125] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1491 gene, herein designated GAM GENE, on one or more GAM1491 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23126] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1491 correlate with, and may be deduced from, the identity of the target genes which GAM1491 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23127] Nucleotide sequences of the GAM1491 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1491 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1491 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1491 are further described hereinbelow with reference to Table Table1.

[23128] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1491 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23129] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1492 (GAM1492) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23130] GAM1492 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1492 was detected is described hereinabove with reference to Figs. 2-8.

[23131] GAM1492 gene, herein designated GAM GENE, and GAM1492 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23132] GAM1492 gene, herein designated GAM GENE, encodes a

GAM1492 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1492 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1492 precursor RNA is designated SEQ ID:1465, and is provided hereinbelow with reference to the sequence listing part.

[23133] GAM1492 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23134] An enzyme complex designated DICER COMPLEX, dices the GAM1492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1492 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1492 RNA is designated SEQ ID:3141, and is provided hereinbelow with reference to the sequence listing part.

[23135] GAM1492 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1492 target RNA, herein designated GAM TARGET RNA. GAM1492 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23136] GAM1492 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1492 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1492 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1492 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1492 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23137] The complementary binding of GAM1492 RNA, herein designated GAM RNA, to target binding sites on GAM1492 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1492 target RNA, herein designated GAM TARGET RNA, into GAM1492 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23138] It is appreciated that GAM1492 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1492 target genes. The mRNA of each one of this plurality of GAM1492 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1492 RNA, herein designated GAM RNA, and which when bound by GAM1492 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1492 target proteins.

[23139] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1492 gene, herein designated GAM GENE, on one or more GAM1492 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[23140] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1492 correlate with, and may be deduced from, the identity of the target genes which GAM1492 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23141] Nucleotide sequences of the GAM1492 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1492 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1492 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1492 are further described hereinbelow with reference to Table Table1.

[23142] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1492 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23143] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1493 (GAM1493) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[23144] GAM1493 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1493 was detected is described hereinabove with reference to Figs. 2-8.

[23145] GAM1493 gene, herein designated GAM GENE, and GAM1493 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23146] GAM1493 gene, herein designated GAM GENE, encodes a GAM1493 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1493 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1493 precursor RNA is designated SEQ ID:1466, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1466 is located at position 5185444 relative to contig NT_005334.11, on chromosome 2.

[23147] GAM1493 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1493 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23148] An enzyme complex designated DICER COMPLEX, dices the GAM1493 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1493 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1493 RNA is designated SEQ ID:3142, and is provided hereinbelow with reference to the sequence listing part.

[23149] GAM1493 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1493 target RNA, herein designated GAM TARGET RNA. GAM1493 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23150] GAM1493 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1493 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1493 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1493 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1493 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23151] The complementary binding of GAM1493 RNA, herein designated GAM RNA, to target binding sites on GAM1493 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1493 target RNA, herein designated GAM TARGET RNA, into GAM1493 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23152] It is appreciated that GAM1493 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1493 target genes. The mRNA of each one of this plurality of GAM1493 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1493 RNA, herein designated GAM RNA, and which when bound by GAM1493 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1493 target proteins.

[23153] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1493 gene, herein designated GAM GENE, on one or more GAM1493 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23154] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1493 correlate with, and may be deduced from, the identity of the target genes which GAM1493 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23155] Nucleotide sequences of the GAM1493 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1493 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1493 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1493 are further described hereinbelow with reference to Table Table1.

[23156] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1493 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23157] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1494 (GAM1494) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23158] GAM1494 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1494 was detected is described hereinabove with reference to Figs. 2-8.

[23159] GAM1494 gene, herein designated GAM GENE, and GAM1494 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23160] GAM1494 gene, herein designated GAM GENE, encodes a GAM1494 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1494 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1494 precursor RNA is designated SEQ ID:1467, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1467 is located at position 23535227 relative to contig NT_033899.3, on chromosome 11.

[23161] GAM1494 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[23162] SEQ ID:100007 detected in mouse EST Accession BI714485.1.

[23163] SEQ ID:100008 detected in mouse EST Accession BE368829.1.

[23164] GAM1494 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23165] An enzyme complex designated DICER COMPLEX, dices the GAM1494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1494 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1494 RNA is designated SEQ ID:3143, and is provided hereinbelow with reference to the sequence listing part.

[23166] GAM1494 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1494 target RNA, herein designated GAM TARGET RNA. GAM1494 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23167] GAM1494 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1494 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1494 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1494 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1494 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23168] The complementary binding of GAM1494 RNA, herein designated GAM RNA, to target binding sites on GAM1494 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1494 target RNA, herein designated GAM TARGET RNA, into GAM1494 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23169] It is appreciated that GAM1494 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1494 target genes. The mRNA of each one of this plurality of GAM1494 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1494 RNA, herein designated GAM RNA, and which when bound by GAM1494 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1494 target proteins.

[23170] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1494 gene, herein designated GAM GENE, on one or more GAM1494 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23171] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1494 correlate with, and may be deduced from, the identity of the target genes which GAM1494 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23172] Nucleotide sequences of the GAM1494 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1494 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1494 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1494 are further described hereinbelow with reference to Table Table1.

[23173] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1494 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23174] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1495 (GAM1495) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23175] GAM1495 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1495 was detected is described hereinabove with reference to Figs. 2-8.

[23176] GAM1495 gene, herein designated GAM GENE, and GAM1495 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23177] GAM1495 gene, herein designated GAM GENE, encodes a GAM1495 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1495 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1495 precursor RNA is designated SEQ ID:1468, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1468 is located at position 6275175 relative to contig NT_034383.2, on chromosome 1.

[23178] GAM1495 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[23179] SEQ ID:100012 detected in mouse EST Accession AI316374.1.

[23180] SEQ ID:100013 detected in mouse EST Accession AA122754.1.

[23181] SEQ ID:100014 detected in mouse EST Accession BI148579.1.

[23182] SEQ ID:100015 detected in mouse EST Accession AW413196.1.

[23183] SEQ ID:100016 detected in mouse EST Accession AA684283.1.

[23184] SEQ ID:99050 detected in mouse EST Accession

BG242574.1.

[23185] SEQ ID:100010 detected in mouse EST Accession AA168500.1.

[23186] SEQ ID:100011 detected in mouse EST Accession AA017943.1.

[23187] GAM1495 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23188] An enzyme complex designated DICER COMPLEX, dices the GAM1495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1495 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1495 RNA is designated SEQ ID:3144, and is provided hereinbelow with reference to the sequence listing part.

[23189] GAM1495 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1495 target RNA, herein designated GAM TARGET RNA. GAM1495 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23190] GAM1495 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1495 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1495 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1495 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1495 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23191] The complementary binding of GAM1495 RNA, herein designated GAM RNA, to target binding sites on GAM1495 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1495 target RNA, herein designated GAM TARGET RNA, into GAM1495 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23192] It is appreciated that GAM1495 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1495 target genes. The mRNA of each one of this plurality of GAM1495 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1495 RNA, herein designated GAM RNA, and which when bound by GAM1495 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1495 target proteins.

[23193] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1495 gene, herein designated GAM GENE, on one or more GAM1495 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23194] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1495 correlate with, and may

be deduced from, the identity of the target genes which GAM1495 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23195] Nucleotide sequences of the GAM1495 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1495 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1495 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1495 are further described hereinbelow with reference to Table Table1.

[23196] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1495 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23197] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1496 (GAM1496) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23198] GAM1496 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1496 was detected is described hereinabove with reference to Figs. 2-8.

[23199] GAM1496 gene, herein designated GAM GENE, and GAM1496 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23200] GAM1496 gene, herein designated GAM GENE, encodes a GAM1496 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1496 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1496 precursor RNA is designated SEQ ID:1469, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1469 is located at position 12183957 relative to contig NT_006576.11, on chromosome 5.

[23201] GAM1496 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23202] An enzyme complex designated DICER COMPLEX, dices the GAM1496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1496 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1496 RNA is designated SEQ ID:3145, and is provided hereinbelow with reference to the sequence listing part.

[23203] GAM1496 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1496 target RNA, herein designated GAM TARGET RNA. GAM1496 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[23204] GAM1496 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1496 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1496 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1496 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1496 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23205] The complementary binding of GAM1496 RNA, herein

designated GAM RNA, to target binding sites on GAM1496 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1496 target RNA, herein designated GAM TARGET RNA, into GAM1496 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23206] It is appreciated that GAM1496 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1496 target genes. The mRNA of each one of this plurality of GAM1496 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1496 RNA, herein designated GAM RNA, and which when bound by GAM1496 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1496 target proteins.

[23207] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1496 gene, herein designated GAM GENE, on one or more GAM1496 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23208] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1496 correlate with, and may be deduced from, the identity of the target genes which GAM1496 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23209] Nucleotide sequences of the GAM1496 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1496 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1496 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1496 are further described hereinbelow with reference to Table Table1.

[23210] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1496 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23211] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1497 (GAM1497) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23212] GAM1497 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1497 was detected is described hereinabove with reference to Figs. 2-8.

[23213] GAM1497 gene, herein designated GAM GENE, and GAM1497 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23214] GAM1497 gene, herein designated GAM GENE, encodes a GAM1497 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1497 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1497 precursor RNA is designated SEQ ID:1470, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1470 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[23215] GAM1497 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23216] An enzyme complex designated DICER COMPLEX, dices the GAM1497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1497 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1497 RNA is designated SEQ ID:3146, and is provided hereinbelow with reference to the sequence listing part.

[23217] GAM1497 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1497 target RNA, herein designated GAM TARGET RNA. GAM1497 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23218] GAM1497 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1497 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1497 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1497 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1497 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23219] The complementary binding of GAM1497 RNA, herein designated GAM RNA, to target binding sites on GAM1497 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1497 target RNA, herein designated GAM TARGET RNA, into GAM1497 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23220] It is appreciated that GAM1497 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1497 target genes. The mRNA of each one of this plurality of GAM1497 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1497 RNA, herein designated GAM RNA, and which when bound by GAM1497 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1497 target proteins.

[23221] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1497 gene, herein designated GAM GENE, on one or more GAM1497 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23222] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1497 correlate with, and may be deduced from, the identity of the target genes which GAM1497 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23223] Nucleotide sequences of the GAM1497 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1497 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1497 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1497 are further described hereinbelow with reference to Table Table1.

[23224] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1497 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23225] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1498 (GAM1498) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23226] GAM1498 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1498 was detected is described hereinabove with reference to Figs. 2-8.

[23227] GAM1498 gene, herein designated GAM GENE, and GAM1498 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23228] GAM1498 gene, herein designated GAM GENE, encodes a GAM1498 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1498 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1498 precursor RNA is designated SEQ ID:1471, and is provided hereinbelow with reference to the sequence listing part.

[23229] GAM1498 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98150, which mouse homolog is detected in mouse EST accession BI654237.1.

[23230] GAM1498 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1498 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23231] An enzyme complex designated DICER COMPLEX, dices the GAM1498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1498 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1498 RNA is designated SEQ ID:3147, and is provided hereinbelow with reference to the sequence listing part.

[23232] GAM1498 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1498 target RNA, herein designated GAM TARGET

RNA. GAM1498 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23233] GAM1498 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1498 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1498 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1498 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1498 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23234] The complementary binding of GAM1498 RNA, herein designated GAM RNA, to target binding sites on GAM1498 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1498 target RNA, herein designated GAM TARGET RNA, into GAM1498 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23235] It is appreciated that GAM1498 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1498 target genes. The mRNA of each one of this plurality of GAM1498 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1498 RNA, herein designated GAM RNA, and which when bound by GAM1498 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1498 target proteins.

[23236] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1498 gene, herein designated GAM GENE, on one or more GAM1498 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23237] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1498 correlate with, and may be deduced from, the identity of the target genes which GAM1498 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23238] Nucleotide sequences of the GAM1498 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1498 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1498 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1498 are further described hereinbelow with reference to Table Table1.

[23239] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1498 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23240] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1499 (GAM1499) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23241] GAM1499 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1499 was detected is described hereinabove with reference to Figs. 2-8.

[23242] GAM1499 gene, herein designated GAM GENE, and GAM1499 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23243] GAM1499 gene, herein designated GAM GENE, encodes a

GAM1499 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1499 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1499 precursor RNA is designated SEQ ID:1472, and is provided hereinbelow with reference to the sequence listing part.

[23244] GAM1499 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[23245] SEQ ID:98372 detected in mouse EST Accession AA682016.1.

[23246] SEQ ID:98659 detected in mouse EST Accession AA682021.1.

[23247] SEQ ID:98660 detected in mouse EST Accession AI526274.1.

[23248] SEQ ID:98661 detected in mouse EST Accession AI526253.1.

[23249] SEQ ID:98662 detected in mouse EST Accession AI526408.1.

[23250] SEQ ID:98663 detected in mouse EST Accession AI526229.1.

[23251] SEQ ID:98664 detected in mouse EST Accession AI526342.1.

[23252] SEQ ID:98665 detected in mouse EST Accession AI526267.1.

[23253] GAM1499 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23254] An enzyme complex designated DICER COMPLEX, dices the GAM1499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1499 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1499 RNA is designated SEQ ID:3148, and is provided hereinbelow with reference to the sequence listing part.

[23255] GAM1499 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1499 target RNA, herein designated GAM TARGET RNA. GAM1499 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23256] GAM1499 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1499 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1499 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1499 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1499 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23257] The complementary binding of GAM1499 RNA, herein designated GAM RNA, to target binding sites on GAM1499 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1499 target RNA, herein designated GAM TARGET RNA, into GAM1499 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23258] It is appreciated that GAM1499 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1499 target genes. The mRNA of each one of this plurality of GAM1499 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1499 RNA, herein designated GAM RNA, and which when bound by GAM1499 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1499 target proteins.

[23259] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1499 gene, herein designated GAM GENE, on one or more GAM1499 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23260] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1499 correlate with, and may be deduced from, the identity of the target genes which GAM1499 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23261] Nucleotide sequences of the GAM1499 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1499 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1499 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1499 are further described hereinbelow with reference to Table Table1.

[23262] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1499 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23263] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1500 (GAM1500) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23264] GAM1500 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1500 was detected is described hereinabove with reference to Figs. 2-8.

[23265] GAM1500 gene, herein designated GAM GENE, and GAM1500 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23266] GAM1500 gene, herein designated GAM GENE, encodes a GAM1500 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1500 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1500 precursor RNA is designated SEQ ID:1473, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1473 is located at position 2394563 relative to contig NT_028050.10, on chromosome 1.

[23267] GAM1500 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23268] An enzyme complex designated DICER COMPLEX, dices the GAM1500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1500 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1500 RNA is designated SEQ ID:3149, and is provided hereinbelow with reference to the sequence listing part.

[23269] GAM1500 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1500 target RNA, herein designated GAM TARGET RNA. GAM1500 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23270] GAM1500 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1500 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1500 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1500 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1500 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23271] The complementary binding of GAM1500 RNA, herein designated GAM RNA, to target binding sites on GAM1500 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1500 target RNA, herein designated GAM TARGET RNA, into GAM1500 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23272] It is appreciated that GAM1500 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1500 target genes. The mRNA of each one of this plurality of GAM1500 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1500 RNA, herein designated GAM RNA, and which when bound by GAM1500 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1500 target proteins.

[23273] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1500 gene, herein designated GAM GENE, on one or more GAM1500 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23274] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1500 correlate with, and may be deduced from, the identity of the target genes which GAM1500 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23275] Nucleotide sequences of the GAM1500 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1500 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1500 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1500 are further described hereinbelow with reference to Table Table1.

[23276] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1500 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23277] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1501 (GAM1501) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23278] GAM1501 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1501 was detected is described hereinabove with reference to Figs. 2-8.

[23279] GAM1501 gene, herein designated GAM GENE, and GAM1501 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23280] GAM1501 gene, herein designated GAM GENE, encodes a GAM1501 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1501 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1501 precursor RNA is designated SEQ ID:1474, and is provided hereinbelow with reference to the sequence listing part.

[23281] GAM1501 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23282] An enzyme complex designated DICER COMPLEX, dices the GAM1501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1501 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1501 RNA is designated SEQ ID:3150, and is provided hereinbelow with reference to the sequence listing part.

[23283] GAM1501 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1501 target RNA, herein designated GAM TARGET RNA. GAM1501 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23284] GAM1501 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1501 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1501 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1501 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1501 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23285] The complementary binding of GAM1501 RNA, herein designated GAM RNA, to target binding sites on GAM1501 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1501 target RNA, herein designated GAM TARGET RNA, into GAM1501 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23286] It is appreciated that GAM1501 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1501 target genes. The mRNA of each one of this plurality of GAM1501 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1501 RNA, herein designated GAM RNA, and which when bound by GAM1501 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1501 target proteins.

[23287] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1501 gene, herein designated GAM GENE, on one or more GAM1501 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23288] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1501 correlate with, and may

be deduced from, the identity of the target genes which GAM1501 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23289] Nucleotide sequences of the GAM1501 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1501 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1501 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1501 are further described hereinbelow with reference to Table Table1.

[23290] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1501 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23291] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1502 (GAM1502) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23292] GAM1502 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1502 was detected is described hereinabove with reference to Figs. 2-8.

[23293] GAM1502 gene, herein designated GAM GENE, and GAM1502 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23294] GAM1502 gene, herein designated GAM GENE, encodes a GAM1502 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1502 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1502 precursor RNA is designated SEQ ID:1475, and is provided hereinbelow with reference to the sequence listing part.

[23295] GAM1502 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23296] An enzyme complex designated DICER COMPLEX, dices the GAM1502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1502 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1502 RNA is designated SEQ ID:3151, and is provided hereinbelow with reference to the sequence listing part.

[23297] GAM1502 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1502 target RNA, herein designated GAM TARGET RNA. GAM1502 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23298] GAM1502 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1502 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1502 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1502 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1502 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23299] The complementary binding of GAM1502 RNA, herein designated GAM RNA, to target binding sites on GAM1502 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1502 target RNA, herein designated GAM TARGET RNA, into GAM1502 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23300] It is appreciated that GAM1502 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1502 target genes. The mRNA of each one of this plurality of GAM1502 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1502 RNA, herein designated GAM RNA, and which when bound by GAM1502 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1502 target proteins.

[23301] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1502 gene, herein designated GAM GENE, on one or more GAM1502 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23302] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1502 correlate with, and may be deduced from, the identity of the target genes which GAM1502 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23303] Nucleotide sequences of the GAM1502 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1502 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1502 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1502 are further described hereinbelow with reference to Table Table1.

[23304] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1502 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23305] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1503 (GAM1503) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23306] GAM1503 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1503 was detected is described hereinabove with reference to Figs. 2-8.

[23307] GAM1503 gene, herein designated GAM GENE, and GAM1503 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23308] GAM1503 gene, herein designated GAM GENE, encodes a GAM1503 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1503 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1503 precursor RNA is

designated SEQ ID:1476, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1476 is located at position 19087830 relative to contig NT_011520.8, on chromosome 22.

[23309] GAM1503 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23310] An enzyme complex designated DICER COMPLEX, dices the GAM1503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1503 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1503 RNA is designated SEQ ID:3152, and is provided hereinbelow with reference to the sequence listing part.

[23311] GAM1503 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1503 target RNA, herein designated GAM TARGET RNA. GAM1503 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23312] GAM1503 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1503 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1503 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1503 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1503 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23313] The complementary binding of GAM1503 RNA, herein designated GAM RNA, to target binding sites on GAM1503 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1503 target RNA, herein designated GAM TARGET RNA, into GAM1503 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23314] It is appreciated that GAM1503 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1503 target genes. The mRNA of each one of this plurality of GAM1503 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1503 RNA,

herein designated GAM RNA, and which when bound by GAM1503 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1503 target proteins.

[23315] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1503 gene, herein designated GAM GENE, on one or more GAM1503 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23316] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1503 correlate with, and may be deduced from, the identity of the target genes which

GAM1503 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23317] Nucleotide sequences of the GAM1503 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1503 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1503 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1503 are further described hereinbelow with reference to Table Table1.

[23318] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1503 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23319] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1504 (GAM1504) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23320] GAM1504 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1504 was detected is described hereinabove with reference to Figs. 2-8.

[23321] GAM1504 gene, herein designated GAM GENE, and GAM1504 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23322] GAM1504 gene, herein designated GAM GENE, encodes a GAM1504 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1504 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1504 precursor RNA is designated SEQ ID:1477, and is provided hereinbelow with reference to the sequence listing part.

[23323] GAM1504 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[23324] SEQ ID:98656 detected in mouse EST Accession AA692083.1.

[23325] SEQ ID:98657 detected in mouse EST Accession BI202421.1.

[23326] GAM1504 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23327] An enzyme complex designated DICER COMPLEX, dices the GAM1504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1504 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1504 RNA is designated SEQ ID:3153, and is provided hereinbelow with reference to the sequence listing part.

[23328] GAM1504 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1504 target RNA, herein designated GAM TARGET RNA. GAM1504 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23329] GAM1504 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1504 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1504 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1504 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1504 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23330] The complementary binding of GAM1504 RNA, herein designated GAM RNA, to target binding sites on GAM1504 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1504 target RNA, herein designated GAM TARGET RNA, into GAM1504 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23331] It is appreciated that GAM1504 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1504 target genes. The mRNA of each one of this plurality of GAM1504 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1504 RNA, herein designated GAM RNA, and which when bound by GAM1504 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1504 target proteins.

[23332] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1504 gene, herein designated GAM GENE, on one or more GAM1504 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23333] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1504 correlate with, and may be deduced from, the identity of the target genes which GAM1504 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23334] Nucleotide sequences of the GAM1504 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1504 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1504 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1504 are further described hereinbelow with reference to Table Table1.

[23335] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1504 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23336] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1505 (GAM1505) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23337] GAM1505 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1505 was detected is described hereinabove with reference to Figs. 2-8.

[23338] GAM1505 gene, herein designated GAM GENE, and GAM1505 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[23339] GAM1505 gene, herein designated GAM GENE, encodes a GAM1505 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1505 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1505 precursor RNA is designated SEQ ID:1478, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1478 is located at position 716965 relative to contig NT_022135.11, on chromosome 2.

[23340] GAM1505 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23341] An enzyme complex designated DICER COMPLEX, dices

the GAM1505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1505 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1505 RNA is designated SEQ ID:3154, and is provided hereinbelow with reference to the sequence listing part.

[23342] GAM1505 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1505 target RNA, herein designated GAM TARGET RNA. GAM1505 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23343] GAM1505 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1505 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1505 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1505 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1505 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23344] The complementary binding of GAM1505 RNA, herein designated GAM RNA, to target binding sites on GAM1505 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1505 target RNA, herein designated GAM TARGET RNA, into GAM1505 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23345] It is appreciated that GAM1505 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1505 target genes. The mRNA of each one of this plurality of GAM1505 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1505 RNA, herein designated GAM RNA, and which when bound by GAM1505 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1505 target proteins.

[23346] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1505 gene, herein designated GAM GENE, on one or more GAM1505 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23347] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1505 correlate with, and may be deduced from, the identity of the target genes which GAM1505 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23348] Nucleotide sequences of the GAM1505 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1505 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1505 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1505 are further described hereinbelow with reference to Table Table1.

[23349] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1505 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23350] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1506 (GAM1506) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23351] GAM1506 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1506 was detected is described hereinabove with reference to Figs. 2-8.

[23352] GAM1506 gene, herein designated GAM GENE, and GAM1506 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23353] GAM1506 gene, herein designated GAM GENE, encodes a GAM1506 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1506 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1506 precursor RNA is designated SEQ ID:1479, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1479 is located at position 4851350 rela-

tive to contig NT_022517.13, on chromosome 3.

[23354] GAM1506 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23355] An enzyme complex designated DICER COMPLEX, dices the GAM1506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1506 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1506 RNA is designated SEQ ID:3155, and is provided hereinbelow with reference to the sequence listing part.

[23356] GAM1506 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1506 target RNA, herein designated GAM TARGET RNA. GAM1506 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23357] GAM1506 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1506 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1506 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1506 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1506 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23358] The complementary binding of GAM1506 RNA, herein designated GAM RNA, to target binding sites on GAM1506 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1506 target RNA, herein designated GAM TARGET RNA, into GAM1506 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23359] It is appreciated that GAM1506 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1506 target genes. The mRNA of each one of this plurality of GAM1506 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1506 RNA, herein designated GAM RNA, and which when bound by GAM1506 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1506

target proteins.

[23360] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1506 gene, herein designated GAM GENE, on one or more GAM1506 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23361] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1506 correlate with, and may be deduced from, the identity of the target genes which GAM1506 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23362] Nucleotide sequences of the GAM1506 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1506 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1506 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1506 are further described hereinbelow with reference to Table Table1.

[23363] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1506 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23364] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1507 (GAM1507) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23365] GAM1507 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1507 was detected is described hereinabove with reference to Figs. 2-8.

[23366] GAM1507 gene, herein designated GAM GENE, and

GAM1507 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23367] GAM1507 gene, herein designated GAM GENE, encodes a GAM1507 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1507 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1507 precursor RNA is designated SEQ ID:1480, and is provided hereinbelow with reference to the sequence listing part.

[23368] GAM1507 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23369] An enzyme complex designated DICER COMPLEX, dices the GAM1507 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1507 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1507 RNA is designated SEQ ID:3156, and is provided hereinbelow with reference to the sequence listing part.

[23370] GAM1507 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1507 target RNA, herein designated GAM TARGET RNA. GAM1507 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23371] GAM1507 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1507 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1507

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1507 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1507 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23372] The complementary binding of GAM1507 RNA, herein designated GAM RNA, to target binding sites on GAM1507 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1507 target RNA, herein designated GAM TARGET RNA, into GAM1507 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[23373] It is appreciated that GAM1507 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1507 target genes. The mRNA of each one of this plurality of GAM1507 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1507 RNA, herein designated GAM RNA, and which when bound by GAM1507 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1507 target proteins.

[23374] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1507 gene, herein designated GAM GENE, on one or more GAM1507 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23375] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1507 correlate with, and may be deduced from, the identity of the target genes which GAM1507 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23376] Nucleotide sequences of the GAM1507 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1507 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1507 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1507 are further described hereinbelow with reference to Table Table1.

[23377] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1507 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23378] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1508 (GAM1508) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23379] GAM1508 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1508 was detected is described hereinabove with reference to Figs. 2-8.

[23380] GAM1508 gene, herein designated GAM GENE, and GAM1508 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23381] GAM1508 gene, herein designated GAM GENE, encodes a GAM1508 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1508 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1508 precursor RNA is designated SEQ ID:1481, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1481 is located at position 1074999 relative to contig NT_028054.10, on chromosome 1.

[23382] GAM1508 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23383] An enzyme complex designated DICER COMPLEX, dices the GAM1508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1508 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1508 RNA is designated SEQ ID:3157, and is provided hereinbelow with reference to the sequence listing part.

[23384] GAM1508 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1508 target RNA, herein designated GAM TARGET RNA. GAM1508 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23385] GAM1508 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1508 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1508 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1508 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1508 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23386] The complementary binding of GAM1508 RNA, herein designated GAM RNA, to target binding sites on GAM1508 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1508 target RNA, herein designated GAM TARGET RNA, into GAM1508 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23387] It is appreciated that GAM1508 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1508 target genes. The mRNA of each one of this plurality of GAM1508 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1508 RNA, herein designated GAM RNA, and which when bound by GAM1508 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1508 target proteins.

[23388] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1508 gene, herein designated GAM GENE, on one or more GAM1508 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23389] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1508 correlate with, and may be deduced from, the identity of the target genes which GAM1508 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23390] Nucleotide sequences of the GAM1508 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1508 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1508 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1508 are further described hereinbelow with reference to Table Table1.

[23391] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1508 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23392] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1509 (GAM1509) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23393] GAM1509 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1509 was detected is described hereinabove with reference to Figs. 2-8.

[23394] GAM1509 gene, herein designated GAM GENE, and GAM1509 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[23395] GAM1509 gene, herein designated GAM GENE, encodes a GAM1509 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1509 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1509 precursor RNA is designated SEQ ID:1482, and is provided hereinbelow with reference to the sequence listing part.

[23396] GAM1509 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23397] An enzyme complex designated DICER COMPLEX, dices the GAM1509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1509 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1509 RNA is designated SEQ ID:3158, and is provided hereinbelow with reference to the sequence listing part.

[23398] GAM1509 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1509 target RNA, herein designated GAM TARGET RNA. GAM1509 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23399] GAM1509 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1509 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1509 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1509 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1509 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23400] The complementary binding of GAM1509 RNA, herein designated GAM RNA, to target binding sites on GAM1509 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1509 target RNA, herein designated GAM TARGET RNA, into GAM1509 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23401] It is appreciated that GAM1509 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1509 target genes. The mRNA of each one of this plurality of GAM1509 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1509 RNA, herein designated GAM RNA, and which when bound by GAM1509 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1509 target proteins.

[23402] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1509 gene, herein designated GAM GENE, on one or more GAM1509 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23403] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1509 correlate with, and may be deduced from, the identity of the target genes which GAM1509 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23404] Nucleotide sequences of the GAM1509 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1509 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1509 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1509 are further described hereinbelow with reference to Table Table1.

[23405] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1509 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23406] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1510 (GAM1510) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23407] GAM1510 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1510 was detected is described hereinabove with reference to Figs. 2-8.

[23408] GAM1510 gene, herein designated GAM GENE, and GAM1510 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23409] GAM1510 gene, herein designated GAM GENE, encodes a GAM1510 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1510 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1510 precursor RNA is designated SEQ ID:1483, and is provided hereinbelow with reference to the sequence listing part.

[23410] GAM1510 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1510 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23411] An enzyme complex designated DICER COMPLEX, dices the GAM1510 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1510 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1510 RNA is designated SEQ ID:3159, and is provided hereinbelow with reference to the sequence listing part.

[23412] GAM1510 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1510 target RNA, herein designated GAM TARGET RNA. GAM1510 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23413] GAM1510 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1510 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1510 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1510 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1510 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23414] The complementary binding of GAM1510 RNA, herein designated GAM RNA, to target binding sites on GAM1510 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1510 target RNA, herein designated GAM TARGET RNA, into GAM1510 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23415] It is appreciated that GAM1510 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1510 target genes. The mRNA of each one of this plurality of GAM1510 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1510 RNA, herein designated GAM RNA, and which when bound by GAM1510 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1510 target proteins.

[23416] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1510 gene, herein designated GAM GENE, on one or more GAM1510 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23417] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1510 correlate with, and may be deduced from, the identity of the target genes which GAM1510 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23418] Nucleotide sequences of the GAM1510 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1510 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1510 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1510 are further described hereinbelow with reference to Table Table1.

[23419] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1510 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23420] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1511 (GAM1511) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23421] GAM1511 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1511 was detected is described hereinabove with reference to Figs. 2-8.

[23422] GAM1511 gene, herein designated GAM GENE, and GAM1511 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23423] GAM1511 gene, herein designated GAM GENE, encodes a GAM1511 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1511 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1511 precursor RNA is designated SEQ ID:1484, and is provided hereinbelow with reference to the sequence listing part.

[23424] GAM1511 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23425] An enzyme complex designated DICER COMPLEX, dices the GAM1511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1511 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1511 RNA is designated SEQ ID:3160, and is provided hereinbelow with reference to the sequence listing part.

[23426] GAM1511 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1511 target RNA, herein designated GAM TARGET RNA. GAM1511 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23427] GAM1511 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1511 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1511 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1511 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1511 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23428] The complementary binding of GAM1511 RNA, herein designated GAM RNA, to target binding sites on GAM1511 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1511 target RNA, herein designated GAM TARGET RNA, into GAM1511 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23429] It is appreciated that GAM1511 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1511 target genes. The mRNA of each one of this

plurality of GAM1511 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1511 RNA, herein designated GAM RNA, and which when bound by GAM1511 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1511 target proteins.

[23430] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1511 gene, herein designated GAM GENE, on one or more GAM1511 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23431] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1511 correlate with, and may be deduced from, the identity of the target genes which GAM1511 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23432] Nucleotide sequences of the GAM1511 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1511 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1511 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1511 are further described hereinbelow with reference to Table Table1.

[23433] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1511 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23434] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1512 (GAM1512) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[23435] GAM1512 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1512 was detected is described hereinabove with reference to Figs. 2-8.

[23436] GAM1512 gene, herein designated GAM GENE, and GAM1512 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23437] GAM1512 gene, herein designated GAM GENE, encodes a GAM1512 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1512 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1512 precursor RNA is designated SEQ ID:1485, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1485 is located at position 3434864 relative to contig NT_009714.13, on chromosome 12.

[23438] GAM1512 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98468, which mouse homolog is detected in

mouse EST accession BG288438.1.

[23439] GAM1512 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23440] An enzyme complex designated DICER COMPLEX, dices the GAM1512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1512 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1512 RNA is designated SEQ ID:3161, and is provided hereinbelow with reference to the sequence listing part.

[23441] GAM1512 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1512 target RNA, herein designated GAM TARGET RNA. GAM1512 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23442] GAM1512 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1512 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1512 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1512 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1512 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23443] The complementary binding of GAM1512 RNA, herein designated GAM RNA, to target binding sites on GAM1512 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1512 target RNA, herein designated GAM TARGET RNA, into GAM1512 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23444] It is appreciated that GAM1512 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1512 target genes. The mRNA of each one of this plurality of GAM1512 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1512 RNA, herein designated GAM RNA, and which when bound by GAM1512 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1512

target proteins.

[23445] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1512 gene, herein designated GAM GENE, on one or more GAM1512 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23446] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1512 correlate with, and may be deduced from, the identity of the target genes which GAM1512 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23447] Nucleotide sequences of the GAM1512 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1512 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1512 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1512 are further described hereinbelow with reference to Table Table1.

[23448] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1512 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23449] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1513 (GAM1513) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23450] GAM1513 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1513 was detected is described hereinabove with reference to Figs. 2-8.

[23451] GAM1513 gene, herein designated GAM GENE, and

GAM1513 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23452] GAM1513 gene, herein designated GAM GENE, encodes a GAM1513 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1513 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1513 precursor RNA is designated SEQ ID:1486, and is provided hereinbelow with reference to the sequence listing part.

[23453] GAM1513 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23454] An enzyme complex designated DICER COMPLEX, dices the GAM1513 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1513 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1513 RNA is designated SEQ ID:3162, and is provided hereinbelow with reference to the sequence listing part.

[23455] GAM1513 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1513 target RNA, herein designated GAM TARGET RNA. GAM1513 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23456] GAM1513 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1513 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1513

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1513 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1513 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23457] The complementary binding of GAM1513 RNA, herein designated GAM RNA, to target binding sites on GAM1513 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1513 target RNA, herein designated GAM TARGET RNA, into GAM1513 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[23458] It is appreciated that GAM1513 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1513 target genes. The mRNA of each one of this plurality of GAM1513 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1513 RNA, herein designated GAM RNA, and which when bound by GAM1513 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1513 target proteins.

[23459] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1513 gene, herein designated GAM GENE, on one or more GAM1513 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23460] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1513 correlate with, and may be deduced from, the identity of the target genes which GAM1513 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23461] Nucleotide sequences of the GAM1513 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1513 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1513 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1513 are further described hereinbelow with reference to Table Table1.

[23462] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1513 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23463] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1514 (GAM1514) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23464] GAM1514 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1514 was detected is described hereinabove with reference to Figs. 2-8.

[23465] GAM1514 gene, herein designated GAM GENE, and GAM1514 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23466] GAM1514 gene, herein designated GAM GENE, encodes a GAM1514 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1514 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1514 precursor RNA is designated SEQ ID:1487, and is provided hereinbelow with reference to the sequence listing part.

[23467] GAM1514 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98481, which mouse homolog is detected in mouse EST accession BF301119.1.

[23468] GAM1514 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1514 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23469] An enzyme complex designated DICER COMPLEX, dices the GAM1514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1514 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 97%) nucleotide sequence of GAM1514 RNA is designated SEQ ID:3163, and is provided hereinbelow with reference to the sequence listing part.

[23470] GAM1514 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1514 target RNA, herein designated GAM TARGET

RNA. GAM1514 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23471] GAM1514 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1514 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1514 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1514 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1514 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23472] The complementary binding of GAM1514 RNA, herein designated GAM RNA, to target binding sites on GAM1514 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1514 target RNA, herein designated GAM TARGET RNA, into GAM1514 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23473] It is appreciated that GAM1514 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1514 target genes. The mRNA of each one of this plurality of GAM1514 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1514 RNA, herein designated GAM RNA, and which when bound by GAM1514 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1514 target proteins.

[23474] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1514 gene, herein designated GAM GENE, on one or more GAM1514 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23475] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1514 correlate with, and may be deduced from, the identity of the target genes which GAM1514 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23476] Nucleotide sequences of the GAM1514 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1514 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1514 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1514 are further described hereinbelow with reference to Table Table1.

[23477] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1514 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23478] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1515 (GAM1515) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23479] GAM1515 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1515 was detected is described hereinabove with reference to Figs. 2-8.

[23480] GAM1515 gene, herein designated GAM GENE, and GAM1515 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23481] GAM1515 gene, herein designated GAM GENE, encodes a

GAM1515 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1515 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1515 precursor RNA is designated SEQ ID:1488, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1488 is located at position 21008692 relative to contig NT_034874.2, on chromosome 6.

[23482] GAM1515 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23483] An enzyme complex designated DICER COMPLEX, dices the GAM1515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1515 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1515 RNA is designated SEQ ID:3164, and is provided hereinbelow with reference to the sequence listing part.

[23484] GAM1515 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1515 target RNA, herein designated GAM TARGET RNA. GAM1515 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23485] GAM1515 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1515 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1515 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1515 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1515 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23486] The complementary binding of GAM1515 RNA, herein designated GAM RNA, to target binding sites on GAM1515 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1515 target RNA, herein designated GAM TARGET RNA, into GAM1515 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23487] It is appreciated that GAM1515 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1515 target genes. The mRNA of each one of this plurality of GAM1515 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1515 RNA, herein designated GAM RNA, and which when bound by GAM1515 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1515 target proteins.

[23488] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1515 gene, herein designated GAM GENE, on one or more GAM1515 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23489] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1515 correlate with, and may be deduced from, the identity of the target genes which GAM1515 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23490] Nucleotide sequences of the GAM1515 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1515 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1515 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1515 are further described hereinbelow with reference to Table Table1.

[23491] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1515 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23492] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1516 (GAM1516) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23493] GAM1516 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1516 was detected is described hereinabove with reference to Figs. 2-8.

[23494] GAM1516 gene, herein designated GAM GENE, and GAM1516 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23495] GAM1516 gene, herein designated GAM GENE, encodes a GAM1516 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1516 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1516 precursor RNA is designated SEQ ID:1489, and is provided hereinbelow with reference to the sequence listing part.

[23496] GAM1516 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1516 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23497] An enzyme complex designated DICER COMPLEX, dices the GAM1516 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1516 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1516 RNA is designated SEQ ID:3165, and is provided hereinbelow with reference to the sequence listing part.

[23498] GAM1516 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1516 target RNA, herein designated GAM TARGET RNA. GAM1516 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23499] GAM1516 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1516 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1516 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1516 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1516 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23500] The complementary binding of GAM1516 RNA, herein designated GAM RNA, to target binding sites on GAM1516 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1516 target RNA, herein designated GAM TARGET RNA, into GAM1516 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23501] It is appreciated that GAM1516 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1516 target genes. The mRNA of each one of this plurality of GAM1516 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1516 RNA, herein designated GAM RNA, and which when bound by GAM1516 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1516 target proteins.

[23502] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1516 gene, herein designated GAM GENE, on one or more GAM1516 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23503] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1516 correlate with, and may be deduced from, the identity of the target genes which GAM1516 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23504] Nucleotide sequences of the GAM1516 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1516 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1516 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1516 are further described hereinbelow with reference to Table Table1.

[23505] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1516 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23506] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1517 (GAM1517) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23507] GAM1517 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1517 was detected is described hereinabove with reference to Figs. 2-8.

[23508] GAM1517 gene, herein designated GAM GENE, and GAM1517 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23509] GAM1517 gene, herein designated GAM GENE, encodes a GAM1517 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1517 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1517 precursor RNA is designated SEQ ID:1490, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1490 is located at position 753752 relative to contig NT_022300.10, on chromosome 2.

[23510] GAM1517 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23511] An enzyme complex designated DICER COMPLEX, dices the GAM1517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1517 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1517 RNA is designated SEQ ID:3166, and is provided hereinbelow with reference to the sequence listing part.

[23512] GAM1517 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1517 target RNA, herein designated GAM TARGET RNA. GAM1517 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23513] GAM1517 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1517 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1517 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1517 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1517 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23514] The complementary binding of GAM1517 RNA, herein designated GAM RNA, to target binding sites on GAM1517 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1517 target RNA, herein designated GAM TARGET RNA, into GAM1517 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23515] It is appreciated that GAM1517 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1517 target genes. The mRNA of each one of this plurality of GAM1517 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1517 RNA, herein designated GAM RNA, and which when bound by GAM1517 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1517 target proteins.

[23516] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1517 gene, herein designated GAM GENE, on one or more GAM1517 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23517] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1517 correlate with, and may be deduced from, the identity of the target genes which GAM1517 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23518] Nucleotide sequences of the GAM1517 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1517 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1517 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1517 are further described hereinbelow with reference to Table Table1.

[23519] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1517 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23520] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1518 (GAM1518) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23521] GAM1518 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1518 was detected is described hereinabove with reference to Figs. 2-8.

[23522] GAM1518 gene, herein designated GAM GENE, and GAM1518 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23523] GAM1518 gene, herein designated GAM GENE, encodes a GAM1518 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1518 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1518 precursor RNA is designated SEQ ID:1491, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1491 is located at position 6080883 relative to contig NT_011812.10, on chromosome X.

[23524] GAM1518 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1518 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23525] An enzyme complex designated DICER COMPLEX, dices the GAM1518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1518 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1518 RNA is designated SEQ ID:3167, and is provided hereinbelow with reference to the sequence listing part.

[23526] GAM1518 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1518 target RNA, herein designated GAM TARGET

RNA. GAM1518 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23527] GAM1518 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1518 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1518 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1518 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1518 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23528] The complementary binding of GAM1518 RNA, herein designated GAM RNA, to target binding sites on GAM1518 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1518 target RNA, herein designated GAM TARGET RNA, into GAM1518 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23529] It is appreciated that GAM1518 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1518 target genes. The mRNA of each one of this plurality of GAM1518 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1518 RNA, herein designated GAM RNA, and which when bound by GAM1518 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1518 target proteins.

[23530] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1518 gene, herein designated GAM GENE, on one or more GAM1518 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23531] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1518 correlate with, and may be deduced from, the identity of the target genes which GAM1518 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23532] Nucleotide sequences of the GAM1518 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1518 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1518 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1518 are further described hereinbelow with reference to Table Table1.

[23533] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1518 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23534] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1519 (GAM1519) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23535] GAM1519 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1519 was detected is described hereinabove with reference to Figs. 2-8.

[23536] GAM1519 gene, herein designated GAM GENE, and GAM1519 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23537] GAM1519 gene, herein designated GAM GENE, encodes a

GAM1519 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1519 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1519 precursor RNA is designated SEQ ID:1492, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1492 is located at position 849933 relative to contig NT_009458.12, on chromosome 12.

[23538] GAM1519 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23539] An enzyme complex designated DICER COMPLEX, dices the GAM1519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1519 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1519 RNA is designated SEQ ID:3168, and is provided hereinbelow with reference to the sequence listing part.

[23540] GAM1519 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1519 target RNA, herein designated GAM TARGET RNA. GAM1519 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23541] GAM1519 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1519 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1519 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1519 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1519 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23542] The complementary binding of GAM1519 RNA, herein designated GAM RNA, to target binding sites on GAM1519 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1519 target RNA, herein designated GAM TARGET RNA, into GAM1519 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23543] It is appreciated that GAM1519 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1519 target genes. The mRNA of each one of this plurality of GAM1519 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1519 RNA, herein designated GAM RNA, and which when bound by GAM1519 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1519 target proteins.

[23544] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1519 gene, herein designated GAM GENE, on one or more GAM1519 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23545] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1519 correlate with, and may be deduced from, the identity of the target genes which GAM1519 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23546] Nucleotide sequences of the GAM1519 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1519 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1519 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1519 are further described hereinbelow with reference to Table Table1.

[23547] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1519 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23548] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1520 (GAM1520) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23549] GAM1520 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1520 was detected is described hereinabove with reference to Figs. 2-8.

[23550] GAM1520 gene, herein designated GAM GENE, and GAM1520 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23551] GAM1520 gene, herein designated GAM GENE, encodes a GAM1520 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1520 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1520 precursor RNA is designated SEQ ID:1493, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1493 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[23552] GAM1520 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23553] An enzyme complex designated DICER COMPLEX, dices the GAM1520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1520 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1520 RNA is designated SEQ ID:3169, and is provided hereinbelow with reference to the sequence listing part.

[23554] GAM1520 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1520 target RNA, herein designated GAM TARGET RNA. GAM1520 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23555] GAM1520 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1520 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1520 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1520 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1520 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23556] The complementary binding of GAM1520 RNA, herein designated GAM RNA, to target binding sites on GAM1520 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1520 target RNA, herein designated GAM TARGET RNA, into GAM1520 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23557] It is appreciated that GAM1520 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1520 target genes. The mRNA of each one of this plurality of GAM1520 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1520 RNA, herein designated GAM RNA, and which when bound by GAM1520 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1520 target proteins.

[23558] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1520 gene, herein designated GAM GENE, on one or more GAM1520 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23559] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1520 correlate with, and may be deduced from, the identity of the target genes which GAM1520 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23560] Nucleotide sequences of the GAM1520 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1520 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1520 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1520 are further described hereinbelow with reference to Table Table1.

[23561] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1520 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23562] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1521 (GAM1521) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23563] GAM1521 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1521 was detected is described hereinabove with reference to Figs. 2-8.

[23564] GAM1521 gene, herein designated GAM GENE, and GAM1521 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23565] GAM1521 gene, herein designated GAM GENE, encodes a GAM1521 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1521 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1521 precursor RNA is designated SEQ ID:1494, and is provided hereinbelow with reference to the sequence listing part.

[23566] GAM1521 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23567] An enzyme complex designated DICER COMPLEX, dices the GAM1521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1521 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1521 RNA is designated SEQ ID:3170, and is provided hereinbelow with reference to the sequence listing part.

[23568] GAM1521 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1521 target RNA, herein designated GAM TARGET RNA. GAM1521 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23569] GAM1521 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1521 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1521 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1521 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1521 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23570] The complementary binding of GAM1521 RNA, herein designated GAM RNA, to target binding sites on GAM1521 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1521 target RNA, herein designated GAM TARGET RNA, into GAM1521 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23571] It is appreciated that GAM1521 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1521 target genes. The mRNA of each one of this plurality of GAM1521 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1521 RNA, herein designated GAM RNA, and which when bound by GAM1521 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1521 target proteins.

[23572] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1521 gene, herein designated GAM GENE, on one or more GAM1521 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23573] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1521 correlate with, and may be deduced from, the identity of the target genes which GAM1521 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23574] Nucleotide sequences of the GAM1521 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1521 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1521 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1521 are further described hereinbelow with reference to Table Table1.

[23575] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1521 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23576] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1522 (GAM1522) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23577] GAM1522 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1522 was detected is described hereinabove with reference to Figs. 2-8.

[23578] GAM1522 gene, herein designated GAM GENE, and GAM1522 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23579] GAM1522 gene, herein designated GAM GENE, encodes a GAM1522 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1522 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1522 precursor RNA is designated SEQ ID:1495, and is provided hereinbelow with reference to the sequence listing part.

[23580] GAM1522 has 45 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse

EST's in which these homologs were detected are:

[23581] SEQ ID:98873 detected in mouse EST Accession AI854392.1.

[23582] SEQ ID:98874 detected in mouse EST Accession BF687351.1.

[23583] SEQ ID:98875 detected in mouse EST Accession AI839406.1.

[23584] SEQ ID:98876 detected in mouse EST Accession AA500195.1.

[23585] SEQ ID:98877 detected in mouse EST Accession AW240734.1.

[23586] SEQ ID:98878 detected in mouse EST Accession AA189505.1.

[23587] SEQ ID:98879 detected in mouse EST Accession AI461779.1.

[23588] SEQ ID:98880 detected in mouse EST Accession AA242320.1.

[23589] SEQ ID:98881 detected in mouse EST Accession BE947946.1.

[23590] SEQ ID:98882 detected in mouse EST Accession AW551192.1.

[23591] SEQ ID:98883 detected in mouse EST Accession AA163022.1.

[23592] SEQ ID:98890 detected in mouse EST Accession W89797.1.

[23593] SEQ ID:98891 detected in mouse EST Accession BI558262.1.

[23594] SEQ ID:98892 detected in mouse EST Accession BI965110.1.

[23595] SEQ ID:98893 detected in mouse EST Accession BF659642.1.

[23596] SEQ ID:98894 detected in mouse EST Accession BG965723.1.

[23597] SEQ ID:98895 detected in mouse EST Accession BG073636.1.

[23598] SEQ ID:98896 detected in mouse EST Accession BF168189.1.

[23599] SEQ ID:98897 detected in mouse EST Accession AA162243.1.

[23600] SEQ ID:98898 detected in mouse EST Accession AA882101.1.

[23601] SEQ ID:98899 detected in mouse EST Accession AA512111.1.

[23602] SEQ ID:98900 detected in mouse EST Accession AA832938.1.

[23603] SEQ ID:98901 detected in mouse EST Accession

AA138504.1.

[23604] SEQ ID:98905 detected in mouse EST Accession W14197.1.

[23605] SEQ ID:98906 detected in mouse EST Accession AI842538.1.

[23606] SEQ ID:98907 detected in mouse EST Accession BF226782.1.

[23607] SEQ ID:98908 detected in mouse EST Accession BF318481.1.

[23608] SEQ ID:98909 detected in mouse EST Accession BF139968.1.

[23609] SEQ ID:98910 detected in mouse EST Accession AI325115.1.

[23610] SEQ ID:98911 detected in mouse EST Accession BF140754.1.

[23611] SEQ ID:98912 detected in mouse EST Accession AI845391.1.

[23612] SEQ ID:98913 detected in mouse EST Accession AW240469.1.

[23613] SEQ ID:98916 detected in mouse EST Accession BE690452.1.

[23614] SEQ ID:98917 detected in mouse EST Accession AA198420.1.

[23615] SEQ ID:98918 detected in mouse EST Accession BE850073.1.

[23616] SEQ ID:98919 detected in mouse EST Accession AW324261.1.

[23617] SEQ ID:98920 detected in mouse EST Accession AA122556.1.

[23618] SEQ ID:98921 detected in mouse EST Accession BE692432.1.

[23619] SEQ ID:98922 detected in mouse EST Accession AA242308.1.

[23620] SEQ ID:98923 detected in mouse EST Accession BI731662.1.

[23621] SEQ ID:98924 detected in mouse EST Accession BG079737.1.

[23622] SEQ ID:98925 detected in mouse EST Accession AW411866.1.

[23623] SEQ ID:98926 detected in mouse EST Accession BF531359.1.

[23624] SEQ ID:98927 detected in mouse EST Accession BI407550.1.

[23625] SEQ ID:98928 detected in mouse EST Accession W64685.1.

[23626] GAM1522 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23627] An enzyme complex designated DICER COMPLEX, dices the GAM1522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1522 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1522 RNA is designated SEQ ID:3171, and is provided hereinbelow with reference to the sequence listing part.

[23628] GAM1522 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1522 target RNA, herein designated GAM TARGET RNA. GAM1522 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23629] GAM1522 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1522 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1522 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1522 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1522 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23630] The complementary binding of GAM1522 RNA, herein designated GAM RNA, to target binding sites on GAM1522 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1522 target RNA, herein designated GAM TARGET RNA, into GAM1522 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23631] It is appreciated that GAM1522 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1522 target genes. The mRNA of each one of this plurality of GAM1522 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1522 RNA, herein designated GAM RNA, and which when bound by GAM1522 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1522 target proteins.

[23632] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1522 gene, herein designated GAM GENE, on one or more GAM1522 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23633] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1522 correlate with, and may be deduced from, the identity of the target genes which GAM1522 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23634] Nucleotide sequences of the GAM1522 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1522 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1522 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1522 are further described hereinbelow with reference to Table Table1.

[23635] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1522 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23636] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1523 (GAM1523) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23637] GAM1523 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1523 was detected is described hereinabove with reference to Figs. 2-8.

[23638] GAM1523 gene, herein designated GAM GENE, and GAM1523 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23639] GAM1523 gene, herein designated GAM GENE, encodes a GAM1523 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1523 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1523 precursor RNA is designated SEQ ID:1496, and is provided hereinbelow with reference to the sequence listing part.

[23640] GAM1523 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23641] An enzyme complex designated DICER COMPLEX, dices the GAM1523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1523 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1523 RNA is designated SEQ ID:3172, and is provided hereinbelow with reference to the sequence listing part.

[23642] GAM1523 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1523 target RNA, herein designated GAM TARGET RNA. GAM1523 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23643] GAM1523 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1523 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1523 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1523 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1523 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23644] The complementary binding of GAM1523 RNA, herein designated GAM RNA, to target binding sites on GAM1523 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1523 target RNA, herein designated GAM TARGET RNA, into GAM1523 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23645] It is appreciated that GAM1523 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1523 target genes. The mRNA of each one of this plurality of GAM1523 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1523 RNA, herein designated GAM RNA, and which when bound by GAM1523 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1523 target proteins.

[23646] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1523 gene, herein designated GAM GENE, on one or more GAM1523 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23647] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1523 correlate with, and may be deduced from, the identity of the target genes which GAM1523 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23648] Nucleotide sequences of the GAM1523 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1523 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1523 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1523 are further described hereinbelow with reference to Table Table1.

[23649] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1523 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23650] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1524 (GAM1524) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23651] GAM1524 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1524 was detected is described hereinabove with reference to Figs. 2-8.

[23652] GAM1524 gene, herein designated GAM GENE, and GAM1524 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23653] GAM1524 gene, herein designated GAM GENE, encodes a GAM1524 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1524 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1524 precursor RNA is designated SEQ ID:1497, and is provided hereinbelow with reference to the sequence listing part.

[23654] GAM1524 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23655] An enzyme complex designated DICER COMPLEX, dices the GAM1524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1524 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1524 RNA is designated SEQ ID:3173, and is provided hereinbelow with reference to the sequence listing part.

[23656] GAM1524 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1524 target RNA, herein designated GAM TARGET RNA. GAM1524 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23657] GAM1524 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1524 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1524 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1524 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1524 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[23658] The complementary binding of GAM1524 RNA, herein designated GAM RNA, to target binding sites on GAM1524 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1524 target RNA, herein designated GAM TARGET RNA, into GAM1524 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23659] It is appreciated that GAM1524 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1524 target genes. The mRNA of each one of this plurality of GAM1524 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1524 RNA, herein designated GAM RNA, and which when bound by GAM1524 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1524 target proteins.

[23660] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1524 gene, herein designated GAM GENE, on one or

more GAM1524 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23661] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1524 correlate with, and may be deduced from, the identity of the target genes which GAM1524 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23662] Nucleotide sequences of the GAM1524 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1524 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1524 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1524 are further de-

scribed hereinbelow with reference to Table Table1.

[23663] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1524 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23664] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1525 (GAM1525) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23665] GAM1525 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1525 was detected is described hereinabove with reference to Figs. 2-8.

[23666] GAM1525 gene, herein designated GAM GENE, and GAM1525 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23667] GAM1525 gene, herein designated GAM GENE, encodes a GAM1525 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1525 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1525 precursor RNA is designated SEQ ID:1498, and is provided hereinbelow with reference to the sequence listing part.

[23668] GAM1525 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23669] An enzyme complex designated DICER COMPLEX, dices the GAM1525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1525 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1525 RNA is designated SEQ ID:3174, and is provided hereinbelow with reference to the sequence listing part.

[23670] GAM1525 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1525 target RNA, herein designated GAM TARGET RNA. GAM1525 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23671] GAM1525 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1525 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1525 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1525 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1525 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23672] The complementary binding of GAM1525 RNA, herein designated GAM RNA, to target binding sites on GAM1525 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1525 target RNA, herein designated GAM TARGET RNA, into GAM1525 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23673] It is appreciated that GAM1525 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1525 target genes. The mRNA of each one of this plurality of GAM1525 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1525 RNA, herein designated GAM RNA, and which when bound by GAM1525 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1525 target proteins.

[23674] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1525 gene, herein designated GAM GENE, on one or more GAM1525 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23675] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1525 correlate with, and may be deduced from, the identity of the target genes which GAM1525 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23676] Nucleotide sequences of the GAM1525 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1525 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1525 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1525 are further described hereinbelow with reference to Table Table1.

[23677] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1525 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23678] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1526 (GAM1526) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23679] GAM1526 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1526 was detected is described hereinabove with reference to Figs. 2-8.

[23680] GAM1526 gene, herein designated GAM GENE, and GAM1526 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23681] GAM1526 gene, herein designated GAM GENE, encodes a GAM1526 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1526 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1526 precursor RNA is designated SEQ ID:1499, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1499 is located at position 6275175 relative to contig NT_034383.2, on chromosome 1.

[23682] GAM1526 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[23683] SEQ ID:98853 detected in mouse EST Accession AA684283.1.

[23684] SEQ ID:98854 detected in mouse EST Accession AA168500.1.

[23685] SEQ ID:98855 detected in mouse EST Accession AA017943.1.

[23686] SEQ ID:98856 detected in mouse EST Accession AI316374.1.

[23687] SEQ ID:98857 detected in mouse EST Accession AA122754.1.

[23688] SEQ ID:98858 detected in mouse EST Accession AW413196.1.

[23689] SEQ ID:98861 detected in mouse EST Accession BI148579.1.

[23690] SEQ ID:98862 detected in mouse EST Accession BG242574.1.

[23691] GAM1526 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23692] An enzyme complex designated DICER COMPLEX, dices the GAM1526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1526 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1526 RNA is designated SEQ ID:3175, and is provided hereinbelow with reference to the sequence listing part.

[23693] GAM1526 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1526 target RNA, herein designated GAM TARGET RNA. GAM1526 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23694] GAM1526 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1526 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1526 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1526 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1526 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23695] The complementary binding of GAM1526 RNA, herein designated GAM RNA, to target binding sites on GAM1526

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1526 target RNA, herein designated GAM TARGET RNA, into GAM1526 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23696] It is appreciated that GAM1526 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1526 target genes. The mRNA of each one of this plurality of GAM1526 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1526 RNA, herein designated GAM RNA, and which when bound by GAM1526 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1526 target proteins.

[23697] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1526 gene, herein designated GAM GENE, on one or more GAM1526 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23698] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1526 correlate with, and may be deduced from, the identity of the target genes which GAM1526 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23699] Nucleotide sequences of the GAM1526 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1526 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1526 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1526 are further described hereinbelow with reference to Table Table1.

[23700] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1526 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23701] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1527 (GAM1527) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23702] GAM1527 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1527 was detected is described hereinabove with reference to Figs. 2-8.

[23703] GAM1527 gene, herein designated GAM GENE, and GAM1527 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23704] GAM1527 gene, herein designated GAM GENE, encodes a GAM1527 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1527 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1527 precursor RNA is designated SEQ ID:1500, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1500 is located at position 3385728 relative to contig NT_006216.12, on chromosome 4.

[23705] GAM1527 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23706] An enzyme complex designated DICER COMPLEX, dices the GAM1527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1527 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1527 RNA is designated SEQ ID:3176, and is provided hereinbelow with reference to the sequence listing part.

[23707] GAM1527 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1527 target RNA, herein designated GAM TARGET RNA. GAM1527 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23708] GAM1527 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1527 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1527 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1527 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1527 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23709] The complementary binding of GAM1527 RNA, herein designated GAM RNA, to target binding sites on GAM1527 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1527 target RNA, herein designated GAM TARGET RNA, into GAM1527 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23710] It is appreciated that GAM1527 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1527 target genes. The mRNA of each one of this plurality of GAM1527 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1527 RNA, herein designated GAM RNA, and which when bound by GAM1527 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1527 target proteins.

[23711] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1527 gene, herein designated GAM GENE, on one or more GAM1527 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23712] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1527 correlate with, and may

be deduced from, the identity of the target genes which GAM1527 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23713] Nucleotide sequences of the GAM1527 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1527 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1527 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1527 are further described hereinbelow with reference to Table Table1.

[23714] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1527 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23715] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1528 (GAM1528) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23716] GAM1528 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1528 was detected is described hereinabove with reference to Figs. 2-8.

[23717] GAM1528 gene, herein designated GAM GENE, and GAM1528 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23718] GAM1528 gene, herein designated GAM GENE, encodes a GAM1528 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1528 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1528 precursor RNA is designated SEQ ID:1501, and is provided hereinbelow with reference to the sequence listing part.

[23719] GAM1528 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23720] An enzyme complex designated DICER COMPLEX, dices the GAM1528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1528 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1528 RNA is designated SEQ ID:3177, and is provided hereinbelow with reference to the sequence listing part.

[23721] GAM1528 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1528 target RNA, herein designated GAM TARGET RNA. GAM1528 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23722] GAM1528 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1528 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1528 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1528 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1528 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23723] The complementary binding of GAM1528 RNA, herein designated GAM RNA, to target binding sites on GAM1528 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1528 target RNA, herein designated GAM TARGET RNA, into GAM1528 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23724] It is appreciated that GAM1528 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1528 target genes. The mRNA of each one of this plurality of GAM1528 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1528 RNA, herein designated GAM RNA, and which when bound by GAM1528 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1528 target proteins.

[23725] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1528 gene, herein designated GAM GENE, on one or more GAM1528 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23726] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1528 correlate with, and may be deduced from, the identity of the target genes which GAM1528 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23727] Nucleotide sequences of the GAM1528 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1528 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1528 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1528 are further described hereinbelow with reference to Table Table1.

[23728] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1528 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23729] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1529 (GAM1529) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23730] GAM1529 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1529 was detected is described hereinabove with reference to Figs. 2-8.

[23731] GAM1529 gene, herein designated GAM GENE, and GAM1529 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23732] GAM1529 gene, herein designated GAM GENE, encodes a GAM1529 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1529 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1529 precursor RNA is

designated SEQ ID:1502, and is provided hereinbelow with reference to the sequence listing part.

[23733] GAM1529 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23734] An enzyme complex designated DICER COMPLEX, dices the GAM1529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1529 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1529 RNA is designated SEQ ID:3178, and is provided hereinbelow with reference to the sequence

listing part.

[23735] GAM1529 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1529 target RNA, herein designated GAM TARGET RNA. GAM1529 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23736] GAM1529 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1529 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1529 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1529 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1529 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23737] The complementary binding of GAM1529 RNA, herein designated GAM RNA, to target binding sites on GAM1529 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1529 target RNA, herein designated GAM TARGET RNA, into GAM1529 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23738] It is appreciated that GAM1529 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1529 target genes. The mRNA of each one of this plurality of GAM1529 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1529 RNA, herein designated GAM RNA, and which when bound by GAM1529 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1529 target proteins.

[23739] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1529 gene, herein designated GAM GENE, on one or more GAM1529 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23740] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1529 correlate with, and may be deduced from, the identity of the target genes which GAM1529 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23741] Nucleotide sequences of the GAM1529 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1529 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1529 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1529 are further described hereinbelow with reference to Table Table1.

[23742] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1529 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23743] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1530 (GAM1530) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23744] GAM1530 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1530 was detected is described hereinabove with reference to Figs. 2-8.

[23745] GAM1530 gene, herein designated GAM GENE, and GAM1530 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23746] GAM1530 gene, herein designated GAM GENE, encodes a GAM1530 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1530 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1530 precursor RNA is designated SEQ ID:1503, and is provided hereinbelow with reference to the sequence listing part.

[23747] GAM1530 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23748] An enzyme complex designated DICER COMPLEX, dices

the GAM1530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1530 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1530 RNA is designated SEQ ID:3179, and is provided hereinbelow with reference to the sequence listing part.

[23749] GAM1530 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1530 target RNA, herein designated GAM TARGET RNA. GAM1530 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23750] GAM1530 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1530 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1530 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1530 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1530 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23751] The complementary binding of GAM1530 RNA, herein designated GAM RNA, to target binding sites on GAM1530 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1530 target RNA, herein designated GAM TARGET RNA, into GAM1530 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23752] It is appreciated that GAM1530 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1530 target genes. The mRNA of each one of this plurality of GAM1530 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1530 RNA, herein designated GAM RNA, and which when bound by GAM1530 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1530 target proteins.

[23753] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1530 gene, herein designated GAM GENE, on one or more GAM1530 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23754] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1530 correlate with, and may be deduced from, the identity of the target genes which GAM1530 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23755] Nucleotide sequences of the GAM1530 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1530 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1530 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1530 are further described hereinbelow with reference to Table Table1.

[23756] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1530 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23757] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1531 (GAM1531) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23758] GAM1531 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1531 was detected is described hereinabove with reference to Figs. 2-8.

[23759] GAM1531 gene, herein designated GAM GENE, and GAM1531 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23760] GAM1531 gene, herein designated GAM GENE, encodes a GAM1531 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1531 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1531 precursor RNA is designated SEQ ID:1504, and is provided hereinbelow with reference to the sequence listing part.

[23761] GAM1531 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23762] An enzyme complex designated DICER COMPLEX, dices the GAM1531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1531 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1531 RNA is designated SEQ ID:3180, and is provided hereinbelow with reference to the sequence listing part.

[23763] GAM1531 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1531 target RNA, herein designated GAM TARGET RNA. GAM1531 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23764] GAM1531 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1531 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1531 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1531 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1531 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23765] The complementary binding of GAM1531 RNA, herein designated GAM RNA, to target binding sites on GAM1531 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1531 target RNA, herein designated GAM TARGET RNA, into GAM1531 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23766] It is appreciated that GAM1531 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1531 target genes. The mRNA of each one of this plurality of GAM1531 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1531 RNA, herein designated GAM RNA, and which when bound by GAM1531 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1531 target proteins.

[23767] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1531 gene, herein designated GAM GENE, on one or more GAM1531 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23768] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1531 correlate with, and may be deduced from, the identity of the target genes which GAM1531 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23769] Nucleotide sequences of the GAM1531 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1531 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1531 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1531 are further described hereinbelow with reference to Table Table1.

[23770] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1531 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23771] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1532 (GAM1532) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23772] GAM1532 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1532 was detected is described hereinabove with reference to Figs. 2-8.

[23773] GAM1532 gene, herein designated GAM GENE, and GAM1532 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23774] GAM1532 gene, herein designated GAM GENE, encodes a GAM1532 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1532 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1532 precursor RNA is designated SEQ ID:1505, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1505 is located at position 532334 relative to contig NT_011520.8, on chromosome 22.

[23775] GAM1532 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23776] An enzyme complex designated DICER COMPLEX, dices the GAM1532 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1532 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1532 RNA is designated SEQ ID:3181, and is provided hereinbelow with reference to the sequence listing part.

[23777] GAM1532 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1532 target RNA, herein designated GAM TARGET RNA. GAM1532 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23778] GAM1532 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1532 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1532

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1532 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1532 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23779] The complementary binding of GAM1532 RNA, herein designated GAM RNA, to target binding sites on GAM1532 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1532 target RNA, herein designated GAM TARGET RNA, into GAM1532 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[23780] It is appreciated that GAM1532 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1532 target genes. The mRNA of each one of this plurality of GAM1532 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1532 RNA, herein designated GAM RNA, and which when bound by GAM1532 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1532 target proteins.

[23781] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1532 gene, herein designated GAM GENE, on one or more GAM1532 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23782] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1532 correlate with, and may be deduced from, the identity of the target genes which GAM1532 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23783] Nucleotide sequences of the GAM1532 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1532 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1532 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1532 are further described hereinbelow with reference to Table Table1.

[23784] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1532 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23785] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1533 (GAM1533) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23786] GAM1533 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1533 was detected is described hereinabove with reference to Figs. 2-8.

[23787] GAM1533 gene, herein designated GAM GENE, and GAM1533 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23788] GAM1533 gene, herein designated GAM GENE, encodes a GAM1533 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1533 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1533 precursor RNA is designated SEQ ID:1506, and is provided hereinbelow with reference to the sequence listing part.

[23789] GAM1533 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1533 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23790] An enzyme complex designated DICER COMPLEX, dices the GAM1533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1533 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1533 RNA is designated SEQ ID:3182, and is provided hereinbelow with reference to the sequence listing part.

[23791] GAM1533 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1533 target RNA, herein designated GAM TARGET

RNA. GAM1533 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23792] GAM1533 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1533 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1533 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1533 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1533 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23793] The complementary binding of GAM1533 RNA, herein designated GAM RNA, to target binding sites on GAM1533 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1533 target RNA, herein designated GAM TARGET RNA, into GAM1533 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23794] It is appreciated that GAM1533 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1533 target genes. The mRNA of each one of this plurality of GAM1533 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1533 RNA, herein designated GAM RNA, and which when bound by GAM1533 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1533 target proteins.

[23795] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1533 gene, herein designated GAM GENE, on one or more GAM1533 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23796] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1533 correlate with, and may be deduced from, the identity of the target genes which GAM1533 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23797] Nucleotide sequences of the GAM1533 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1533 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1533 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1533 are further described hereinbelow with reference to Table Table1.

[23798] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1533 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23799] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1534 (GAM1534) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23800] GAM1534 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1534 was detected is described hereinabove with reference to Figs. 2-8.

[23801] GAM1534 gene, herein designated GAM GENE, and GAM1534 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23802] GAM1534 gene, herein designated GAM GENE, encodes a

GAM1534 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1534 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1534 precursor RNA is designated SEQ ID:1507, and is provided hereinbelow with reference to the sequence listing part.

[23803] GAM1534 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[23804] SEQ ID:99087 detected in mouse EST Accession AA823029.1.

[23805] SEQ ID:99088 detected in mouse EST Accession BE625629.1.

[23806] SEQ ID:99089 detected in mouse EST Accession BE380224.1.

[23807] SEQ ID:99090 detected in mouse EST Accession BE309708.1.

[23808] SEQ ID:99091 detected in mouse EST Accession BI100916.1.

[23809] SEQ ID:99104 detected in mouse EST Accession BG296866.1.

[23810] SEQ ID:99107 detected in mouse EST Accession AA068787.1.

[23811] SEQ ID:99108 detected in mouse EST Accession BI792530.1.

[23812] GAM1534 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23813] An enzyme complex designated DICER COMPLEX, dices the GAM1534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1534 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 97%) nucleotide sequence of GAM1534 RNA is designated SEQ ID:3183, and is provided hereinbelow with reference to the sequence listing part.

[23814] GAM1534 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1534 target RNA, herein designated GAM TARGET RNA. GAM1534 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23815] GAM1534 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1534 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1534 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1534 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1534 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23816] The complementary binding of GAM1534 RNA, herein designated GAM RNA, to target binding sites on GAM1534 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1534 target RNA, herein designated GAM TARGET RNA, into GAM1534 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23817] It is appreciated that GAM1534 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1534 target genes. The mRNA of each one of this plurality of GAM1534 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1534 RNA, herein designated GAM RNA, and which when bound by GAM1534 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1534 target proteins.

[23818] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1534 gene, herein designated GAM GENE, on one or more GAM1534 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23819] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1534 correlate with, and may be deduced from, the identity of the target genes which GAM1534 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23820] Nucleotide sequences of the GAM1534 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1534 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1534 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1534 are further described hereinbelow with reference to Table Table1.

[23821] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1534 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23822] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1535 (GAM1535) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23823] GAM1535 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1535 was detected is described hereinabove with reference to Figs. 2-8.

[23824] GAM1535 gene, herein designated GAM GENE, and GAM1535 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23825] GAM1535 gene, herein designated GAM GENE, encodes a GAM1535 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1535 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1535 precursor RNA is designated SEQ ID:1508, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1508 is located at position 4851374 relative to contig NT_022517.13, on chromosome 3.

[23826] GAM1535 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23827] An enzyme complex designated DICER COMPLEX, dices the GAM1535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1535 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1535 RNA is designated SEQ ID:3184, and is provided hereinbelow with reference to the sequence listing part.

[23828] GAM1535 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1535 target RNA, herein designated GAM TARGET RNA. GAM1535 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23829] GAM1535 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1535 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1535 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1535 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1535 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23830] The complementary binding of GAM1535 RNA, herein designated GAM RNA, to target binding sites on GAM1535 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1535 target RNA, herein designated GAM TARGET RNA, into GAM1535 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23831] It is appreciated that GAM1535 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1535 target genes. The mRNA of each one of this plurality of GAM1535 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1535 RNA, herein designated GAM RNA, and which when bound by GAM1535 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1535 target proteins.

[23832] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1535 gene, herein designated GAM GENE, on one or more GAM1535 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23833] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1535 correlate with, and may be deduced from, the identity of the target genes which GAM1535 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23834] Nucleotide sequences of the GAM1535 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1535 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1535 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1535 are further described hereinbelow with reference to Table Table1.

[23835] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1535 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23836] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1536 (GAM1536) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23837] GAM1536 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1536 was detected is described hereinabove with reference to Figs. 2-8.

[23838] GAM1536 gene, herein designated GAM GENE, and GAM1536 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23839] GAM1536 gene, herein designated GAM GENE, encodes a GAM1536 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1536 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1536 precursor RNA is designated SEQ ID:1509, and is provided hereinbelow with reference to the sequence listing part.

[23840] GAM1536 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23841] An enzyme complex designated DICER COMPLEX, dices the GAM1536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1536 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1536 RNA is designated SEQ ID:3185, and is provided hereinbelow with reference to the sequence listing part.

[23842] GAM1536 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1536 target RNA, herein designated GAM TARGET RNA. GAM1536 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23843] GAM1536 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1536 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1536 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1536 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1536 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23844] The complementary binding of GAM1536 RNA, herein designated GAM RNA, to target binding sites on GAM1536 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1536 target RNA, herein designated GAM TARGET RNA, into GAM1536 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23845] It is appreciated that GAM1536 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1536 target genes. The mRNA of each one of this plurality of GAM1536 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1536 RNA, herein designated GAM RNA, and which when bound by GAM1536 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1536 target proteins.

[23846] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1536 gene, herein designated GAM GENE, on one or more GAM1536 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23847] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1536 correlate with, and may

be deduced from, the identity of the target genes which GAM1536 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23848] Nucleotide sequences of the GAM1536 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1536 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1536 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1536 are further described hereinbelow with reference to Table Table1.

[23849] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1536 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23850] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1537 (GAM1537) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23851] GAM1537 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1537 was detected is described hereinabove with reference to Figs. 2-8.

[23852] GAM1537 gene, herein designated GAM GENE, and GAM1537 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23853] GAM1537 gene, herein designated GAM GENE, encodes a GAM1537 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1537 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1537 precursor RNA is designated SEQ ID:1510, and is provided hereinbelow with reference to the sequence listing part.

[23854] GAM1537 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23855] An enzyme complex designated DICER COMPLEX, dices the GAM1537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1537 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1537 RNA is designated SEQ ID:3186, and is provided hereinbelow with reference to the sequence listing part.

[23856] GAM1537 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1537 target RNA, herein designated GAM TARGET RNA. GAM1537 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23857] GAM1537 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1537 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1537 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1537 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1537 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23858] The complementary binding of GAM1537 RNA, herein designated GAM RNA, to target binding sites on GAM1537 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1537 target RNA, herein designated GAM TARGET RNA, into GAM1537 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23859] It is appreciated that GAM1537 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1537 target genes. The mRNA of each one of this plurality of GAM1537 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1537 RNA, herein designated GAM RNA, and which when bound by GAM1537 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1537 target proteins.

[23860] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1537 gene, herein designated GAM GENE, on one or more GAM1537 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23861] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1537 correlate with, and may be deduced from, the identity of the target genes which GAM1537 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23862] Nucleotide sequences of the GAM1537 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1537 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1537 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1537 are further described hereinbelow with reference to Table Table1.

[23863] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1537 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23864] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1538 (GAM1538) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23865] GAM1538 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1538 was detected is described hereinabove with reference to Figs. 2-8.

[23866] GAM1538 gene, herein designated GAM GENE, and GAM1538 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23867] GAM1538 gene, herein designated GAM GENE, encodes a GAM1538 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1538 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1538 precursor RNA is

designated SEQ ID:1511, and is provided hereinbelow with reference to the sequence listing part.

[23868] GAM1538 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23869] An enzyme complex designated DICER COMPLEX, dices the GAM1538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1538 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1538 RNA is designated SEQ ID:3187, and is provided hereinbelow with reference to the sequence

listing part.

[23870] GAM1538 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1538 target RNA, herein designated GAM TARGET RNA. GAM1538 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23871] GAM1538 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1538 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1538 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1538 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1538 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23872] The complementary binding of GAM1538 RNA, herein designated GAM RNA, to target binding sites on GAM1538 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1538 target RNA, herein designated GAM TARGET RNA, into GAM1538 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23873] It is appreciated that GAM1538 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1538 target genes. The mRNA of each one of this plurality of GAM1538 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1538 RNA, herein designated GAM RNA, and which when bound by GAM1538 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1538 target proteins.

[23874] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1538 gene, herein designated GAM GENE, on one or more GAM1538 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23875] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1538 correlate with, and may be deduced from, the identity of the target genes which GAM1538 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23876] Nucleotide sequences of the GAM1538 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1538 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1538 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1538 are further described hereinbelow with reference to Table Table1.

[23877] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1538 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23878] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1539 (GAM1539) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23879] GAM1539 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1539 was detected is described hereinabove with reference to Figs. 2-8.

[23880] GAM1539 gene, herein designated GAM GENE, and GAM1539 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23881] GAM1539 gene, herein designated GAM GENE, encodes a GAM1539 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1539 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1539 precursor RNA is designated SEQ ID:1512, and is provided hereinbelow with reference to the sequence listing part.

[23882] GAM1539 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23883] An enzyme complex designated DICER COMPLEX, dices

the GAM1539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1539 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1539 RNA is designated SEQ ID:3188, and is provided hereinbelow with reference to the sequence listing part.

[23884] GAM1539 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1539 target RNA, herein designated GAM TARGET RNA. GAM1539 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23885] GAM1539 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1539 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1539 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1539 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1539 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23886] The complementary binding of GAM1539 RNA, herein designated GAM RNA, to target binding sites on GAM1539 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1539 target RNA, herein designated GAM TARGET RNA, into GAM1539 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23887] It is appreciated that GAM1539 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1539 target genes. The mRNA of each one of this plurality of GAM1539 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1539 RNA, herein designated GAM RNA, and which when bound by GAM1539 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1539 target proteins.

[23888] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1539 gene, herein designated GAM GENE, on one or more GAM1539 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23889] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1539 correlate with, and may be deduced from, the identity of the target genes which GAM1539 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23890] Nucleotide sequences of the GAM1539 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1539 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1539 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1539 are further described hereinbelow with reference to Table Table1.

[23891] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1539 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23892] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1540 (GAM1540) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23893] GAM1540 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1540 was detected is described hereinabove with reference to Figs. 2-8.

[23894] GAM1540 gene, herein designated GAM GENE, and GAM1540 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23895] GAM1540 gene, herein designated GAM GENE, encodes a GAM1540 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1540 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1540 precursor RNA is designated SEQ ID:1513, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1513 is located at position 3434852 rela-

tive to contig NT_009714.13, on chromosome 12.

[23896] GAM1540 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99155, which mouse homolog is detected in mouse EST accession BG288438.1.

[23897] GAM1540 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23898] An enzyme complex designated DICER COMPLEX, dices the GAM1540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1540 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1540 RNA is designated SEQ ID:3189, and is provided hereinbelow with reference to the sequence listing part.

[23899] GAM1540 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1540 target RNA, herein designated GAM TARGET RNA. GAM1540 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23900] GAM1540 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1540 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1540 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1540 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1540 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23901] The complementary binding of GAM1540 RNA, herein designated GAM RNA, to target binding sites on GAM1540 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1540 target RNA, herein designated GAM TARGET RNA, into GAM1540 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23902] It is appreciated that GAM1540 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1540 target genes. The mRNA of each one of this plurality of GAM1540 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1540 RNA, herein designated GAM RNA, and which when bound by GAM1540 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1540 target proteins.

[23903] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1540 gene, herein designated GAM GENE, on one or more GAM1540 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23904] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1540 correlate with, and may be deduced from, the identity of the target genes which GAM1540 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23905] Nucleotide sequences of the GAM1540 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1540 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1540 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1540 are further described hereinbelow with reference to Table Table1.

[23906] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1540 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23907] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1541 (GAM1541) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23908] GAM1541 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1541 was detected is described hereinabove with reference to Figs. 2-8.

[23909] GAM1541 gene, herein designated GAM GENE, and GAM1541 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23910] GAM1541 gene, herein designated GAM GENE, encodes a GAM1541 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1541 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1541 precursor RNA is designated SEQ ID:1514, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1514 is located at position 763088 relative to contig NT_022676.12, on chromosome 3.

[23911] GAM1541 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23912] An enzyme complex designated DICER COMPLEX, dices the GAM1541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1541 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1541 RNA is designated SEQ ID:3190, and is provided hereinbelow with reference to the sequence listing part.

[23913] GAM1541 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1541 target RNA, herein designated GAM TARGET RNA. GAM1541 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23914] GAM1541 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1541 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1541 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1541 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1541 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23915] The complementary binding of GAM1541 RNA, herein designated GAM RNA, to target binding sites on GAM1541 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1541 target RNA, herein designated GAM TARGET RNA, into GAM1541 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23916] It is appreciated that GAM1541 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1541 target genes. The mRNA of each one of this plurality of GAM1541 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1541 RNA, herein designated GAM RNA, and which when bound by GAM1541 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1541 target proteins.

[23917] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1541 gene, herein designated GAM GENE, on one or more GAM1541 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23918] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1541 correlate with, and may be deduced from, the identity of the target genes which GAM1541 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23919] Nucleotide sequences of the GAM1541 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1541 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1541 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1541 are further described hereinbelow with reference to Table Table1.

[23920] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1541 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23921] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1542 (GAM1542) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23922] GAM1542 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1542 was detected is described hereinabove with reference to Figs. 2-8.

[23923] GAM1542 gene, herein designated GAM GENE, and GAM1542 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23924] GAM1542 gene, herein designated GAM GENE, encodes a GAM1542 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1542 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1542 precursor RNA is designated SEQ ID:1515, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1515 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[23925] GAM1542 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23926] An enzyme complex designated DICER COMPLEX, dices the GAM1542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1542 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1542 RNA is designated SEQ ID:3191, and is provided hereinbelow with reference to the sequence listing part.

[23927] GAM1542 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1542 target RNA, herein designated GAM TARGET RNA. GAM1542 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23928] GAM1542 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1542 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1542 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1542 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1542 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23929] The complementary binding of GAM1542 RNA, herein designated GAM RNA, to target binding sites on GAM1542 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1542 target RNA, herein designated GAM TARGET RNA, into GAM1542 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23930] It is appreciated that GAM1542 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1542 target genes. The mRNA of each one of this

plurality of GAM1542 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1542 RNA, herein designated GAM RNA, and which when bound by GAM1542 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1542 target proteins.

[23931] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1542 gene, herein designated GAM GENE, on one or more GAM1542 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23932] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1542 correlate with, and may be deduced from, the identity of the target genes which GAM1542 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23933] Nucleotide sequences of the GAM1542 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1542 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1542 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1542 are further described hereinbelow with reference to Table Table1.

[23934] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1542 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23935] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1543 (GAM1543) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[23936] GAM1543 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1543 was detected is described hereinabove with reference to Figs. 2-8.

[23937] GAM1543 gene, herein designated GAM GENE, and GAM1543 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23938] GAM1543 gene, herein designated GAM GENE, encodes a GAM1543 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1543 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1543 precursor RNA is designated SEQ ID:1516, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1516 is located at position 9102844 relative to contig NT_017568.11, on chromosome 9.

[23939] GAM1543 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23940] An enzyme complex designated DICER COMPLEX, dices the GAM1543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1543 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1543 RNA is designated SEQ ID:3192, and is provided hereinbelow with reference to the sequence listing part.

[23941] GAM1543 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1543 target RNA, herein designated GAM TARGET RNA. GAM1543 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23942] GAM1543 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1543 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1543 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1543 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1543 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[23943] The complementary binding of GAM1543 RNA, herein designated GAM RNA, to target binding sites on GAM1543 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1543 target RNA, herein designated GAM TARGET RNA, into GAM1543 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23944] It is appreciated that GAM1543 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1543 target genes. The mRNA of each one of this plurality of GAM1543 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1543 RNA, herein designated GAM RNA, and which when bound by GAM1543 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1543 target proteins.

[23945] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1543 gene, herein designated GAM GENE, on one or

more GAM1543 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23946] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1543 correlate with, and may be deduced from, the identity of the target genes which GAM1543 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23947] Nucleotide sequences of the GAM1543 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1543 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1543 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1543 are further de-

scribed hereinbelow with reference to Table Table1.

[23948] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1543 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23949] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1544 (GAM1544) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23950] GAM1544 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1544 was detected is described hereinabove with reference to Figs. 2-8.

[23951] GAM1544 gene, herein designated GAM GENE, and GAM1544 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23952] GAM1544 gene, herein designated GAM GENE, encodes a GAM1544 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1544 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1544 precursor RNA is designated SEQ ID:1517, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1517 is located at position 365849 relative to contig NT_010799.11, on chromosome 17.

[23953] GAM1544 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[23954] SEQ ID:99657 detected in mouse EST Accession AA144533.1.

[23955] SEQ ID:99658 detected in mouse EST Accession AA671455.1.

[23956] SEQ ID:99659 detected in mouse EST Accession AW824753.1.

[23957] SEQ ID:99660 detected in mouse EST Accession BE943987.1.

[23958] SEQ ID:99661 detected in mouse EST Accession BE691447.1.

[23959] SEQ ID:99662 detected in mouse EST Accession BE691413.1.

[23960] SEQ ID:99663 detected in mouse EST Accession BG808025.1.

[23961] SEQ ID:99664 detected in mouse EST Accession BG808010.1.

[23962] SEQ ID:99665 detected in mouse EST Accession BG807850.1.

[23963] SEQ ID:99666 detected in mouse EST Accession BG805970.1.

[23964] SEQ ID:99667 detected in mouse EST Accession BB610842.1.

[23965] SEQ ID:99668 detected in mouse EST Accession BB609859.1.

[23966] SEQ ID:99669 detected in mouse EST Accession BG145596.1.

[23967] SEQ ID:99670 detected in mouse EST Accession BE692802.1.

[23968] SEQ ID:99671 detected in mouse EST Accession AW208601.1.

[23969] GAM1544 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1544 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23970] An enzyme complex designated DICER COMPLEX, dices the GAM1544 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1544 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1544 RNA is designated SEQ ID:3193, and is provided hereinbelow with reference to the sequence listing part.

[23971] GAM1544 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1544 target RNA, herein designated GAM TARGET RNA. GAM1544 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23972] GAM1544 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1544 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1544 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1544 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1544 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23973] The complementary binding of GAM1544 RNA, herein designated GAM RNA, to target binding sites on GAM1544 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1544 target RNA, herein designated GAM TARGET RNA, into GAM1544 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23974] It is appreciated that GAM1544 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1544 target genes. The mRNA of each one of this plurality of GAM1544 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1544 RNA, herein designated GAM RNA, and which when bound by GAM1544 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1544 target proteins.

[23975] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1544 gene, herein designated GAM GENE, on one or more GAM1544 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23976] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1544 correlate with, and may be deduced from, the identity of the target genes which GAM1544 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23977] Nucleotide sequences of the GAM1544 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1544 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1544 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1544 are further described hereinbelow with reference to Table Table1.

[23978] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1544 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23979] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1545 (GAM1545) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23980] GAM1545 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1545 was detected is described hereinabove with reference to Figs. 2-8.

[23981] GAM1545 gene, herein designated GAM GENE, and GAM1545 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23982] GAM1545 gene, herein designated GAM GENE, encodes a GAM1545 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1545 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1545 precursor RNA is designated SEQ ID:1518, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1518 is located at position 2183835 relative to contig NT_034383.2, on chromosome 1.

[23983] GAM1545 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23984] An enzyme complex designated DICER COMPLEX, dices the GAM1545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1545 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1545 RNA is designated SEQ ID:3194, and is provided hereinbelow with reference to the sequence listing part.

[23985] GAM1545 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1545 target RNA, herein designated GAM TARGET RNA. GAM1545 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[23986] GAM1545 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1545 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1545 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1545 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1545 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[23987] The complementary binding of GAM1545 RNA, herein designated GAM RNA, to target binding sites on GAM1545 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1545 target RNA, herein designated GAM TARGET RNA, into GAM1545 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[23988] It is appreciated that GAM1545 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1545 target genes. The mRNA of each one of this plurality of GAM1545 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1545 RNA, herein designated GAM RNA, and which when bound by GAM1545 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1545 target proteins.

[23989] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1545 gene, herein designated GAM GENE, on one or more GAM1545 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[23990] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1545 correlate with, and may be deduced from, the identity of the target genes which GAM1545 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[23991] Nucleotide sequences of the GAM1545 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1545 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1545 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1545 are further described hereinbelow with reference to Table Table1.

[23992] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1545 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[23993] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1546 (GAM1546) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[23994] GAM1546 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1546 was detected is described hereinabove with reference to Figs. 2-8.

[23995] GAM1546 gene, herein designated GAM GENE, and GAM1546 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[23996] GAM1546 gene, herein designated GAM GENE, encodes a GAM1546 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1546 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1546 precursor RNA is designated SEQ ID:1519, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1519 is located at position 19308883 relative to contig NT_033899.3, on chromosome 11.

[23997] GAM1546 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1546 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[23998] An enzyme complex designated DICER COMPLEX, dices the GAM1546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1546 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1546 RNA is designated SEQ ID:3195, and is provided hereinbelow with reference to the sequence listing part.

[23999] GAM1546 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1546 target RNA, herein designated GAM TARGET

RNA. GAM1546 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24000] GAM1546 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1546 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1546 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1546 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1546 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24001] The complementary binding of GAM1546 RNA, herein designated GAM RNA, to target binding sites on GAM1546 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1546 target RNA, herein designated GAM TARGET RNA, into GAM1546 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24002] It is appreciated that GAM1546 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1546 target genes. The mRNA of each one of this plurality of GAM1546 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1546 RNA, herein designated GAM RNA, and which when bound by GAM1546 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1546 target proteins.

[24003] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1546 gene, herein designated GAM GENE, on one or more GAM1546 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24004] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1546 correlate with, and may be deduced from, the identity of the target genes which GAM1546 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24005] Nucleotide sequences of the GAM1546 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1546 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1546 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1546 are further described hereinbelow with reference to Table Table1.

[24006] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1546 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24007] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1547 (GAM1547) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24008] GAM1547 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1547 was detected is described hereinabove with reference to Figs. 2-8.

[24009] GAM1547 gene, herein designated GAM GENE, and GAM1547 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24010] GAM1547 gene, herein designated GAM GENE, encodes a

GAM1547 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1547 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1547 precursor RNA is designated SEQ ID:1520, and is provided hereinbelow with reference to the sequence listing part.

[24011] GAM1547 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[24012] SEQ ID:97949 detected in mouse EST Accession BE625629.1.

[24013] SEQ ID:97950 detected in mouse EST Accession BI792530.1.

[24014] SEQ ID:97951 detected in mouse EST Accession BE380224.1.

[24015] SEQ ID:97952 detected in mouse EST Accession AA068787.1.

[24016] SEQ ID:97953 detected in mouse EST Accession AA823029.1.

[24017] SEQ ID:97954 detected in mouse EST Accession BE309708.1.

[24018] SEQ ID:97955 detected in mouse EST Accession BI100916.1.

[24019] SEQ ID:97956 detected in mouse EST Accession BG296866.1.

[24020] GAM1547 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24021] An enzyme complex designated DICER COMPLEX, dices the GAM1547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1547 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 97%) nucleotide sequence of GAM1547 RNA is designated SEQ ID:3196, and is provided hereinbelow with reference to the sequence listing part.

[24022] GAM1547 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1547 target RNA, herein designated GAM TARGET RNA. GAM1547 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24023] GAM1547 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1547 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1547 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1547 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1547 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24024] The complementary binding of GAM1547 RNA, herein designated GAM RNA, to target binding sites on GAM1547 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1547 target RNA, herein designated GAM TARGET RNA, into GAM1547 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24025] It is appreciated that GAM1547 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1547 target genes. The mRNA of each one of this plurality of GAM1547 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1547 RNA, herein designated GAM RNA, and which when bound by GAM1547 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1547 target proteins.

[24026] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1547 gene, herein designated GAM GENE, on one or more GAM1547 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24027] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1547 correlate with, and may be deduced from, the identity of the target genes which GAM1547 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24028] Nucleotide sequences of the GAM1547 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1547 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1547 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1547 are further described hereinbelow with reference to Table Table1.

[24029] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1547 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24030] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1548 (GAM1548) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24031] GAM1548 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1548 was detected is described hereinabove with reference to Figs. 2-8.

[24032] GAM1548 gene, herein designated GAM GENE, and GAM1548 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24033] GAM1548 gene, herein designated GAM GENE, encodes a GAM1548 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1548 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1548 precursor RNA is designated SEQ ID:1521, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1521 is located at position 11259458 relative to contig NT_007592.11, on chromosome 6.

[24034] GAM1548 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24035] An enzyme complex designated DICER COMPLEX, dices the GAM1548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1548 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1548 RNA is designated SEQ ID:3197, and is provided hereinbelow with reference to the sequence listing part.

[24036] GAM1548 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1548 target RNA, herein designated GAM TARGET RNA. GAM1548 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24037] GAM1548 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1548 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1548 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1548 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1548 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24038] The complementary binding of GAM1548 RNA, herein designated GAM RNA, to target binding sites on GAM1548 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1548 target RNA, herein designated GAM TARGET RNA, into GAM1548 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24039] It is appreciated that GAM1548 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1548 target genes. The mRNA of each one of this plurality of GAM1548 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1548 RNA, herein designated GAM RNA, and which when bound by GAM1548 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1548 target proteins.

[24040] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1548 gene, herein designated GAM GENE, on one or more GAM1548 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24041] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1548 correlate with, and may be deduced from, the identity of the target genes which GAM1548 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24042] Nucleotide sequences of the GAM1548 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1548 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1548 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1548 are further described hereinbelow with reference to Table Table1.

[24043] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1548 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24044] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1549 (GAM1549) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24045] GAM1549 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1549 was detected is described hereinabove with reference to Figs. 2-8.

[24046] GAM1549 gene, herein designated GAM GENE, and GAM1549 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24047] GAM1549 gene, herein designated GAM GENE, encodes a GAM1549 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1549 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1549 precursor RNA is designated SEQ ID:1522, and is provided hereinbelow with reference to the sequence listing part.

[24048] GAM1549 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24049] An enzyme complex designated DICER COMPLEX, dices the GAM1549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1549 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1549 RNA is designated SEQ ID:3198, and is provided hereinbelow with reference to the sequence listing part.

[24050] GAM1549 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1549 target RNA, herein designated GAM TARGET RNA. GAM1549 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24051] GAM1549 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1549 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1549 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1549 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1549 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24052] The complementary binding of GAM1549 RNA, herein designated GAM RNA, to target binding sites on GAM1549 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1549 target RNA, herein designated GAM TARGET RNA, into GAM1549 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24053] It is appreciated that GAM1549 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1549 target genes. The mRNA of each one of this plurality of GAM1549 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1549 RNA, herein designated GAM RNA, and which when bound by GAM1549 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1549 target proteins.

[24054] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1549 gene, herein designated GAM GENE, on one or more GAM1549 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24055] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1549 correlate with, and may

be deduced from, the identity of the target genes which GAM1549 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24056] Nucleotide sequences of the GAM1549 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1549 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1549 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1549 are further described hereinbelow with reference to Table Table1.

[24057] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1549 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24058] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1550 (GAM1550) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24059] GAM1550 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1550 was detected is described hereinabove with reference to Figs. 2-8.

[24060] GAM1550 gene, herein designated GAM GENE, and GAM1550 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24061] GAM1550 gene, herein designated GAM GENE, encodes a GAM1550 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1550 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1550 precursor RNA is designated SEQ ID:1523, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1523 is located at position 6160001 relative to contig NT_011176.13, on chromosome 19.

[24062] GAM1550 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24063] An enzyme complex designated DICER COMPLEX, dices the GAM1550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1550 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1550 RNA is designated SEQ ID:3199, and is provided hereinbelow with reference to the sequence listing part.

[24064] GAM1550 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1550 target RNA, herein designated GAM TARGET RNA. GAM1550 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[24065] GAM1550 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1550 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1550 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1550 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1550 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24066] The complementary binding of GAM1550 RNA, herein

designated GAM RNA, to target binding sites on GAM1550 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1550 target RNA, herein designated GAM TARGET RNA, into GAM1550 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24067] It is appreciated that GAM1550 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1550 target genes. The mRNA of each one of this plurality of GAM1550 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1550 RNA, herein designated GAM RNA, and which when bound by GAM1550 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1550 target proteins.

[24068] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1550 gene, herein designated GAM GENE, on one or more GAM1550 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24069] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1550 correlate with, and may be deduced from, the identity of the target genes which GAM1550 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24070] Nucleotide sequences of the GAM1550 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1550 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1550 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1550 are further described hereinbelow with reference to Table Table1.

[24071] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1550 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24072] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1551 (GAM1551) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24073] GAM1551 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1551 was detected is described hereinabove with reference to Figs. 2-8.

[24074] GAM1551 gene, herein designated GAM GENE, and GAM1551 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24075] GAM1551 gene, herein designated GAM GENE, encodes a GAM1551 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1551 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1551 precursor RNA is designated SEQ ID:1524, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1524 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[24076] GAM1551 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24077] An enzyme complex designated DICER COMPLEX, dices the GAM1551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1551 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1551 RNA is designated SEQ ID:3200, and is provided hereinbelow with reference to the sequence listing part.

[24078] GAM1551 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1551 target RNA, herein designated GAM TARGET RNA. GAM1551 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24079] GAM1551 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1551 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1551 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1551 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1551 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24080] The complementary binding of GAM1551 RNA, herein designated GAM RNA, to target binding sites on GAM1551 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1551 target RNA, herein designated GAM TARGET RNA, into GAM1551 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24081] It is appreciated that GAM1551 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1551 target genes. The mRNA of each one of this plurality of GAM1551 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1551 RNA, herein designated GAM RNA, and which when bound by GAM1551 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1551 target proteins.

[24082] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1551 gene, herein designated GAM GENE, on one or more GAM1551 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24083] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1551 correlate with, and may be deduced from, the identity of the target genes which GAM1551 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24084] Nucleotide sequences of the GAM1551 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1551 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1551 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1551 are further described hereinbelow with reference to Table Table1.

[24085] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1551 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24086] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1552 (GAM1552) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24087] GAM1552 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1552 was detected is described hereinabove with reference to Figs. 2-8.

[24088] GAM1552 gene, herein designated GAM GENE, and GAM1552 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24089] GAM1552 gene, herein designated GAM GENE, encodes a GAM1552 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1552 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1552 precursor RNA is designated SEQ ID:1525, and is provided hereinbelow with reference to the sequence listing part.

[24090] GAM1552 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24091] An enzyme complex designated DICER COMPLEX, dices the GAM1552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1552 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1552 RNA is designated SEQ ID:3201, and is provided hereinbelow with reference to the sequence listing part.

[24092] GAM1552 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1552 target RNA, herein designated GAM TARGET RNA. GAM1552 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24093] GAM1552 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1552 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1552 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1552 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1552 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24094] The complementary binding of GAM1552 RNA, herein designated GAM RNA, to target binding sites on GAM1552

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1552 target RNA, herein designated GAM TARGET RNA, into GAM1552 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24095] It is appreciated that GAM1552 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1552 target genes. The mRNA of each one of this plurality of GAM1552 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1552 RNA, herein designated GAM RNA, and which when bound by GAM1552 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1552 target proteins.

[24096] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1552 gene, herein designated GAM GENE, on one or more GAM1552 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24097] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1552 correlate with, and may be deduced from, the identity of the target genes which GAM1552 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24098] Nucleotide sequences of the GAM1552 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1552 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1552 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1552 are further described hereinbelow with reference to Table Table1.

[24099] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1552 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24100] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1553 (GAM1553) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24101] GAM1553 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1553 was detected is described hereinabove with reference to Figs. 2-8.

[24102] GAM1553 gene, herein designated GAM GENE, and GAM1553 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24103] GAM1553 gene, herein designated GAM GENE, encodes a GAM1553 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1553 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1553 precursor RNA is designated SEQ ID:1526, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1526 is located at position 4851355 relative to contig NT_022517.13, on chromosome 3.

[24104] GAM1553 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24105] An enzyme complex designated DICER COMPLEX, dices the GAM1553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1553 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1553 RNA is designated SEQ ID:3202, and is provided hereinbelow with reference to the sequence listing part.

[24106] GAM1553 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1553 target RNA, herein designated GAM TARGET RNA. GAM1553 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24107] GAM1553 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1553 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1553 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1553 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1553 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24108] The complementary binding of GAM1553 RNA, herein designated GAM RNA, to target binding sites on GAM1553 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1553 target RNA, herein designated GAM TARGET RNA, into GAM1553 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24109] It is appreciated that GAM1553 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1553 target genes. The mRNA of each one of this plurality of GAM1553 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1553 RNA, herein designated GAM RNA, and which when bound by GAM1553 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1553 target proteins.

[24110] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1553 gene, herein designated GAM GENE, on one or more GAM1553 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24111] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1553 correlate with, and may

be deduced from, the identity of the target genes which GAM1553 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24112] Nucleotide sequences of the GAM1553 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1553 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1553 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1553 are further described hereinbelow with reference to Table Table1.

[24113] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1553 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24114] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1554 (GAM1554) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24115] GAM1554 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1554 was detected is described hereinabove with reference to Figs. 2-8.

[24116] GAM1554 gene, herein designated GAM GENE, and GAM1554 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24117] GAM1554 gene, herein designated GAM GENE, encodes a GAM1554 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1554 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1554 precursor RNA is designated SEQ ID:1527, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1527 is located at position 755874 relative to contig NT_005416.8, on chromosome 2.

[24118] GAM1554 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24119] An enzyme complex designated DICER COMPLEX, dices the GAM1554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1554 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1554 RNA is designated SEQ ID:3203, and is provided hereinbelow with reference to the sequence listing part.

[24120] GAM1554 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1554 target RNA, herein designated GAM TARGET RNA. GAM1554 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[24121] GAM1554 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1554 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1554 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1554 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1554 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24122] The complementary binding of GAM1554 RNA, herein

designated GAM RNA, to target binding sites on GAM1554 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1554 target RNA, herein designated GAM TARGET RNA, into GAM1554 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24123] It is appreciated that GAM1554 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1554 target genes. The mRNA of each one of this plurality of GAM1554 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1554 RNA, herein designated GAM RNA, and which when bound by GAM1554 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1554 target proteins.

[24124] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1554 gene, herein designated GAM GENE, on one or more GAM1554 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24125] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1554 correlate with, and may be deduced from, the identity of the target genes which GAM1554 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24126] Nucleotide sequences of the GAM1554 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1554 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1554 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1554 are further described hereinbelow with reference to Table Table1.

[24127] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1554 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24128] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1555 (GAM1555) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24129] GAM1555 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1555 was detected is described hereinabove with reference to Figs. 2-8.

[24130] GAM1555 gene, herein designated GAM GENE, and GAM1555 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24131] GAM1555 gene, herein designated GAM GENE, encodes a GAM1555 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1555 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1555 precursor RNA is designated SEQ ID:1528, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1528 is located at position 4256965 relative to contig NT_008046.11, on chromosome 8.

[24132] GAM1555 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98144, which mouse homolog is detected in mouse EST accession AW476224.1.

[24133] GAM1555 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24134] An enzyme complex designated DICER COMPLEX, dices the GAM1555 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1555 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1555 RNA is designated SEQ ID:3204, and is provided hereinbelow with reference to the sequence listing part.

[24135] GAM1555 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1555 target RNA, herein designated GAM TARGET RNA. GAM1555 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24136] GAM1555 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1555 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1555

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1555 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1555 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24137] The complementary binding of GAM1555 RNA, herein designated GAM RNA, to target binding sites on GAM1555 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1555 target RNA, herein designated GAM TARGET RNA, into GAM1555 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[24138] It is appreciated that GAM1555 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1555 target genes. The mRNA of each one of this plurality of GAM1555 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1555 RNA, herein designated GAM RNA, and which when bound by GAM1555 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1555 target proteins.

[24139] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1555 gene, herein designated GAM GENE, on one or more GAM1555 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24140] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1555 correlate with, and may be deduced from, the identity of the target genes which GAM1555 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24141] Nucleotide sequences of the GAM1555 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1555 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1555 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1555 are further described hereinbelow with reference to Table Table1.

[24142] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1555 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24143] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1556 (GAM1556) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24144] GAM1556 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1556 was detected is described hereinabove with reference to Figs. 2-8.

[24145] GAM1556 gene, herein designated GAM GENE, and GAM1556 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24146] GAM1556 gene, herein designated GAM GENE, encodes a GAM1556 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1556 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1556 precursor RNA is designated SEQ ID:1529, and is provided hereinbelow with reference to the sequence listing part.

[24147] GAM1556 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1556 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24148] An enzyme complex designated DICER COMPLEX, dices the GAM1556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1556 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1556 RNA is designated SEQ ID:3205, and is provided hereinbelow with reference to the sequence listing part.

[24149] GAM1556 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1556 target RNA, herein designated GAM TARGET

RNA. GAM1556 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24150] GAM1556 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1556 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1556 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1556 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1556 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24151] The complementary binding of GAM1556 RNA, herein designated GAM RNA, to target binding sites on GAM1556 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1556 target RNA, herein designated GAM TARGET RNA, into GAM1556 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24152] It is appreciated that GAM1556 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1556 target genes. The mRNA of each one of this plurality of GAM1556 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1556 RNA, herein designated GAM RNA, and which when bound by GAM1556 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1556 target proteins.

[24153] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1556 gene, herein designated GAM GENE, on one or more GAM1556 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24154] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1556 correlate with, and may be deduced from, the identity of the target genes which GAM1556 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24155] Nucleotide sequences of the GAM1556 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1556 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1556 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1556 are further described hereinbelow with reference to Table Table1.

[24156] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1556 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24157] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1557 (GAM1557) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24158] GAM1557 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1557 was detected is described hereinabove with reference to Figs. 2-8.

[24159] GAM1557 gene, herein designated GAM GENE, and GAM1557 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24160] GAM1557 gene, herein designated GAM GENE, encodes a

GAM1557 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1557 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1557 precursor RNA is designated SEQ ID:1530, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1530 is located at position 6961159 relative to contig NT_011196.11, on chromosome 19.

[24161] GAM1557 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24162] An enzyme complex designated DICER COMPLEX, dices the GAM1557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1557 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1557 RNA is designated SEQ ID:3206, and is provided hereinbelow with reference to the sequence listing part.

[24163] GAM1557 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1557 target RNA, herein designated GAM TARGET RNA. GAM1557 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24164] GAM1557 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1557 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1557 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1557 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1557 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24165] The complementary binding of GAM1557 RNA, herein designated GAM RNA, to target binding sites on GAM1557 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1557 target RNA, herein designated GAM TARGET RNA, into GAM1557 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24166] It is appreciated that GAM1557 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1557 target genes. The mRNA of each one of this plurality of GAM1557 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1557 RNA, herein designated GAM RNA, and which when bound by GAM1557 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1557 target proteins.

[24167] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1557 gene, herein designated GAM GENE, on one or more GAM1557 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24168] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1557 correlate with, and may be deduced from, the identity of the target genes which GAM1557 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24169] Nucleotide sequences of the GAM1557 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1557 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1557 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1557 are further described hereinbelow with reference to Table Table1.

[24170] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1557 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24171] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1558 (GAM1558) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24172] GAM1558 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1558 was detected is described hereinabove with reference to Figs. 2-8.

[24173] GAM1558 gene, herein designated GAM GENE, and GAM1558 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24174] GAM1558 gene, herein designated GAM GENE, encodes a GAM1558 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1558 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1558 precursor RNA is designated SEQ ID:1531, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1531 is located at position 2948497 relative to contig NT_034383.2, on chromosome 1.

[24175] GAM1558 has 8 highly conserved, expressed mouse ho-

mologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[24176] SEQ ID:98859 detected in mouse EST Accession AA017943.1.

[24177] SEQ ID:98860 detected in mouse EST Accession AA122754.1.

[24178] SEQ ID:98863 detected in mouse EST Accession AA684283.1.

[24179] SEQ ID:98864 detected in mouse EST Accession AA168500.1.

[24180] SEQ ID:98865 detected in mouse EST Accession AI316374.1.

[24181] SEQ ID:98866 detected in mouse EST Accession BG242574.1.

[24182] SEQ ID:98867 detected in mouse EST Accession AW413196.1.

[24183] SEQ ID:98872 detected in mouse EST Accession BI148579.1.

[24184] GAM1558 precursor RNA, herein designated GAM PRE-CURSOR RNA, folds onto itself, forming GAM1558 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24185] An enzyme complex designated DICER COMPLEX, dices the GAM1558 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1558 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1558 RNA is designated SEQ ID:3207, and is provided hereinbelow with reference to the sequence listing part.

[24186] GAM1558 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1558 target RNA, herein designated GAM TARGET RNA. GAM1558 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24187] GAM1558 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1558 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1558 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1558 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1558 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24188] The complementary binding of GAM1558 RNA, herein designated GAM RNA, to target binding sites on GAM1558 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1558 target RNA, herein designated GAM TARGET RNA, into GAM1558 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24189] It is appreciated that GAM1558 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1558 target genes. The mRNA of each one of this plurality of GAM1558 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1558 RNA, herein designated GAM RNA, and which when bound by GAM1558 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1558 target proteins.

[24190] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1558 gene, herein designated GAM GENE, on one or more GAM1558 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24191] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1558 correlate with, and may be deduced from, the identity of the target genes which GAM1558 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24192] Nucleotide sequences of the GAM1558 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1558 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1558 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1558 are further described hereinbelow with reference to Table Table1.

[24193] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1558 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24194] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1559 (GAM1559) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24195] GAM1559 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1559 was detected is described hereinabove with reference to Figs. 2-8.

[24196] GAM1559 gene, herein designated GAM GENE, and GAM1559 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24197] GAM1559 gene, herein designated GAM GENE, encodes a GAM1559 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1559 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1559 precursor RNA is designated SEQ ID:1532, and is provided hereinbelow with reference to the sequence listing part.

[24198] GAM1559 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24199] An enzyme complex designated DICER COMPLEX, dices the GAM1559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1559 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1559 RNA is designated SEQ ID:3208, and is provided hereinbelow with reference to the sequence listing part.

[24200] GAM1559 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1559 target RNA, herein designated GAM TARGET RNA. GAM1559 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24201] GAM1559 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1559 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1559 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1559 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1559 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24202] The complementary binding of GAM1559 RNA, herein designated GAM RNA, to target binding sites on GAM1559 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1559 target RNA, herein designated GAM TARGET RNA, into GAM1559 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24203] It is appreciated that GAM1559 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1559 target genes. The mRNA of each one of this

plurality of GAM1559 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1559 RNA, herein designated GAM RNA, and which when bound by GAM1559 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1559 target proteins.

[24204] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1559 gene, herein designated GAM GENE, on one or more GAM1559 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24205] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1559 correlate with, and may be deduced from, the identity of the target genes which GAM1559 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24206] Nucleotide sequences of the GAM1559 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1559 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1559 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1559 are further described hereinbelow with reference to Table Table1.

[24207] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1559 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24208] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1560 (GAM1560) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[24209] GAM1560 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1560 was detected is described hereinabove with reference to Figs. 2-8.

[24210] GAM1560 gene, herein designated GAM GENE, and GAM1560 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24211] GAM1560 gene, herein designated GAM GENE, encodes a GAM1560 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1560 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1560 precursor RNA is designated SEQ ID:1533, and is provided hereinbelow with reference to the sequence listing part.

[24212] GAM1560 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24213] An enzyme complex designated DICER COMPLEX, dices the GAM1560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1560 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1560 RNA is designated SEQ ID:3209, and is provided hereinbelow with reference to the sequence listing part.

[24214] GAM1560 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1560 target RNA, herein designated GAM TARGET RNA. GAM1560 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[24215] GAM1560 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1560 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1560 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1560 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1560 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24216] The complementary binding of GAM1560 RNA, herein

designated GAM RNA, to target binding sites on GAM1560 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1560 target RNA, herein designated GAM TARGET RNA, into GAM1560 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24217] It is appreciated that GAM1560 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1560 target genes. The mRNA of each one of this plurality of GAM1560 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1560 RNA, herein designated GAM RNA, and which when bound by GAM1560 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1560 target proteins.

[24218] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1560 gene, herein designated GAM GENE, on one or more GAM1560 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24219] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1560 correlate with, and may be deduced from, the identity of the target genes which GAM1560 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24220] Nucleotide sequences of the GAM1560 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1560 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1560 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1560 are further described hereinbelow with reference to Table Table1.

[24221] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1560 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24222] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1561 (GAM1561) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24223] GAM1561 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1561 was detected is described hereinabove with reference to Figs. 2-8.

[24224] GAM1561 gene, herein designated GAM GENE, and GAM1561 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24225] GAM1561 gene, herein designated GAM GENE, encodes a GAM1561 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1561 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1561 precursor RNA is designated SEQ ID:1534, and is provided hereinbelow with reference to the sequence listing part.

[24226] GAM1561 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24227] An enzyme complex designated DICER COMPLEX, dices the GAM1561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1561 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1561 RNA is designated SEQ ID:3210, and is provided hereinbelow with reference to the sequence listing part.

[24228] GAM1561 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1561 target RNA, herein designated GAM TARGET RNA. GAM1561 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24229] GAM1561 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1561 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1561 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1561 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1561 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24230] The complementary binding of GAM1561 RNA, herein designated GAM RNA, to target binding sites on GAM1561 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1561 target RNA, herein designated GAM TARGET RNA, into GAM1561 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24231] It is appreciated that GAM1561 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1561 target genes. The mRNA of each one of this plurality of GAM1561 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1561 RNA,

herein designated GAM RNA, and which when bound by GAM1561 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1561 target proteins.

[24232] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1561 gene, herein designated GAM GENE, on one or more GAM1561 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24233] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1561 correlate with, and may be deduced from, the identity of the target genes which

GAM1561 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24234] Nucleotide sequences of the GAM1561 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1561 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1561 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1561 are further described hereinbelow with reference to Table Table1.

[24235] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1561 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24236] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1562 (GAM1562) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24237] GAM1562 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1562 was detected is described hereinabove with reference to Figs. 2-8.

[24238] GAM1562 gene, herein designated GAM GENE, and GAM1562 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24239] GAM1562 gene, herein designated GAM GENE, encodes a GAM1562 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1562 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1562 precursor RNA is designated SEQ ID:1535, and is provided hereinbelow with reference to the sequence listing part.

[24240] GAM1562 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1562 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[24241] An enzyme complex designated DICER COMPLEX, dices the GAM1562 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1562 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1562 RNA is designated SEQ ID:3211, and is provided hereinbelow with reference to the sequence listing part.

[24242] GAM1562 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1562 target RNA, herein designated GAM TARGET RNA. GAM1562 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24243] GAM1562 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1562 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1562 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1562 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1562 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24244] The complementary binding of GAM1562 RNA, herein designated GAM RNA, to target binding sites on GAM1562 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1562 target RNA, herein designated GAM TARGET RNA, into GAM1562 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24245] It is appreciated that GAM1562 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1562 target genes. The mRNA of each one of this plurality of GAM1562 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1562 RNA, herein designated GAM RNA, and which when bound by GAM1562 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1562 target proteins.

[24246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1562 gene, herein designated GAM GENE, on one or more GAM1562 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24247] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1562 correlate with, and may be deduced from, the identity of the target genes which GAM1562 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24248] Nucleotide sequences of the GAM1562 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1562 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1562 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1562 are further described hereinbelow with reference to Table Table1.

[24249] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1562 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24250] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1563 (GAM1563) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24251] GAM1563 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1563 was detected is described hereinabove with reference to Figs. 2-8.

[24252] GAM1563 gene, herein designated GAM GENE, and GAM1563 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24253] GAM1563 gene, herein designated GAM GENE, encodes a GAM1563 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1563 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1563 precursor RNA is designated SEQ ID:1536, and is provided hereinbelow with

reference to the sequence listing part. Nucleotide sequence SEQ ID:1536 is located at position 5764679 relative to contig NT_008984.13, on chromosome 11.

[24254] GAM1563 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24255] An enzyme complex designated DICER COMPLEX, dices the GAM1563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1563 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1563 RNA is designated SEQ ID:3212, and

is provided hereinbelow with reference to the sequence listing part.

[24256] GAM1563 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1563 target RNA, herein designated GAM TARGET RNA. GAM1563 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24257] GAM1563 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1563 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1563 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1563 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1563 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24258] The complementary binding of GAM1563 RNA, herein designated GAM RNA, to target binding sites on GAM1563 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1563 target RNA, herein designated GAM TARGET RNA, into GAM1563 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24259] It is appreciated that GAM1563 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1563 target genes. The mRNA of each one of this plurality of GAM1563 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1563 RNA, herein designated GAM RNA, and which when bound by

GAM1563 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1563 target proteins.

[24260] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1563 gene, herein designated GAM GENE, on one or more GAM1563 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24261] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1563 correlate with, and may be deduced from, the identity of the target genes which GAM1563 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[24262] Nucleotide sequences of the GAM1563 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1563 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1563 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1563 are further described hereinbelow with reference to Table Table1.

[24263] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1563 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24264] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1564 (GAM1564) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24265] GAM1564 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1564 was detected is described hereinabove

with reference to Figs. 2-8.

[24266] GAM1564 gene, herein designated GAM GENE, and GAM1564 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24267] GAM1564 gene, herein designated GAM GENE, encodes a GAM1564 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1564 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1564 precursor RNA is designated SEQ ID:1537, and is provided hereinbelow with reference to the sequence listing part.

[24268] GAM1564 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24269] An enzyme complex designated DICER COMPLEX, dices the GAM1564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1564 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1564 RNA is designated SEQ ID:3213, and is provided hereinbelow with reference to the sequence listing part.

[24270] GAM1564 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1564 target RNA, herein designated GAM TARGET RNA. GAM1564 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24271] GAM1564 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1564 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1564 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1564 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1564 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24272] The complementary binding of GAM1564 RNA, herein designated GAM RNA, to target binding sites on GAM1564 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1564 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1564 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24273] It is appreciated that GAM1564 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1564 target genes. The mRNA of each one of this plurality of GAM1564 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1564 RNA, herein designated GAM RNA, and which when bound by GAM1564 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1564 target proteins.

[24274] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1564 gene, herein designated GAM GENE, on one or more GAM1564 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24275] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1564 correlate with, and may be deduced from, the identity of the target genes which GAM1564 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24276] Nucleotide sequences of the GAM1564 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1564 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1564 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1564 are further described hereinbelow with reference to Table Table1.

[24277] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1564 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[24278] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1565 (GAM1565) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24279] GAM1565 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1565 was detected is described hereinabove with reference to Figs. 2-8.

[24280] GAM1565 gene, herein designated GAM GENE, and GAM1565 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24281] GAM1565 gene, herein designated GAM GENE, encodes a GAM1565 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1565 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1565 precursor RNA is designated SEQ ID:1538, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1538 is located at position 365837 relative to contig NT_010799.11, on chromosome 17.

[24282] GAM1565 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24283] An enzyme complex designated DICER COMPLEX, dices the GAM1565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1565 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1565 RNA is designated SEQ ID:3214, and is provided hereinbelow with reference to the sequence

listing part.

[24284] GAM1565 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1565 target RNA, herein designated GAM TARGET RNA. GAM1565 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24285] GAM1565 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1565 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1565 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1565 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1565 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24286] The complementary binding of GAM1565 RNA, herein designated GAM RNA, to target binding sites on GAM1565 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1565 target RNA, herein designated GAM TARGET RNA, into GAM1565 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24287] It is appreciated that GAM1565 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1565 target genes. The mRNA of each one of this plurality of GAM1565 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1565 RNA, herein designated GAM RNA, and which when bound by GAM1565 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1565 target proteins.

[24288] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1565 gene, herein designated GAM GENE, on one or more GAM1565 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24289] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1565 correlate with, and may be deduced from, the identity of the target genes which GAM1565 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24290] Nucleotide sequences of the GAM1565 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1565 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1565 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1565 are further described hereinbelow with reference to Table Table1.

[24291] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1565 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24292] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1566 (GAM1566) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24293] GAM1566 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1566 was detected is described hereinabove with reference to Figs. 2-8.

[24294] GAM1566 gene, herein designated GAM GENE, and GAM1566 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24295] GAM1566 gene, herein designated GAM GENE, encodes a GAM1566 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1566 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1566 precursor RNA is designated SEQ ID:1539, and is provided hereinbelow with reference to the sequence listing part.

[24296] GAM1566 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24297] An enzyme complex designated DICER COMPLEX, dices

the GAM1566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1566 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1566 RNA is designated SEQ ID:3215, and is provided hereinbelow with reference to the sequence listing part.

[24298] GAM1566 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1566 target RNA, herein designated GAM TARGET RNA. GAM1566 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24299] GAM1566 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1566 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1566 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1566 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1566 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24300] The complementary binding of GAM1566 RNA, herein designated GAM RNA, to target binding sites on GAM1566 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1566 target RNA, herein designated GAM TARGET RNA, into GAM1566 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24301] It is appreciated that GAM1566 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1566 target genes. The mRNA of each one of this plurality of GAM1566 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1566 RNA, herein designated GAM RNA, and which when bound by GAM1566 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1566 target proteins.

[24302] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1566 gene, herein designated GAM GENE, on one or more GAM1566 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24303] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1566 correlate with, and may be deduced from, the identity of the target genes which GAM1566 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24304] Nucleotide sequences of the GAM1566 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1566 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1566 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1566 are further described hereinbelow with reference to Table Table1.

[24305] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1566 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24306] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1567 (GAM1567) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24307] GAM1567 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1567 was detected is described hereinabove with reference to Figs. 2-8.

[24308] GAM1567 gene, herein designated GAM GENE, and GAM1567 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24309] GAM1567 gene, herein designated GAM GENE, encodes a GAM1567 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1567 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1567 precursor RNA is designated SEQ ID:1540, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1540 is located at position 365849 relative

to contig NT_010799.11, on chromosome 17.

[24310] GAM1567 has 15 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[24311] SEQ ID:99052 detected in mouse EST Accession AA671455.1.

[24312] SEQ ID:99053 detected in mouse EST Accession AW824753.1.

[24313] SEQ ID:99054 detected in mouse EST Accession AW208601.1.

[24314] SEQ ID:99055 detected in mouse EST Accession BB609859.1.

[24315] SEQ ID:99056 detected in mouse EST Accession AA144533.1.

[24316] SEQ ID:99057 detected in mouse EST Accession BE943987.1.

[24317] SEQ ID:99058 detected in mouse EST Accession BE691413.1.

[24318] SEQ ID:99059 detected in mouse EST Accession BE691447.1.

[24319] SEQ ID:99060 detected in mouse EST Accession

BG808025.1.

[24320] SEQ ID:99061 detected in mouse EST Accession BG808010.1.

[24321] SEQ ID:99062 detected in mouse EST Accession BG807850.1.

[24322] SEQ ID:99063 detected in mouse EST Accession BG805970.1.

[24323] SEQ ID:99064 detected in mouse EST Accession BG145596.1.

[24324] SEQ ID:99065 detected in mouse EST Accession BE692802.1.

[24325] SEQ ID:99066 detected in mouse EST Accession BB610842.1.

[24326] GAM1567 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24327] An enzyme complex designated DICER COMPLEX, dices the GAM1567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1567 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1567 RNA is designated SEQ ID:3216, and is provided hereinbelow with reference to the sequence listing part.

[24328] GAM1567 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1567 target RNA, herein designated GAM TARGET RNA. GAM1567 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24329] GAM1567 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1567 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1567 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1567 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1567 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24330] The complementary binding of GAM1567 RNA, herein designated GAM RNA, to target binding sites on GAM1567 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1567 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1567 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24331] It is appreciated that GAM1567 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1567 target genes. The mRNA of each one of this plurality of GAM1567 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1567 RNA, herein designated GAM RNA, and which when bound by GAM1567 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1567 target proteins.

[24332] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1567 gene, herein designated GAM GENE, on one or more GAM1567 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24333] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1567 correlate with, and may be deduced from, the identity of the target genes which GAM1567 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24334] Nucleotide sequences of the GAM1567 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1567 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1567 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1567 are further described hereinbelow with reference to Table Table1.

[24335] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1567 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[24336] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1568 (GAM1568) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24337] GAM1568 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1568 was detected is described hereinabove with reference to Figs. 2-8.

[24338] GAM1568 gene, herein designated GAM GENE, and GAM1568 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24339] GAM1568 gene, herein designated GAM GENE, encodes a GAM1568 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1568 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1568 precursor RNA is designated SEQ ID:1541, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1541 is located at position 4851356 relative to contig NT_022517.13, on chromosome 3.

[24340] GAM1568 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24341] An enzyme complex designated DICER COMPLEX, dices the GAM1568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1568 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1568 RNA is designated SEQ ID:3217, and is provided hereinbelow with reference to the sequence

listing part.

[24342] GAM1568 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1568 target RNA, herein designated GAM TARGET RNA. GAM1568 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24343] GAM1568 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1568 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1568 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1568 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1568 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24344] The complementary binding of GAM1568 RNA, herein designated GAM RNA, to target binding sites on GAM1568 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1568 target RNA, herein designated GAM TARGET RNA, into GAM1568 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24345] It is appreciated that GAM1568 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1568 target genes. The mRNA of each one of this plurality of GAM1568 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1568 RNA, herein designated GAM RNA, and which when bound by GAM1568 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1568 target proteins.

[24346] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1568 gene, herein designated GAM GENE, on one or more GAM1568 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24347] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1568 correlate with, and may be deduced from, the identity of the target genes which GAM1568 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24348] Nucleotide sequences of the GAM1568 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1568 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1568 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1568 are further described hereinbelow with reference to Table Table1.

[24349] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1568 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24350] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1569 (GAM1569) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24351] GAM1569 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1569 was detected is described hereinabove with reference to Figs. 2-8.

[24352] GAM1569 gene, herein designated GAM GENE, and GAM1569 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24353] GAM1569 gene, herein designated GAM GENE, encodes a GAM1569 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1569 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1569 precursor RNA is designated SEQ ID:1542, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1542 is located at position 4851366 relative to contig NT_022517.13, on chromosome 3.

[24354] GAM1569 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[24355] An enzyme complex designated DICER COMPLEX, dices the GAM1569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1569 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1569 RNA is designated SEQ ID:3218, and is provided hereinbelow with reference to the sequence listing part.

[24356] GAM1569 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1569 target RNA, herein designated GAM TARGET RNA. GAM1569 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24357] GAM1569 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1569 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1569 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1569 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1569 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24358] The complementary binding of GAM1569 RNA, herein designated GAM RNA, to target binding sites on GAM1569 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1569 target RNA, herein designated GAM TARGET RNA, into GAM1569 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24359] It is appreciated that GAM1569 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1569 target genes. The mRNA of each one of this plurality of GAM1569 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1569 RNA, herein designated GAM RNA, and which when bound by GAM1569 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1569 target proteins.

[24360] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1569 gene, herein designated GAM GENE, on one or more GAM1569 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24361] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1569 correlate with, and may be deduced from, the identity of the target genes which GAM1569 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24362] Nucleotide sequences of the GAM1569 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1569 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1569 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1569 are further described hereinbelow with reference to Table Table1.

[24363] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1569 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24364] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1570 (GAM1570) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24365] GAM1570 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1570 was detected is described hereinabove with reference to Figs. 2-8.

[24366] GAM1570 gene, herein designated GAM GENE, and GAM1570 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24367] GAM1570 gene, herein designated GAM GENE, encodes a GAM1570 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1570 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1570 precursor RNA is designated SEQ ID:1543, and is provided hereinbelow with

reference to the sequence listing part.

[24368] GAM1570 has 4 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[24369] SEQ ID:100075 detected in mouse EST Accession BG242453.1.

[24370] SEQ ID:100146 detected in mouse EST Accession BE862202.1.

[24371] SEQ ID:100147 detected in mouse EST Accession AW229351.1.

[24372] SEQ ID:100148 detected in mouse EST Accession BI413638.1.

[24373] GAM1570 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of

the second half thereof.

[24374] An enzyme complex designated DICER COMPLEX, dices the GAM1570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1570 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1570 RNA is designated SEQ ID:3219, and is provided hereinbelow with reference to the sequence listing part.

[24375] GAM1570 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1570 target RNA, herein designated GAM TARGET RNA. GAM1570 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24376] GAM1570 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in

untranslated regions of GAM1570 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1570 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1570 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1570 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24377] The complementary binding of GAM1570 RNA, herein designated GAM RNA, to target binding sites on GAM1570 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, in-

hibits translation of GAM1570 target RNA, herein designated GAM TARGET RNA, into GAM1570 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24378] It is appreciated that GAM1570 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1570 target genes. The mRNA of each one of this plurality of GAM1570 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1570 RNA, herein designated GAM RNA, and which when bound by GAM1570 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1570 target proteins.

[24379] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1570 gene, herein designated GAM GENE, on one or more GAM1570 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the

known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24380] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1570 correlate with, and may be deduced from, the identity of the target genes which GAM1570 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24381] Nucleotide sequences of the GAM1570 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1570 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1570 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1570 are further described hereinbelow with reference to Table Table1.

[24382] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to

GAM1570 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24383] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1571 (GAM1571) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24384] GAM1571 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1571 was detected is described hereinabove with reference to Figs. 2-8.

[24385] GAM1571 gene, herein designated GAM GENE, and GAM1571 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24386] GAM1571 gene, herein designated GAM GENE, encodes a GAM1571 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1571 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1571 precursor RNA is designated SEQ ID:1544, and is provided hereinbelow with

reference to the sequence listing part.

[24387] GAM1571 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24388] An enzyme complex designated DICER COMPLEX, dices the GAM1571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1571 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1571 RNA is designated SEQ ID:3220, and is provided hereinbelow with reference to the sequence listing part.

[24389] GAM1571 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1571 target RNA, herein designated GAM TARGET RNA. GAM1571 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24390] GAM1571 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1571 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1571 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1571 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a

GAM1571 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24391] The complementary binding of GAM1571 RNA, herein designated GAM RNA, to target binding sites on GAM1571 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1571 target RNA, herein designated GAM TARGET RNA, into GAM1571 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24392] It is appreciated that GAM1571 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1571 target genes. The mRNA of each one of this plurality of GAM1571 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1571 RNA, herein designated GAM RNA, and which when bound by GAM1571 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1571

target proteins.

[24393] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1571 gene, herein designated GAM GENE, on one or more GAM1571 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24394] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1571 correlate with, and may be deduced from, the identity of the target genes which GAM1571 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24395] Nucleotide sequences of the GAM1571 precursor RNA,

herein designated GAM PRECURSOR RNA, and of the diced GAM1571 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1571 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1571 are further described hereinbelow with reference to Table Table1.

[24396] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1571 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24397] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1572 (GAM1572) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24398] GAM1572 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1572 was detected is described hereinabove with reference to Figs. 2-8.

[24399] GAM1572 gene, herein designated GAM GENE, and

GAM1572 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24400] GAM1572 gene, herein designated GAM GENE, encodes a GAM1572 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1572 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1572 precursor RNA is designated SEQ ID:1545, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1545 is located at position 2349689 relative to contig NT_021907.13, on chromosome 1.

[24401] GAM1572 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24402] An enzyme complex designated DICER COMPLEX, dices the GAM1572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1572 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1572 RNA is designated SEQ ID:3221, and is provided hereinbelow with reference to the sequence listing part.

[24403] GAM1572 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1572 target RNA, herein designated GAM TARGET RNA. GAM1572 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24404] GAM1572 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1572 target RNA, herein des-

ignated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1572 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1572 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1572 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24405] The complementary binding of GAM1572 RNA, herein designated GAM RNA, to target binding sites on GAM1572 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1572 target RNA, herein desig-

nated GAM TARGET RNA, into GAM1572 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24406] It is appreciated that GAM1572 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1572 target genes. The mRNA of each one of this plurality of GAM1572 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1572 RNA, herein designated GAM RNA, and which when bound by GAM1572 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1572 target proteins.

[24407] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1572 gene, herein designated GAM GENE, on one or more GAM1572 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other

recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24408] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1572 correlate with, and may be deduced from, the identity of the target genes which GAM1572 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24409] Nucleotide sequences of the GAM1572 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1572 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1572 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1572 are further described hereinbelow with reference to Table Table1.

[24410] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1572 RNA, herein designated GAM RNA, are de-

scribed hereinbelow with reference to Table Table2.

[24411] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1573 (GAM1573) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24412] GAM1573 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1573 was detected is described hereinabove with reference to Figs. 2-8.

[24413] GAM1573 gene, herein designated GAM GENE, and GAM1573 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24414] GAM1573 gene, herein designated GAM GENE, encodes a GAM1573 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1573 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1573 precursor RNA is designated SEQ ID:1546, and is provided hereinbelow with reference to the sequence listing part. Nucleotide se-

quence SEQ ID:1546 is located at position 5764678 relative to contig NT_008984.13, on chromosome 11.

[24415] GAM1573 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24416] An enzyme complex designated DICER COMPLEX, dices the GAM1573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1573 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1573 RNA is designated SEQ ID:3222, and is provided hereinbelow with reference to the sequence

listing part.

[24417] GAM1573 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1573 target RNA, herein designated GAM TARGET RNA. GAM1573 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24418] GAM1573 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1573 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1573 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1573 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1573 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24419] The complementary binding of GAM1573 RNA, herein designated GAM RNA, to target binding sites on GAM1573 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1573 target RNA, herein designated GAM TARGET RNA, into GAM1573 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24420] It is appreciated that GAM1573 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1573 target genes. The mRNA of each one of this plurality of GAM1573 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1573 RNA, herein designated GAM RNA, and which when bound by GAM1573 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1573 target proteins.

[24421] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1573 gene, herein designated GAM GENE, on one or more GAM1573 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24422] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1573 correlate with, and may be deduced from, the identity of the target genes which GAM1573 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24423] Nucleotide sequences of the GAM1573 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1573 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1573 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1573 are further described hereinbelow with reference to Table Table1.

[24424] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1573 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24425] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1574 (GAM1574) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24426] GAM1574 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1574 was detected is described hereinabove with reference to Figs. 2-8.

[24427] GAM1574 gene, herein designated GAM GENE, and GAM1574 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24428] GAM1574 gene, herein designated GAM GENE, encodes a GAM1574 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1574 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1574 precursor RNA is designated SEQ ID:1547, and is provided hereinbelow with reference to the sequence listing part.

[24429] GAM1574 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24430] An enzyme complex designated DICER COMPLEX, dices

the GAM1574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1574 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1574 RNA is designated SEQ ID:3223, and is provided hereinbelow with reference to the sequence listing part.

[24431] GAM1574 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1574 target RNA, herein designated GAM TARGET RNA. GAM1574 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24432] GAM1574 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1574 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1574 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1574 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1574 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24433] The complementary binding of GAM1574 RNA, herein designated GAM RNA, to target binding sites on GAM1574 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1574 target RNA, herein designated GAM TARGET RNA, into GAM1574 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24434] It is appreciated that GAM1574 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1574 target genes. The mRNA of each one of this plurality of GAM1574 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1574 RNA, herein designated GAM RNA, and which when bound by GAM1574 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1574 target proteins.

[24435] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1574 gene, herein designated GAM GENE, on one or more GAM1574 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24436] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1574 correlate with, and may be deduced from, the identity of the target genes which GAM1574 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24437] Nucleotide sequences of the GAM1574 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1574 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1574 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1574 are further described hereinbelow with reference to Table Table1.

[24438] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1574 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24439] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1575 (GAM1575) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24440] GAM1575 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1575 was detected is described hereinabove with reference to Figs. 2-8.

[24441] GAM1575 gene, herein designated GAM GENE, and GAM1575 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24442] GAM1575 gene, herein designated GAM GENE, encodes a GAM1575 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1575 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1575 precursor RNA is designated SEQ ID:1548, and is provided hereinbelow with reference to the sequence listing part.

[24443] GAM1575 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24444] An enzyme complex designated DICER COMPLEX, dices the GAM1575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1575 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1575 RNA is designated SEQ ID:3224, and is provided hereinbelow with reference to the sequence listing part.

[24445] GAM1575 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1575 target RNA, herein designated GAM TARGET RNA. GAM1575 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24446] GAM1575 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1575 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1575 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1575 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1575 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24447] The complementary binding of GAM1575 RNA, herein designated GAM RNA, to target binding sites on GAM1575 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1575 target RNA, herein designated GAM TARGET RNA, into GAM1575 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24448] It is appreciated that GAM1575 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1575 target genes. The mRNA of each one of this plurality of GAM1575 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1575 RNA, herein designated GAM RNA, and which when bound by GAM1575 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1575 target proteins.

[24449] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1575 gene, herein designated GAM GENE, on one or more GAM1575 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24450] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1575 correlate with, and may be deduced from, the identity of the target genes which GAM1575 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24451] Nucleotide sequences of the GAM1575 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1575 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1575 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1575 are further described hereinbelow with reference to Table Table1.

[24452] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1575 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24453] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1576 (GAM1576) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24454] GAM1576 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1576 was detected is described hereinabove with reference to Figs. 2-8.

[24455] GAM1576 gene, herein designated GAM GENE, and GAM1576 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24456] GAM1576 gene, herein designated GAM GENE, encodes a GAM1576 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1576 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1576 precursor RNA is designated SEQ ID:1549, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1549 is located at position 2934173 relative to contig NT_009458.12, on chromosome 12.

[24457] GAM1576 has 2 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[24458] SEQ ID:98749 detected in mouse EST Accession AA692083.1.

[24459] SEQ ID:98750 detected in mouse EST Accession BI202421.1.

[24460] GAM1576 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1576 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24461] An enzyme complex designated DICER COMPLEX, dices the GAM1576 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1576 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1576 RNA is designated SEQ ID:3225, and is provided hereinbelow with reference to the sequence listing part.

[24462] GAM1576 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1576 target RNA, herein designated GAM TARGET RNA. GAM1576 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24463] GAM1576 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1576 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1576 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1576 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1576 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24464] The complementary binding of GAM1576 RNA, herein designated GAM RNA, to target binding sites on GAM1576 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1576 target RNA, herein designated GAM TARGET RNA, into GAM1576 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24465] It is appreciated that GAM1576 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1576 target genes. The mRNA of each one of this plurality of GAM1576 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1576 RNA, herein designated GAM RNA, and which when bound by GAM1576 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1576 target proteins.

[24466] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1576 gene, herein designated GAM GENE, on one or more GAM1576 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24467] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1576 correlate with, and may be deduced from, the identity of the target genes which GAM1576 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24468] Nucleotide sequences of the GAM1576 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1576 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1576 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1576 are further described hereinbelow with reference to Table Table1.

[24469] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1576 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24470] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1577 (GAM1577) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24471] GAM1577 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1577 was detected is described hereinabove with reference to Figs. 2-8.

[24472] GAM1577 gene, herein designated GAM GENE, and GAM1577 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24473] GAM1577 gene, herein designated GAM GENE, encodes a GAM1577 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1577 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1577 precursor RNA is designated SEQ ID:1550, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1550 is located at position 6275175 relative to contig NT_034383.2, on chromosome 1.

[24474] GAM1577 has 8 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[24475] SEQ ID:99141 detected in mouse EST Accession AA168500.1.

[24476] SEQ ID:100076 detected in mouse EST Accession AA684283.1.

[24477] SEQ ID:100077 detected in mouse EST Accession AA017943.1.

[24478] SEQ ID:100149 detected in mouse EST Accession AI316374.1.

[24479] SEQ ID:100150 detected in mouse EST Accession

AA122754.1.

[24480] SEQ ID:100151 detected in mouse EST Accession BI148579.1.

[24481] SEQ ID:100152 detected in mouse EST Accession BG242574.1.

[24482] SEQ ID:100153 detected in mouse EST Accession AW413196.1.

[24483] GAM1577 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1577 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24484] An enzyme complex designated DICER COMPLEX, dices the GAM1577 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1577 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1577 RNA is designated SEQ ID:3226, and is provided hereinbelow with reference to the sequence listing part.

[24485] GAM1577 target gene, herein designated GAM TARGET

GENE, encodes a corresponding messenger RNA, GAM1577 target RNA, herein designated GAM TARGET RNA. GAM1577 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24486] GAM1577 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1577 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1577 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1577 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1577 target RNA, herein designated GAM TARGET

RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24487] The complementary binding of GAM1577 RNA, herein designated GAM RNA, to target binding sites on GAM1577 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1577 target RNA, herein designated GAM TARGET RNA, into GAM1577 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24488] It is appreciated that GAM1577 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1577 target genes. The mRNA of each one of this plurality of GAM1577 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1577 RNA, herein designated GAM RNA, and which when bound by GAM1577 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1577 target proteins.

[24489] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1577 gene, herein designated GAM GENE, on one or more GAM1577 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24490] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1577 correlate with, and may be deduced from, the identity of the target genes which GAM1577 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24491] Nucleotide sequences of the GAM1577 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced

GAM1577 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1577 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1577 are further described hereinbelow with reference to Table Table1.

[24492] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1577 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24493] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1578 (GAM1578) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24494] GAM1578 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1578 was detected is described hereinabove with reference to Figs. 2-8.

[24495] GAM1578 gene, herein designated GAM GENE, and GAM1578 target gene, herein designated GAM TARGET

GENE, are human genes contained in the human genome.

[24496] GAM1578 gene, herein designated GAM GENE, encodes a GAM1578 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1578 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1578 precursor RNA is designated SEQ ID:1551, and is provided hereinbelow with reference to the sequence listing part.

[24497] GAM1578 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:100009, which mouse homolog is detected in mouse EST accession AA265311.1.

[24498] GAM1578 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24499] An enzyme complex designated DICER COMPLEX, dices the GAM1578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1578 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1578 RNA is designated SEQ ID:3227, and is provided hereinbelow with reference to the sequence listing part.

[24500] GAM1578 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1578 target RNA, herein designated GAM TARGET RNA. GAM1578 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24501] GAM1578 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1578 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1578 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1578 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1578 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24502] The complementary binding of GAM1578 RNA, herein designated GAM RNA, to target binding sites on GAM1578 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1578 target RNA, herein designated GAM TARGET RNA, into GAM1578 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24503] It is appreciated that GAM1578 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1578 target genes. The mRNA of each one of this plurality of GAM1578 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1578 RNA, herein designated GAM RNA, and which when bound by GAM1578 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1578 target proteins.

[24504] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1578 gene, herein designated GAM GENE, on one or more GAM1578 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24505] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1578 correlate with, and may be deduced from, the identity of the target genes which GAM1578 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24506] Nucleotide sequences of the GAM1578 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1578 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1578 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1578 are further described hereinbelow with reference to Table Table1.

[24507] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1578 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24508] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1579 (GAM1579) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24509] GAM1579 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1579 was detected is described hereinabove with reference to Figs. 2-8.

[24510] GAM1579 gene, herein designated GAM GENE, and GAM1579 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24511] GAM1579 gene, herein designated GAM GENE, encodes a GAM1579 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1579 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1579 precursor RNA is

designated SEQ ID:1552, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1552 is located at position 1062857 relative to contig NT_004671.13, on chromosome 1.

[24512] GAM1579 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:97957, which mouse homolog is detected in mouse EST accession AW476724.1.

[24513] GAM1579 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24514] An enzyme complex designated DICER COMPLEX, dices the GAM1579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1579 RNA, herein designated GAM RNA, a single stranded ~22 nt

long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1579 RNA is designated SEQ ID:3228, and is provided hereinbelow with reference to the sequence listing part.

[24515] GAM1579 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1579 target RNA, herein designated GAM TARGET RNA. GAM1579 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24516] GAM1579 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1579 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1579 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1579 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1579 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24517] The complementary binding of GAM1579 RNA, herein designated GAM RNA, to target binding sites on GAM1579 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1579 target RNA, herein designated GAM TARGET RNA, into GAM1579 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24518] It is appreciated that GAM1579 target gene, herein desig-

nated GAM TARGET GENE, in fact represents a plurality of GAM1579 target genes. The mRNA of each one of this plurality of GAM1579 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1579 RNA, herein designated GAM RNA, and which when bound by GAM1579 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1579 target proteins.

[24519] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1579 gene, herein designated GAM GENE, on one or more GAM1579 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have

not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24520] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1579 correlate with, and may be deduced from, the identity of the target genes which GAM1579 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24521] Nucleotide sequences of the GAM1579 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1579 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1579 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1579 are further described hereinbelow with reference to Table Table1.

[24522] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1579 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24523] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger

1580 (GAM1580) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24524] GAM1580 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1580 was detected is described hereinabove with reference to Figs. 2-8.

[24525] GAM1580 gene, herein designated GAM GENE, and GAM1580 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24526] GAM1580 gene, herein designated GAM GENE, encodes a GAM1580 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1580 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1580 precursor RNA is designated SEQ ID:1553, and is provided hereinbelow with reference to the sequence listing part.

[24527] GAM1580 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure.

As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24528] An enzyme complex designated DICER COMPLEX, dices the GAM1580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1580 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1580 RNA is designated SEQ ID:3229, and is provided hereinbelow with reference to the sequence listing part.

[24529] GAM1580 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1580 target RNA, herein designated GAM TARGET RNA. GAM1580 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA

of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24530] GAM1580 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1580 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1580 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1580 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1580 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and

5UTR regions.

[24531] The complementary binding of GAM1580 RNA, herein designated GAM RNA, to target binding sites on GAM1580 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1580 target RNA, herein designated GAM TARGET RNA, into GAM1580 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24532] It is appreciated that GAM1580 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1580 target genes. The mRNA of each one of this plurality of GAM1580 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1580 RNA, herein designated GAM RNA, and which when bound by GAM1580 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1580 target proteins.

[24533] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1580 gene, herein designated GAM GENE, on one or

more GAM1580 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24534] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1580 correlate with, and may be deduced from, the identity of the target genes which GAM1580 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24535] Nucleotide sequences of the GAM1580 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1580 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1580 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1580 are further de-

scribed hereinbelow with reference to Table Table1.

[24536] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1580 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24537] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1581 (GAM1581) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24538] GAM1581 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1581 was detected is described hereinabove with reference to Figs. 2-8.

[24539] GAM1581 gene, herein designated GAM GENE, and GAM1581 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24540] GAM1581 gene, herein designated GAM GENE, encodes a GAM1581 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike

most ordinary genes, GAM1581 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1581 precursor RNA is designated SEQ ID:1554, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1554 is located at position 8271484 relative to contig NT_011109.13, on chromosome 19.

[24541] GAM1581 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24542] An enzyme complex designated DICER COMPLEX, dices the GAM1581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1581 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1581 RNA is designated SEQ ID:3230, and is provided hereinbelow with reference to the sequence listing part.

[24543] GAM1581 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1581 target RNA, herein designated GAM TARGET RNA. GAM1581 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24544] GAM1581 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1581 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1581 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1581 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1581 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24545] The complementary binding of GAM1581 RNA, herein designated GAM RNA, to target binding sites on GAM1581 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1581 target RNA, herein designated GAM TARGET RNA, into GAM1581 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24546] It is appreciated that GAM1581 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1581 target genes. The mRNA of each one of this plurality of GAM1581 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1581 RNA, herein designated GAM RNA, and which when bound by GAM1581 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1581 target proteins.

[24547] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1581 gene, herein designated GAM GENE, on one or more GAM1581 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[24548] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1581 correlate with, and may be deduced from, the identity of the target genes which GAM1581 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24549] Nucleotide sequences of the GAM1581 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1581 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1581 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1581 are further described hereinbelow with reference to Table Table1.

[24550] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1581 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24551] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1582 (GAM1582) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[24552] GAM1582 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1582 was detected is described hereinabove with reference to Figs. 2-8.

[24553] GAM1582 gene, herein designated GAM GENE, and GAM1582 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24554] GAM1582 gene, herein designated GAM GENE, encodes a GAM1582 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1582 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1582 precursor RNA is designated SEQ ID:1555, and is provided hereinbelow with reference to the sequence listing part.

[24555] GAM1582 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24556] An enzyme complex designated DICER COMPLEX, dices the GAM1582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1582 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1582 RNA is designated SEQ ID:3231, and is provided hereinbelow with reference to the sequence listing part.

[24557] GAM1582 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1582 target RNA, herein designated GAM TARGET RNA. GAM1582 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24558] GAM1582 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1582 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1582 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1582 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1582 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24559] The complementary binding of GAM1582 RNA, herein designated GAM RNA, to target binding sites on GAM1582 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1582 target RNA, herein designated GAM TARGET RNA, into GAM1582 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24560] It is appreciated that GAM1582 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1582 target genes. The mRNA of each one of this plurality of GAM1582 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1582 RNA, herein designated GAM RNA, and which when bound by GAM1582 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1582 target proteins.

[24561] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1582 gene, herein designated GAM GENE, on one or more GAM1582 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24562] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1582 correlate with, and may be deduced from, the identity of the target genes which GAM1582 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24563] Nucleotide sequences of the GAM1582 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1582 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1582 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1582 are further described hereinbelow with reference to Table Table1.

[24564] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1582 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24565] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1583 (GAM1583) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24566] GAM1583 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1583 was detected is described hereinabove with reference to Figs. 2-8.

[24567] GAM1583 gene, herein designated GAM GENE, and GAM1583 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24568] GAM1583 gene, herein designated GAM GENE, encodes a GAM1583 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1583 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1583 precursor RNA is designated SEQ ID:1556, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1556 is located at position 2907544 relative to contig NT_015805.11, on chromosome 2.

[24569] GAM1583 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24570] An enzyme complex designated DICER COMPLEX, dices the GAM1583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1583 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1583 RNA is designated SEQ ID:3232, and is provided hereinbelow with reference to the sequence listing part.

[24571] GAM1583 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1583 target RNA, herein designated GAM TARGET RNA. GAM1583 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24572] GAM1583 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1583 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1583 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1583 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1583 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24573] The complementary binding of GAM1583 RNA, herein designated GAM RNA, to target binding sites on GAM1583 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1583 target RNA, herein designated GAM TARGET RNA, into GAM1583 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24574] It is appreciated that GAM1583 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1583 target genes. The mRNA of each one of this

plurality of GAM1583 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1583 RNA, herein designated GAM RNA, and which when bound by GAM1583 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1583 target proteins.

[24575] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1583 gene, herein designated GAM GENE, on one or more GAM1583 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24576] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1583 correlate with, and may be deduced from, the identity of the target genes which GAM1583 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24577] Nucleotide sequences of the GAM1583 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1583 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1583 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1583 are further described hereinbelow with reference to Table Table1.

[24578] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1583 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24579] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1584 (GAM1584) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[24580] GAM1584 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1584 was detected is described hereinabove with reference to Figs. 2-8.

[24581] GAM1584 gene, herein designated GAM GENE, and GAM1584 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24582] GAM1584 gene, herein designated GAM GENE, encodes a GAM1584 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1584 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1584 precursor RNA is designated SEQ ID:1557, and is provided hereinbelow with reference to the sequence listing part.

[24583] GAM1584 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24584] An enzyme complex designated DICER COMPLEX, dices the GAM1584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1584 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1584 RNA is designated SEQ ID:3233, and is provided hereinbelow with reference to the sequence listing part.

[24585] GAM1584 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1584 target RNA, herein designated GAM TARGET RNA. GAM1584 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[24586] GAM1584 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1584 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1584 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1584 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1584 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24587] The complementary binding of GAM1584 RNA, herein

designated GAM RNA, to target binding sites on GAM1584 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1584 target RNA, herein designated GAM TARGET RNA, into GAM1584 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24588] It is appreciated that GAM1584 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1584 target genes. The mRNA of each one of this plurality of GAM1584 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1584 RNA, herein designated GAM RNA, and which when bound by GAM1584 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1584 target proteins.

[24589] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1584 gene, herein designated GAM GENE, on one or more GAM1584 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24590] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1584 correlate with, and may be deduced from, the identity of the target genes which GAM1584 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24591] Nucleotide sequences of the GAM1584 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1584 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1584 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1584 are further described hereinbelow with reference to Table Table1.

[24592] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1584 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24593] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1585 (GAM1585) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24594] GAM1585 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1585 was detected is described hereinabove with reference to Figs. 2-8.

[24595] GAM1585 gene, herein designated GAM GENE, and GAM1585 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24596] GAM1585 gene, herein designated GAM GENE, encodes a GAM1585 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1585 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1585 precursor RNA is designated SEQ ID:1558, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1558 is located at position 6008532 relative to contig NT_010498.11, on chromosome 16.

[24597] GAM1585 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24598] An enzyme complex designated DICER COMPLEX, dices the GAM1585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1585 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1585 RNA is designated SEQ ID:3234, and is provided hereinbelow with reference to the sequence listing part.

[24599] GAM1585 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1585 target RNA, herein designated GAM TARGET RNA. GAM1585 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24600] GAM1585 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1585 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1585 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1585 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1585 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24601] The complementary binding of GAM1585 RNA, herein designated GAM RNA, to target binding sites on GAM1585 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1585 target RNA, herein designated GAM TARGET RNA, into GAM1585 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24602] It is appreciated that GAM1585 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1585 target genes. The mRNA of each one of this plurality of GAM1585 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1585 RNA, herein designated GAM RNA, and which when bound by GAM1585 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1585 target proteins.

[24603] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1585 gene, herein designated GAM GENE, on one or more GAM1585 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24604] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1585 correlate with, and may be deduced from, the identity of the target genes which GAM1585 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24605] Nucleotide sequences of the GAM1585 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1585 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1585 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1585 are further described hereinbelow with reference to Table Table1.

[24606] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1585 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24607] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1586 (GAM1586) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24608] GAM1586 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1586 was detected is described hereinabove with reference to Figs. 2-8.

[24609] GAM1586 gene, herein designated GAM GENE, and GAM1586 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24610] GAM1586 gene, herein designated GAM GENE, encodes a GAM1586 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1586 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1586 precursor RNA is designated SEQ ID:1559, and is provided hereinbelow with reference to the sequence listing part.

[24611] GAM1586 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24612] An enzyme complex designated DICER COMPLEX, dices the GAM1586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1586 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1586 RNA is designated SEQ ID:3235, and is provided hereinbelow with reference to the sequence listing part.

[24613] GAM1586 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1586 target RNA, herein designated GAM TARGET RNA. GAM1586 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24614] GAM1586 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1586 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1586 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1586 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1586 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24615] The complementary binding of GAM1586 RNA, herein designated GAM RNA, to target binding sites on GAM1586

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1586 target RNA, herein designated GAM TARGET RNA, into GAM1586 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24616] It is appreciated that GAM1586 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1586 target genes. The mRNA of each one of this plurality of GAM1586 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1586 RNA, herein designated GAM RNA, and which when bound by GAM1586 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1586 target proteins.

[24617] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1586 gene, herein designated GAM GENE, on one or more GAM1586 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24618] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1586 correlate with, and may be deduced from, the identity of the target genes which GAM1586 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24619] Nucleotide sequences of the GAM1586 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1586 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1586 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1586 are further described hereinbelow with reference to Table Table1.

[24620] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1586 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24621] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1587 (GAM1587) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24622] GAM1587 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1587 was detected is described hereinabove with reference to Figs. 2-8.

[24623] GAM1587 gene, herein designated GAM GENE, and GAM1587 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24624] GAM1587 gene, herein designated GAM GENE, encodes a GAM1587 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1587 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1587 precursor RNA is designated SEQ ID:1560, and is provided hereinbelow with reference to the sequence listing part.

[24625] GAM1587 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24626] An enzyme complex designated DICER COMPLEX, dices the GAM1587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1587 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1587 RNA is designated SEQ ID:3236, and

is provided hereinbelow with reference to the sequence listing part.

[24627] GAM1587 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1587 target RNA, herein designated GAM TARGET RNA. GAM1587 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24628] GAM1587 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1587 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1587 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1587 RNA,

herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1587 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24629] The complementary binding of GAM1587 RNA, herein designated GAM RNA, to target binding sites on GAM1587 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1587 target RNA, herein designated GAM TARGET RNA, into GAM1587 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24630] It is appreciated that GAM1587 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1587 target genes. The mRNA of each one of this plurality of GAM1587 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1587 RNA, herein designated GAM RNA, and which when bound by

GAM1587 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1587 target proteins.

[24631] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1587 gene, herein designated GAM GENE, on one or more GAM1587 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24632] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1587 correlate with, and may be deduced from, the identity of the target genes which GAM1587 binds and inhibits, and the function of these

target genes, as elaborated hereinbelow.

[24633] Nucleotide sequences of the GAM1587 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1587 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1587 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1587 are further described hereinbelow with reference to Table Table1.

[24634] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1587 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24635] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1588 (GAM1588) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24636] GAM1588 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1588 was detected is described hereinabove

with reference to Figs. 2-8.

[24637] GAM1588 gene, herein designated GAM GENE, and GAM1588 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24638] GAM1588 gene, herein designated GAM GENE, encodes a GAM1588 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1588 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1588 precursor RNA is designated SEQ ID:1561, and is provided hereinbelow with reference to the sequence listing part.

[24639] GAM1588 has 38 highly conserved, expressed mouse homologs (>90% sequence similarity), found in mouse EST's. Nucleotide sequences similar to the nucleotide sequences of which mouse homologs, and the respective mouse EST's in which these homologs were detected are:

[24640] SEQ ID:99627 detected in mouse EST Accession AI314714.1.

[24641] SEQ ID:99628 detected in mouse EST Accession AA414773.1.

[24642] SEQ ID:99629 detected in mouse EST Accession

AV225454.1.

[24643] SEQ ID:99630 detected in mouse EST Accession BE860595.1.

[24644] SEQ ID:99631 detected in mouse EST Accession AU016124.1.

[24645] SEQ ID:99632 detected in mouse EST Accession AW988911.1.

[24646] SEQ ID:99633 detected in mouse EST Accession BF016642.1.

[24647] SEQ ID:99634 detected in mouse EST Accession AI573357.1.

[24648] SEQ ID:99635 detected in mouse EST Accession AA122854.1.

[24649] SEQ ID:99636 detected in mouse EST Accession BG083946.1.

[24650] SEQ ID:99637 detected in mouse EST Accession BG078060.1.

[24651] SEQ ID:99638 detected in mouse EST Accession AL024328.1.

[24652] SEQ ID:99639 detected in mouse EST Accession BG071084.1.

[24653] SEQ ID:99642 detected in mouse EST Accession BE573540.1.

[24654] SEQ ID:99643 detected in mouse EST Accession BF120559.1.

[24655] SEQ ID:99644 detected in mouse EST Accession BF785462.1.

[24656] SEQ ID:99645 detected in mouse EST Accession AW681385.1.

[24657] SEQ ID:99646 detected in mouse EST Accession BF454862.1.

[24658] SEQ ID:99647 detected in mouse EST Accession AA589031.1.

[24659] SEQ ID:99648 detected in mouse EST Accession AA120399.1.

[24660] SEQ ID:99649 detected in mouse EST Accession AA692748.1.

[24661] SEQ ID:99650 detected in mouse EST Accession AA589661.1.

[24662] SEQ ID:99651 detected in mouse EST Accession AA646147.1.

[24663] SEQ ID:99652 detected in mouse EST Accession AU018118.1.

[24664] SEQ ID:99653 detected in mouse EST Accession BG802025.1.

[24665] SEQ ID:99654 detected in mouse EST Accession

AA106981.1.

[24666] SEQ ID:99655 detected in mouse EST Accession BI660487.1.

[24667] SEQ ID:99656 detected in mouse EST Accession BI693070.1.

[24668] SEQ ID:98756 detected in mouse EST Accession BG082539.1.

[24669] SEQ ID:98757 detected in mouse EST Accession AA545087.1.

[24670] SEQ ID:98758 detected in mouse EST Accession BG295832.1.

[24671] SEQ ID:98759 detected in mouse EST Accession BI158190.1.

[24672] SEQ ID:98760 detected in mouse EST Accession BI078320.1.

[24673] SEQ ID:98761 detected in mouse EST Accession BG077811.1.

[24674] SEQ ID:98762 detected in mouse EST Accession BE911048.1.

[24675] SEQ ID:98763 detected in mouse EST Accession BI452791.1.

[24676] SEQ ID:98764 detected in mouse EST Accession BI661798.1.

[24677] SEQ ID:98765 detected in mouse EST Accession BI156043.1.

[24678] GAM1588 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24679] An enzyme complex designated DICER COMPLEX, dices the GAM1588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1588 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1588 RNA is designated SEQ ID:3237, and is provided hereinbelow with reference to the sequence

listing part.

[24680] GAM1588 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1588 target RNA, herein designated GAM TARGET RNA. GAM1588 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24681] GAM1588 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1588 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1588 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1588 RNA, herein designated GAM RNA, may have a different number

of target binding sites in untranslated regions of a GAM1588 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24682] The complementary binding of GAM1588 RNA, herein designated GAM RNA, to target binding sites on GAM1588 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1588 target RNA, herein designated GAM TARGET RNA, into GAM1588 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24683] It is appreciated that GAM1588 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1588 target genes. The mRNA of each one of this plurality of GAM1588 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1588 RNA, herein designated GAM RNA, and which when bound by GAM1588 RNA, herein designated GAM RNA, causes inhi-

bition of translation of respective one or more GAM1588 target proteins.

[24684] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1588 gene, herein designated GAM GENE, on one or more GAM1588 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24685] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1588 correlate with, and may be deduced from, the identity of the target genes which GAM1588 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24686] Nucleotide sequences of the GAM1588 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1588 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1588 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1588 are further described hereinbelow with reference to Table Table1.

[24687] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1588 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24688] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1589 (GAM1589) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24689] GAM1589 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1589 was detected is described hereinabove with reference to Figs. 2-8.

[24690] GAM1589 gene, herein designated GAM GENE, and GAM1589 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24691] GAM1589 gene, herein designated GAM GENE, encodes a GAM1589 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1589 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1589 precursor RNA is designated SEQ ID:1562, and is provided hereinbelow with reference to the sequence listing part.

[24692] GAM1589 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24693] An enzyme complex designated DICER COMPLEX, dices

the GAM1589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1589 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1589 RNA is designated SEQ ID:3238, and is provided hereinbelow with reference to the sequence listing part.

[24694] GAM1589 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1589 target RNA, herein designated GAM TARGET RNA. GAM1589 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24695] GAM1589 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1589 target RNA, herein designated GAM TARGET RNA. This complementary binding is

due to the fact that the nucleotide sequence of GAM1589 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1589 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1589 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24696] The complementary binding of GAM1589 RNA, herein designated GAM RNA, to target binding sites on GAM1589 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1589 target RNA, herein designated GAM TARGET RNA, into GAM1589 target protein,

herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24697] It is appreciated that GAM1589 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1589 target genes. The mRNA of each one of this plurality of GAM1589 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1589 RNA, herein designated GAM RNA, and which when bound by GAM1589 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1589 target proteins.

[24698] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1589 gene, herein designated GAM GENE, on one or more GAM1589 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by

those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24699] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1589 correlate with, and may be deduced from, the identity of the target genes which GAM1589 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24700] Nucleotide sequences of the GAM1589 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1589 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1589 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1589 are further described hereinbelow with reference to Table Table1.

[24701] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1589 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24702] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1590 (GAM1590) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24703] GAM1590 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1590 was detected is described hereinabove with reference to Figs. 2-8.

[24704] GAM1590 gene, herein designated GAM GENE, and GAM1590 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24705] GAM1590 gene, herein designated GAM GENE, encodes a GAM1590 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1590 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1590 precursor RNA is designated SEQ ID:1563, and is provided hereinbelow with reference to the sequence listing part.

[24706] GAM1590 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24707] An enzyme complex designated DICER COMPLEX, dices the GAM1590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1590 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1590 RNA is designated SEQ ID:3239, and is provided hereinbelow with reference to the sequence listing part.

[24708] GAM1590 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1590 target RNA, herein designated GAM TARGET RNA. GAM1590 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24709] GAM1590 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1590 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1590 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1590 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1590 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24710] The complementary binding of GAM1590 RNA, herein designated GAM RNA, to target binding sites on GAM1590 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1590 target RNA, herein designated GAM TARGET RNA, into GAM1590 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24711] It is appreciated that GAM1590 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1590 target genes. The mRNA of each one of this plurality of GAM1590 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1590 RNA, herein designated GAM RNA, and which when bound by GAM1590 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1590 target proteins.

[24712] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1590 gene, herein designated GAM GENE, on one or more GAM1590 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24713] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1590 correlate with, and may be deduced from, the identity of the target genes which GAM1590 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24714] Nucleotide sequences of the GAM1590 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1590 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1590 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1590 are further described hereinbelow with reference to Table Table1.

[24715] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1590 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24716] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1591 (GAM1591) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24717] GAM1591 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1591 was detected is described hereinabove with reference to Figs. 2-8.

[24718] GAM1591 gene, herein designated GAM GENE, and GAM1591 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24719] GAM1591 gene, herein designated GAM GENE, encodes a GAM1591 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1591 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1591 precursor RNA is designated SEQ ID:1564, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1564 is located at position 444755 relative to contig NT_031728.6, on chromosome 1.

[24720] GAM1591 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24721] An enzyme complex designated DICER COMPLEX, dices the GAM1591 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1591 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1591 RNA is designated SEQ ID:3240, and is provided hereinbelow with reference to the sequence listing part.

[24722] GAM1591 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1591 target RNA, herein designated GAM TARGET RNA. GAM1591 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24723] GAM1591 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1591 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1591

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1591 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1591 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24724] The complementary binding of GAM1591 RNA, herein designated GAM RNA, to target binding sites on GAM1591 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1591 target RNA, herein designated GAM TARGET RNA, into GAM1591 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[24725] It is appreciated that GAM1591 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1591 target genes. The mRNA of each one of this plurality of GAM1591 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1591 RNA, herein designated GAM RNA, and which when bound by GAM1591 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1591 target proteins.

[24726] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1591 gene, herein designated GAM GENE, on one or more GAM1591 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24727] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1591 correlate with, and may be deduced from, the identity of the target genes which GAM1591 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24728] Nucleotide sequences of the GAM1591 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1591 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1591 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1591 are further described hereinbelow with reference to Table Table1.

[24729] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1591 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24730] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1592 (GAM1592) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24731] GAM1592 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1592 was detected is described hereinabove with reference to Figs. 2-8.

[24732] GAM1592 gene, herein designated GAM GENE, and GAM1592 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24733] GAM1592 gene, herein designated GAM GENE, encodes a GAM1592 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1592 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1592 precursor RNA is designated SEQ ID:1565, and is provided hereinbelow with reference to the sequence listing part.

[24734] GAM1592 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1592 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24735] An enzyme complex designated DICER COMPLEX, dices the GAM1592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1592 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1592 RNA is designated SEQ ID:3241, and is provided hereinbelow with reference to the sequence listing part.

[24736] GAM1592 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1592 target RNA, herein designated GAM TARGET

RNA. GAM1592 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24737] GAM1592 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1592 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1592 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1592 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1592 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24738] The complementary binding of GAM1592 RNA, herein designated GAM RNA, to target binding sites on GAM1592 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1592 target RNA, herein designated GAM TARGET RNA, into GAM1592 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24739] It is appreciated that GAM1592 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1592 target genes. The mRNA of each one of this plurality of GAM1592 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1592 RNA, herein designated GAM RNA, and which when bound by GAM1592 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1592 target proteins.

[24740] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1592 gene, herein designated GAM GENE, on one or more GAM1592 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24741] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1592 correlate with, and may be deduced from, the identity of the target genes which GAM1592 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24742] Nucleotide sequences of the GAM1592 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1592 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1592 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1592 are further described hereinbelow with reference to Table Table1.

[24743] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1592 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24744] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1593 (GAM1593) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24745] GAM1593 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1593 was detected is described hereinabove with reference to Figs. 2-8.

[24746] GAM1593 gene, herein designated GAM GENE, and GAM1593 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24747] GAM1593 gene, herein designated GAM GENE, encodes a

GAM1593 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1593 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1593 precursor RNA is designated SEQ ID:1566, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1566 is located at position 9807620 relative to contig NT_011812.10, on chromosome X.

[24748] GAM1593 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24749] An enzyme complex designated DICER COMPLEX, dices the GAM1593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1593 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1593 RNA is designated SEQ ID:3242, and is provided hereinbelow with reference to the sequence listing part.

[24750] GAM1593 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1593 target RNA, herein designated GAM TARGET RNA. GAM1593 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24751] GAM1593 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1593 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1593 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1593 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1593 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24752] The complementary binding of GAM1593 RNA, herein designated GAM RNA, to target binding sites on GAM1593 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1593 target RNA, herein designated GAM TARGET RNA, into GAM1593 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24753] It is appreciated that GAM1593 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1593 target genes. The mRNA of each one of this plurality of GAM1593 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1593 RNA, herein designated GAM RNA, and which when bound by GAM1593 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1593 target proteins.

[24754] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1593 gene, herein designated GAM GENE, on one or more GAM1593 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24755] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1593 correlate with, and may be deduced from, the identity of the target genes which GAM1593 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24756] Nucleotide sequences of the GAM1593 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1593 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1593 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1593 are further described hereinbelow with reference to Table Table1.

[24757] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1593 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24758] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1594 (GAM1594) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24759] GAM1594 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1594 was detected is described hereinabove with reference to Figs. 2-8.

[24760] GAM1594 gene, herein designated GAM GENE, and GAM1594 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24761] GAM1594 gene, herein designated GAM GENE, encodes a GAM1594 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1594 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1594 precursor RNA is designated SEQ ID:1567, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1567 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[24762] GAM1594 precursor RNA, herein designated GAM PRE-

CURSOR RNA, folds onto itself, forming GAM1594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24763] An enzyme complex designated DICER COMPLEX, dices the GAM1594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1594 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1594 RNA is designated SEQ ID:3243, and is provided hereinbelow with reference to the sequence listing part.

[24764] GAM1594 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA,

GAM1594 target RNA, herein designated GAM TARGET RNA. GAM1594 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24765] GAM1594 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1594 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1594 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1594 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1594 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts tar-

get binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24766] The complementary binding of GAM1594 RNA, herein designated GAM RNA, to target binding sites on GAM1594 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1594 target RNA, herein designated GAM TARGET RNA, into GAM1594 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24767] It is appreciated that GAM1594 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1594 target genes. The mRNA of each one of this plurality of GAM1594 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1594 RNA, herein designated GAM RNA, and which when bound by GAM1594 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1594 target proteins.

[24768] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1594 gene, herein designated GAM GENE, on one or more GAM1594 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24769] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1594 correlate with, and may be deduced from, the identity of the target genes which GAM1594 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24770] Nucleotide sequences of the GAM1594 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1594 RNA, herein designated GAM RNA, and a

schematic representation of the secondary folding of GAM1594 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1594 are further described hereinbelow with reference to Table Table1.

[24771] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1594 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24772] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1595 (GAM1595) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24773] GAM1595 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1595 was detected is described hereinabove with reference to Figs. 2-8.

[24774] GAM1595 gene, herein designated GAM GENE, and GAM1595 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24775] GAM1595 gene, herein designated GAM GENE, encodes a GAM1595 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1595 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1595 precursor RNA is designated SEQ ID:1568, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1568 is located at position 1698742 relative to contig NT_028309.8, on chromosome 11.

[24776] GAM1595 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24777] An enzyme complex designated DICER COMPLEX, dices the GAM1595 folded precursor RNA, herein designated

GAM FOLDED PRECURSOR RNA, into GAM1595 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1595 RNA is designated SEQ ID:3244, and is provided hereinbelow with reference to the sequence listing part.

[24778] GAM1595 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1595 target RNA, herein designated GAM TARGET RNA. GAM1595 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24779] GAM1595 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1595 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1595

RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1595 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1595 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24780] The complementary binding of GAM1595 RNA, herein designated GAM RNA, to target binding sites on GAM1595 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1595 target RNA, herein designated GAM TARGET RNA, into GAM1595 target protein, herein designated GAM TARGET PROTEIN. GAM target

protein is therefore outlined by a broken line.

[24781] It is appreciated that GAM1595 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1595 target genes. The mRNA of each one of this plurality of GAM1595 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1595 RNA, herein designated GAM RNA, and which when bound by GAM1595 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1595 target proteins.

[24782] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1595 gene, herein designated GAM GENE, on one or more GAM1595 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other

genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24783] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1595 correlate with, and may be deduced from, the identity of the target genes which GAM1595 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24784] Nucleotide sequences of the GAM1595 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1595 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1595 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1595 are further described hereinbelow with reference to Table Table1.

[24785] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1595 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24786] Fig. 8 further provides a conceptual description of another

novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1596 (GAM1596) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24787] GAM1596 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1596 was detected is described hereinabove with reference to Figs. 2-8.

[24788] GAM1596 gene, herein designated GAM GENE, and GAM1596 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24789] GAM1596 gene, herein designated GAM GENE, encodes a GAM1596 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1596 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1596 precursor RNA is designated SEQ ID:1569, and is provided hereinbelow with reference to the sequence listing part.

[24790] GAM1596 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1596 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24791] An enzyme complex designated DICER COMPLEX, dices the GAM1596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1596 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1596 RNA is designated SEQ ID:3245, and is provided hereinbelow with reference to the sequence listing part.

[24792] GAM1596 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1596 target RNA, herein designated GAM TARGET

RNA. GAM1596 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24793] GAM1596 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1596 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1596 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1596 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1596 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24794] The complementary binding of GAM1596 RNA, herein designated GAM RNA, to target binding sites on GAM1596 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1596 target RNA, herein designated GAM TARGET RNA, into GAM1596 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24795] It is appreciated that GAM1596 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1596 target genes. The mRNA of each one of this plurality of GAM1596 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1596 RNA, herein designated GAM RNA, and which when bound by GAM1596 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1596 target proteins.

[24796] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1596 gene, herein designated GAM GENE, on one or more GAM1596 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24797] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1596 correlate with, and may be deduced from, the identity of the target genes which GAM1596 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24798] Nucleotide sequences of the GAM1596 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1596 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1596 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1596 are further described hereinbelow with reference to Table Table1.

[24799] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1596 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24800] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1597 (GAM1597) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24801] GAM1597 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1597 was detected is described hereinabove with reference to Figs. 2-8.

[24802] GAM1597 gene, herein designated GAM GENE, and GAM1597 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24803] GAM1597 gene, herein designated GAM GENE, encodes a

GAM1597 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1597 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1597 precursor RNA is designated SEQ ID:1570, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1570 is located at position 2865607 relative to contig NT_011512.7, on chromosome 21.

[24804] GAM1597 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24805] An enzyme complex designated DICER COMPLEX, dices the GAM1597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1597 RNA,

herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1597 RNA is designated SEQ ID:3246, and is provided hereinbelow with reference to the sequence listing part.

[24806] GAM1597 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1597 target RNA, herein designated GAM TARGET RNA. GAM1597 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24807] GAM1597 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1597 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1597 RNA, herein designated GAM RNA, is an accurate or a par-

tial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1597 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1597 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24808] The complementary binding of GAM1597 RNA, herein designated GAM RNA, to target binding sites on GAM1597 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1597 target RNA, herein designated GAM TARGET RNA, into GAM1597 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24809] It is appreciated that GAM1597 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1597 target genes. The mRNA of each one of this plurality of GAM1597 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1597 RNA, herein designated GAM RNA, and which when bound by GAM1597 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1597 target proteins.

[24810] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1597 gene, herein designated GAM GENE, on one or more GAM1597 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific com-

plementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24811] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1597 correlate with, and may be deduced from, the identity of the target genes which GAM1597 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24812] Nucleotide sequences of the GAM1597 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1597 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1597 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1597 are further described hereinbelow with reference to Table Table1.

[24813] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1597 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24814] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present in-

vention, referred to here as Genomic Address Messenger 1598 (GAM1598) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24815] GAM1598 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1598 was detected is described hereinabove with reference to Figs. 2-8.

[24816] GAM1598 gene, herein designated GAM GENE, and GAM1598 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24817] GAM1598 gene, herein designated GAM GENE, encodes a GAM1598 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1598 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1598 precursor RNA is designated SEQ ID:1571, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1571 is located at position 4256984 relative to contig NT_008046.11, on chromosome 8.

[24818] GAM1598 has a highly conserved, expressed mouse ho-

molog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99051, which mouse homolog is detected in mouse EST accession AW476224.1.

[24819] GAM1598 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24820] An enzyme complex designated DICER COMPLEX, dices the GAM1598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1598 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1598 RNA is designated SEQ ID:3247, and is provided hereinbelow with reference to the sequence listing part.

[24821] GAM1598 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1598 target RNA, herein designated GAM TARGET RNA. GAM1598 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24822] GAM1598 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1598 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1598 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1598 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1598 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24823] The complementary binding of GAM1598 RNA, herein designated GAM RNA, to target binding sites on GAM1598 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1598 target RNA, herein designated GAM TARGET RNA, into GAM1598 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24824] It is appreciated that GAM1598 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1598 target genes. The mRNA of each one of this plurality of GAM1598 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1598 RNA,

herein designated GAM RNA, and which when bound by GAM1598 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1598 target proteins.

[24825] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1598 gene, herein designated GAM GENE, on one or more GAM1598 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24826] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1598 correlate with, and may be deduced from, the identity of the target genes which

GAM1598 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24827] Nucleotide sequences of the GAM1598 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1598 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1598 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1598 are further described hereinbelow with reference to Table Table1.

[24828] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1598 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24829] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1599 (GAM1599) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24830] GAM1599 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1599 was detected is described hereinabove with reference to Figs. 2-8.

[24831] GAM1599 gene, herein designated GAM GENE, and GAM1599 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24832] GAM1599 gene, herein designated GAM GENE, encodes a GAM1599 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1599 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1599 precursor RNA is designated SEQ ID:1572, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1572 is located at position 3804016 relative to contig NT_029289.7, on chromosome 5.

[24833] GAM1599 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:98407, which mouse homolog is detected in mouse EST accession BE572814.1.

[24834] GAM1599 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1599 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24835] An enzyme complex designated DICER COMPLEX, dices the GAM1599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1599 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1599 RNA is designated SEQ ID:3248, and is provided hereinbelow with reference to the sequence listing part.

[24836] GAM1599 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1599 target RNA, herein designated GAM TARGET

RNA. GAM1599 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24837] GAM1599 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1599 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1599 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1599 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1599 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24838] The complementary binding of GAM1599 RNA, herein designated GAM RNA, to target binding sites on GAM1599 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1599 target RNA, herein designated GAM TARGET RNA, into GAM1599 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24839] It is appreciated that GAM1599 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1599 target genes. The mRNA of each one of this plurality of GAM1599 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1599 RNA, herein designated GAM RNA, and which when bound by GAM1599 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1599 target proteins.

[24840] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1599 gene, herein designated GAM GENE, on one or more GAM1599 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24841] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1599 correlate with, and may be deduced from, the identity of the target genes which GAM1599 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24842] Nucleotide sequences of the GAM1599 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1599 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1599 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1599 are further described hereinbelow with reference to Table Table1.

[24843] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1599 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24844] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1600 (GAM1600) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24845] GAM1600 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1600 was detected is described hereinabove with reference to Figs. 2-8.

[24846] GAM1600 gene, herein designated GAM GENE, and GAM1600 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24847] GAM1600 gene, herein designated GAM GENE, encodes a

GAM1600 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1600 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1600 precursor RNA is designated SEQ ID:1573, and is provided hereinbelow with reference to the sequence listing part.

[24848] GAM1600 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24849] An enzyme complex designated DICER COMPLEX, dices the GAM1600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1600 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1600 RNA is designated SEQ ID:3249, and is provided hereinbelow with reference to the sequence listing part.

[24850] GAM1600 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1600 target RNA, herein designated GAM TARGET RNA. GAM1600 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24851] GAM1600 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1600 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1600 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1600 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1600 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24852] The complementary binding of GAM1600 RNA, herein designated GAM RNA, to target binding sites on GAM1600 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1600 target RNA, herein designated GAM TARGET RNA, into GAM1600 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24853] It is appreciated that GAM1600 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1600 target genes. The mRNA of each one of this plurality of GAM1600 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1600 RNA, herein designated GAM RNA, and which when bound by GAM1600 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1600 target proteins.

[24854] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1600 gene, herein designated GAM GENE, on one or more GAM1600 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[24855] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1600 correlate with, and may be deduced from, the identity of the target genes which GAM1600 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24856] Nucleotide sequences of the GAM1600 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1600 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1600 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1600 are further described hereinbelow with reference to Table Table1.

[24857] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1600 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24858] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1601 (GAM1601) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[24859] GAM1601 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1601 was detected is described hereinabove with reference to Figs. 2-8.

[24860] GAM1601 gene, herein designated GAM GENE, and GAM1601 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24861] GAM1601 gene, herein designated GAM GENE, encodes a GAM1601 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1601 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1601 precursor RNA is designated SEQ ID:1574, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1574 is located at position 2045037 relative to contig NT_005962.13, on chromosome 3.

[24862] GAM1601 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1601 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24863] An enzyme complex designated DICER COMPLEX, dices the GAM1601 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1601 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1601 RNA is designated SEQ ID:3250, and is provided hereinbelow with reference to the sequence listing part.

[24864] GAM1601 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1601 target RNA, herein designated GAM TARGET RNA. GAM1601 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24865] GAM1601 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1601 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1601 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1601 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1601 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24866] The complementary binding of GAM1601 RNA, herein designated GAM RNA, to target binding sites on GAM1601 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1601 target RNA, herein designated GAM TARGET RNA, into GAM1601 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24867] It is appreciated that GAM1601 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1601 target genes. The mRNA of each one of this plurality of GAM1601 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1601 RNA, herein designated GAM RNA, and which when bound by GAM1601 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1601 target proteins.

[24868] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1601 gene, herein designated GAM GENE, on one or more GAM1601 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24869] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1601 correlate with, and may be deduced from, the identity of the target genes which GAM1601 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24870] Nucleotide sequences of the GAM1601 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1601 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1601 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1601 are further described hereinbelow with reference to Table Table1.

[24871] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1601 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24872] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1602 (GAM1602) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24873] GAM1602 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1602 was detected is described hereinabove with reference to Figs. 2-8.

[24874] GAM1602 gene, herein designated GAM GENE, and GAM1602 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24875] GAM1602 gene, herein designated GAM GENE, encodes a GAM1602 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1602 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1602 precursor RNA is designated SEQ ID:1575, and is provided hereinbelow with reference to the sequence listing part.

[24876] GAM1602 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24877] An enzyme complex designated DICER COMPLEX, dices the GAM1602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1602 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1602 RNA is designated SEQ ID:3251, and is provided hereinbelow with reference to the sequence listing part.

[24878] GAM1602 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1602 target RNA, herein designated GAM TARGET RNA. GAM1602 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24879] GAM1602 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1602 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1602 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1602 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1602 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24880] The complementary binding of GAM1602 RNA, herein designated GAM RNA, to target binding sites on GAM1602 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1602 target RNA, herein designated GAM TARGET RNA, into GAM1602 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24881] It is appreciated that GAM1602 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1602 target genes. The mRNA of each one of this

plurality of GAM1602 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1602 RNA, herein designated GAM RNA, and which when bound by GAM1602 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1602 target proteins.

[24882] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1602 gene, herein designated GAM GENE, on one or more GAM1602 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24883] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1602 correlate with, and may be deduced from, the identity of the target genes which GAM1602 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24884] Nucleotide sequences of the GAM1602 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1602 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1602 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1602 are further described hereinbelow with reference to Table Table1.

[24885] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1602 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24886] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1603 (GAM1603) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[24887] GAM1603 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1603 was detected is described hereinabove with reference to Figs. 2-8.

[24888] GAM1603 gene, herein designated GAM GENE, and GAM1603 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24889] GAM1603 gene, herein designated GAM GENE, encodes a GAM1603 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1603 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1603 precursor RNA is designated SEQ ID:1576, and is provided hereinbelow with reference to the sequence listing part.

[24890] GAM1603 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1603 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24891] An enzyme complex designated DICER COMPLEX, dices the GAM1603 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1603 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1603 RNA is designated SEQ ID:3252, and is provided hereinbelow with reference to the sequence listing part.

[24892] GAM1603 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1603 target RNA, herein designated GAM TARGET RNA. GAM1603 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[24893] GAM1603 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1603 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1603 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1603 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1603 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24894] The complementary binding of GAM1603 RNA, herein

designated GAM RNA, to target binding sites on GAM1603 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1603 target RNA, herein designated GAM TARGET RNA, into GAM1603 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24895] It is appreciated that GAM1603 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1603 target genes. The mRNA of each one of this plurality of GAM1603 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1603 RNA, herein designated GAM RNA, and which when bound by GAM1603 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1603 target proteins.

[24896] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1603 gene, herein designated GAM GENE, on one or more GAM1603 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24897] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1603 correlate with, and may be deduced from, the identity of the target genes which GAM1603 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24898] Nucleotide sequences of the GAM1603 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1603 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1603 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1603 are further described hereinbelow with reference to Table Table1.

[24899] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1603 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24900] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1604 (GAM1604) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24901] GAM1604 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1604 was detected is described hereinabove with reference to Figs. 2-8.

[24902] GAM1604 gene, herein designated GAM GENE, and GAM1604 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24903] GAM1604 gene, herein designated GAM GENE, encodes a GAM1604 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1604 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1604 precursor RNA is designated SEQ ID:1577, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1577 is located at position 2349674 relative to contig NT_021907.13, on chromosome 1.

[24904] GAM1604 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24905] An enzyme complex designated DICER COMPLEX, dices the GAM1604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1604 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1604 RNA is designated SEQ ID:3253, and is provided hereinbelow with reference to the sequence listing part.

[24906] GAM1604 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1604 target RNA, herein designated GAM TARGET RNA. GAM1604 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24907] GAM1604 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1604 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1604 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1604 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1604 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24908] The complementary binding of GAM1604 RNA, herein designated GAM RNA, to target binding sites on GAM1604 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1604 target RNA, herein designated GAM TARGET RNA, into GAM1604 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24909] It is appreciated that GAM1604 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1604 target genes. The mRNA of each one of this plurality of GAM1604 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1604 RNA, herein designated GAM RNA, and which when bound by GAM1604 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1604 target proteins.

[24910] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1604 gene, herein designated GAM GENE, on one or more GAM1604 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24911] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1604 correlate with, and may be deduced from, the identity of the target genes which GAM1604 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24912] Nucleotide sequences of the GAM1604 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1604 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1604 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1604 are further described hereinbelow with reference to Table Table1.

[24913] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1604 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24914] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1605 (GAM1605) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24915] GAM1605 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1605 was detected is described hereinabove with reference to Figs. 2-8.

[24916] GAM1605 gene, herein designated GAM GENE, and GAM1605 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24917] GAM1605 gene, herein designated GAM GENE, encodes a GAM1605 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1605 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1605 precursor RNA is designated SEQ ID:1578, and is provided hereinbelow with reference to the sequence listing part.

[24918] GAM1605 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24919] An enzyme complex designated DICER COMPLEX, dices the GAM1605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1605 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1605 RNA is designated SEQ ID:3254, and is provided hereinbelow with reference to the sequence listing part.

[24920] GAM1605 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1605 target RNA, herein designated GAM TARGET RNA. GAM1605 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24921] GAM1605 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1605 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1605 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1605 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1605 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24922] The complementary binding of GAM1605 RNA, herein designated GAM RNA, to target binding sites on GAM1605

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1605 target RNA, herein designated GAM TARGET RNA, into GAM1605 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24923] It is appreciated that GAM1605 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1605 target genes. The mRNA of each one of this plurality of GAM1605 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1605 RNA, herein designated GAM RNA, and which when bound by GAM1605 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1605 target proteins.

[24924] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1605 gene, herein designated GAM GENE, on one or more GAM1605 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the

background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24925] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1605 correlate with, and may be deduced from, the identity of the target genes which GAM1605 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24926] Nucleotide sequences of the GAM1605 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1605 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1605 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1605 are further described hereinbelow with reference to Table Table1.

[24927] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1605 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24928] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1606 (GAM1606) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24929] GAM1606 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1606 was detected is described hereinabove with reference to Figs. 2-8.

[24930] GAM1606 gene, herein designated GAM GENE, and GAM1606 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24931] GAM1606 gene, herein designated GAM GENE, encodes a GAM1606 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1606 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to

the nucleotide sequence of GAM1606 precursor RNA is designated SEQ ID:1579, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1579 is located at position 8166585 relative to contig NT_009781.13, on chromosome 12.

[24932] GAM1606 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24933] An enzyme complex designated DICER COMPLEX, dices the GAM1606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1606 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1606 RNA is designated SEQ ID:3255, and is provided hereinbelow with reference to the sequence listing part.

[24934] GAM1606 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1606 target RNA, herein designated GAM TARGET RNA. GAM1606 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24935] GAM1606 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1606 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1606 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1606 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1606 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24936] The complementary binding of GAM1606 RNA, herein designated GAM RNA, to target binding sites on GAM1606 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1606 target RNA, herein designated GAM TARGET RNA, into GAM1606 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24937] It is appreciated that GAM1606 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1606 target genes. The mRNA of each one of this plurality of GAM1606 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1606 RNA, herein designated GAM RNA, and which when bound by GAM1606 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1606 target proteins.

[24938] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1606 gene, herein designated GAM GENE, on one or more GAM1606 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24939] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1606 correlate with, and may

be deduced from, the identity of the target genes which GAM1606 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24940] Nucleotide sequences of the GAM1606 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1606 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1606 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1606 are further described hereinbelow with reference to Table Table1.

[24941] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1606 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24942] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1607 (GAM1607) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24943] GAM1607 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1607 was detected is described hereinabove with reference to Figs. 2-8.

[24944] GAM1607 gene, herein designated GAM GENE, and GAM1607 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24945] GAM1607 gene, herein designated GAM GENE, encodes a GAM1607 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1607 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1607 precursor RNA is designated SEQ ID:1580, and is provided hereinbelow with reference to the sequence listing part.

[24946] GAM1607 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial

inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24947] An enzyme complex designated DICER COMPLEX, dices the GAM1607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1607 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1607 RNA is designated SEQ ID:3256, and is provided hereinbelow with reference to the sequence listing part.

[24948] GAM1607 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1607 target RNA, herein designated GAM TARGET RNA. GAM1607 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24949] GAM1607 RNA, herein designated GAM RNA, binds com-

plementarily to one or more target binding sites located in untranslated regions of GAM1607 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1607 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1607 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1607 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24950] The complementary binding of GAM1607 RNA, herein designated GAM RNA, to target binding sites on GAM1607 target RNA, herein designated GAM TARGET RNA, such as

BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1607 target RNA, herein designated GAM TARGET RNA, into GAM1607 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24951] It is appreciated that GAM1607 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1607 target genes. The mRNA of each one of this plurality of GAM1607 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1607 RNA, herein designated GAM RNA, and which when bound by GAM1607 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1607 target proteins.

[24952] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1607 gene, herein designated GAM GENE, on one or more GAM1607 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary

binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24953] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1607 correlate with, and may be deduced from, the identity of the target genes which GAM1607 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24954] Nucleotide sequences of the GAM1607 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1607 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1607 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1607 are further described hereinbelow with reference to Table Table1.

[24955] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the

complementarity of each of these target binding sites to GAM1607 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24956] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1608 (GAM1608) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24957] GAM1608 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1608 was detected is described hereinabove with reference to Figs. 2-8.

[24958] GAM1608 gene, herein designated GAM GENE, and GAM1608 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24959] GAM1608 gene, herein designated GAM GENE, encodes a GAM1608 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1608 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1608 precursor RNA is

designated SEQ ID:1581, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1581 is located at position 8166585 relative to contig NT_009781.13, on chromosome 12.

[24960] GAM1608 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24961] An enzyme complex designated DICER COMPLEX, dices the GAM1608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1608 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1608 RNA is designated SEQ ID:3257, and is provided hereinbelow with reference to the sequence listing part.

[24962] GAM1608 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1608 target RNA, herein designated GAM TARGET RNA. GAM1608 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24963] GAM1608 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1608 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1608 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1608 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1608 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24964] The complementary binding of GAM1608 RNA, herein designated GAM RNA, to target binding sites on GAM1608 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1608 target RNA, herein designated GAM TARGET RNA, into GAM1608 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24965] It is appreciated that GAM1608 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1608 target genes. The mRNA of each one of this plurality of GAM1608 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1608 RNA,

herein designated GAM RNA, and which when bound by GAM1608 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1608 target proteins.

[24966] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1608 gene, herein designated GAM GENE, on one or more GAM1608 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24967] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1608 correlate with, and may be deduced from, the identity of the target genes which

GAM1608 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24968] Nucleotide sequences of the GAM1608 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1608 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1608 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1608 are further described hereinbelow with reference to Table Table1.

[24969] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1608 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24970] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1609 (GAM1609) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24971] GAM1609 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1609 was detected is described hereinabove with reference to Figs. 2-8.

[24972] GAM1609 gene, herein designated GAM GENE, and GAM1609 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24973] GAM1609 gene, herein designated GAM GENE, encodes a GAM1609 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1609 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1609 precursor RNA is designated SEQ ID:1582, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1582 is located at position 3434864 relative to contig NT_009714.13, on chromosome 12.

[24974] GAM1609 has a highly conserved, expressed mouse homolog (>90% sequence similarity), the nucleotide sequence of which is similar to the nucleotide sequence of SEQ ID:99067, which mouse homolog is detected in mouse EST accession BG288438.1.

[24975] GAM1609 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1609 folded

precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24976] An enzyme complex designated DICER COMPLEX, dices the GAM1609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1609 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1609 RNA is designated SEQ ID:3258, and is provided hereinbelow with reference to the sequence listing part.

[24977] GAM1609 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1609 target RNA, herein designated GAM TARGET

RNA. GAM1609 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24978] GAM1609 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1609 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1609 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1609 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1609 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an

example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24979] The complementary binding of GAM1609 RNA, herein designated GAM RNA, to target binding sites on GAM1609 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1609 target RNA, herein designated GAM TARGET RNA, into GAM1609 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24980] It is appreciated that GAM1609 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1609 target genes. The mRNA of each one of this plurality of GAM1609 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1609 RNA, herein designated GAM RNA, and which when bound by GAM1609 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1609 target proteins.

[24981] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with

specific reference to translational inhibition exerted by GAM1609 gene, herein designated GAM GENE, on one or more GAM1609 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[24982] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1609 correlate with, and may be deduced from, the identity of the target genes which GAM1609 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24983] Nucleotide sequences of the GAM1609 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1609 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of

GAM1609 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1609 are further described hereinbelow with reference to Table Table1.

[24984] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1609 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24985] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1610 (GAM1610) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[24986] GAM1610 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1610 was detected is described hereinabove with reference to Figs. 2-8.

[24987] GAM1610 gene, herein designated GAM GENE, and GAM1610 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[24988] GAM1610 gene, herein designated GAM GENE, encodes a

GAM1610 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1610 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1610 precursor RNA is designated SEQ ID:1583, and is provided hereinbelow with reference to the sequence listing part.

[24989] GAM1610 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[24990] An enzyme complex designated DICER COMPLEX, dices the GAM1610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1610 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1610 RNA is designated SEQ ID:3259, and is provided hereinbelow with reference to the sequence listing part.

[24991] GAM1610 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1610 target RNA, herein designated GAM TARGET RNA. GAM1610 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[24992] GAM1610 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1610 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1610 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustra-

tion, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1610 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1610 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[24993] The complementary binding of GAM1610 RNA, herein designated GAM RNA, to target binding sites on GAM1610 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1610 target RNA, herein designated GAM TARGET RNA, into GAM1610 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[24994] It is appreciated that GAM1610 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of

GAM1610 target genes. The mRNA of each one of this plurality of GAM1610 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1610 RNA, herein designated GAM RNA, and which when bound by GAM1610 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1610 target proteins.

[24995] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1610 gene, herein designated GAM GENE, on one or more GAM1610 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a

tiny RNA world, Science 294,779 (2001)).

[24996] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1610 correlate with, and may be deduced from, the identity of the target genes which GAM1610 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[24997] Nucleotide sequences of the GAM1610 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1610 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1610 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1610 are further described hereinbelow with reference to Table Table1.

[24998] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1610 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[24999] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1611 (GAM1611) gene, which modulates expression of

respective target genes thereof, the function and utility of which target genes is known in the art.

[25000] GAM1611 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1611 was detected is described hereinabove with reference to Figs. 2-8.

[25001] GAM1611 gene, herein designated GAM GENE, and GAM1611 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25002] GAM1611 gene, herein designated GAM GENE, encodes a GAM1611 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1611 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1611 precursor RNA is designated SEQ ID:1584, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1584 is located at position 5080787 relative to contig NT_006383.13, on chromosome 4.

[25003] GAM1611 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1611 folded precursor RNA, herein designated GAM FOLDED PRECUR-

SOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25004] An enzyme complex designated DICER COMPLEX, dices the GAM1611 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1611 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1611 RNA is designated SEQ ID:3260, and is provided hereinbelow with reference to the sequence listing part.

[25005] GAM1611 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1611 target RNA, herein designated GAM TARGET RNA. GAM1611 target RNA, herein designated GAM TAR-

GET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25006] GAM1611 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1611 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1611 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1611 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1611 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in

the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25007] The complementary binding of GAM1611 RNA, herein designated GAM RNA, to target binding sites on GAM1611 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1611 target RNA, herein designated GAM TARGET RNA, into GAM1611 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25008] It is appreciated that GAM1611 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1611 target genes. The mRNA of each one of this plurality of GAM1611 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1611 RNA, herein designated GAM RNA, and which when bound by GAM1611 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1611 target proteins.

[25009] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by

GAM1611 gene, herein designated GAM GENE, on one or more GAM1611 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25010] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1611 correlate with, and may be deduced from, the identity of the target genes which GAM1611 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25011] Nucleotide sequences of the GAM1611 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1611 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1611 folded precursor RNA, herein designated GAM

FOLDED PRECURSOR RNA, of GAM1611 are further described hereinbelow with reference to Table Table1.

[25012] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1611 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25013] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1612 (GAM1612) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25014] GAM1612 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1612 was detected is described hereinabove with reference to Figs. 2-8.

[25015] GAM1612 gene, herein designated GAM GENE, and GAM1612 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25016] GAM1612 gene, herein designated GAM GENE, encodes a GAM1612 precursor RNA, herein designated GAM PRE-

CURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1612 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1612 precursor RNA is designated SEQ ID:1585, and is provided hereinbelow with reference to the sequence listing part.

[25017] GAM1612 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1612 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25018] An enzyme complex designated DICER COMPLEX, dices the GAM1612 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1612 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1612 RNA is designated SEQ ID:3261, and is provided hereinbelow with reference to the sequence listing part.

[25019] GAM1612 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1612 target RNA, herein designated GAM TARGET RNA. GAM1612 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25020] GAM1612 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1612 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1612 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated

BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1612 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1612 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25021] The complementary binding of GAM1612 RNA, herein designated GAM RNA, to target binding sites on GAM1612 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1612 target RNA, herein designated GAM TARGET RNA, into GAM1612 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25022] It is appreciated that GAM1612 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1612 target genes. The mRNA of each one of this

plurality of GAM1612 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1612 RNA, herein designated GAM RNA, and which when bound by GAM1612 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1612 target proteins.

[25023] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1612 gene, herein designated GAM GENE, on one or more GAM1612 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25024] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1612 correlate with, and may be deduced from, the identity of the target genes which GAM1612 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25025] Nucleotide sequences of the GAM1612 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1612 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1612 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1612 are further described hereinbelow with reference to Table Table1.

[25026] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1612 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25027] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1613 (GAM1613) gene, which modulates expression of respective target genes thereof, the function and utility of

which target genes is known in the art.

[25028] GAM1613 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1613 was detected is described hereinabove with reference to Figs. 2-8.

[25029] GAM1613 gene, herein designated GAM GENE, and GAM1613 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25030] GAM1613 gene, herein designated GAM GENE, encodes a GAM1613 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1613 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1613 precursor RNA is designated SEQ ID:1586, and is provided hereinbelow with reference to the sequence listing part.

[25031] GAM1613 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25032] An enzyme complex designated DICER COMPLEX, dices the GAM1613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1613 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 94%) nucleotide sequence of GAM1613 RNA is designated SEQ ID:3262, and is provided hereinbelow with reference to the sequence listing part.

[25033] GAM1613 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1613 target RNA, herein designated GAM TARGET RNA. GAM1613 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[25034] GAM1613 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1613 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1613 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1613 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1613 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25035] The complementary binding of GAM1613 RNA, herein

designated GAM RNA, to target binding sites on GAM1613 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1613 target RNA, herein designated GAM TARGET RNA, into GAM1613 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25036] It is appreciated that GAM1613 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1613 target genes. The mRNA of each one of this plurality of GAM1613 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1613 RNA, herein designated GAM RNA, and which when bound by GAM1613 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1613 target proteins.

[25037] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1613 gene, herein designated GAM GENE, on one or more GAM1613 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25038] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1613 correlate with, and may be deduced from, the identity of the target genes which GAM1613 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25039] Nucleotide sequences of the GAM1613 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1613 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1613 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1613 are further described hereinbelow with reference to Table Table1.

[25040] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1613 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25041] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1614 (GAM1614) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25042] GAM1614 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1614 was detected is described hereinabove with reference to Figs. 2-8.

[25043] GAM1614 gene, herein designated GAM GENE, and GAM1614 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25044] GAM1614 gene, herein designated GAM GENE, encodes a GAM1614 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1614 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1614 precursor RNA is designated SEQ ID:1587, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1587 is located at position 8166585 relative to contig NT_009781.13, on chromosome 12.

[25045] GAM1614 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25046] An enzyme complex designated DICER COMPLEX, dices the GAM1614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1614 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1614 RNA is designated SEQ ID:3263, and is provided hereinbelow with reference to the sequence listing part.

[25047] GAM1614 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1614 target RNA, herein designated GAM TARGET RNA. GAM1614 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25048] GAM1614 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1614 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1614 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III re-

spectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1614 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1614 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25049] The complementary binding of GAM1614 RNA, herein designated GAM RNA, to target binding sites on GAM1614 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1614 target RNA, herein designated GAM TARGET RNA, into GAM1614 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25050] It is appreciated that GAM1614 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1614 target genes. The mRNA of each one of this plurality of GAM1614 target genes comprises one or more

target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1614 RNA, herein designated GAM RNA, and which when bound by GAM1614 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1614 target proteins.

[25051] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1614 gene, herein designated GAM GENE, on one or more GAM1614 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25052] It is yet further appreciated that specific functions, and

accordingly utilities, of GAM1614 correlate with, and may be deduced from, the identity of the target genes which GAM1614 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25053] Nucleotide sequences of the GAM1614 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1614 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1614 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1614 are further described hereinbelow with reference to Table Table1.

[25054] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1614 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25055] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1615 (GAM1615) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25056] GAM1615 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1615 was detected is described hereinabove with reference to Figs. 2-8.

[25057] GAM1615 gene, herein designated GAM GENE, and GAM1615 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25058] GAM1615 gene, herein designated GAM GENE, encodes a GAM1615 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1615 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1615 precursor RNA is designated SEQ ID:1588, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1588 is located at position 5362451 relative to contig NT_010498.11, on chromosome 16.

[25059] GAM1615 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typi-

cal of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25060] An enzyme complex designated DICER COMPLEX, dices the GAM1615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1615 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1615 RNA is designated SEQ ID:3264, and is provided hereinbelow with reference to the sequence listing part.

[25061] GAM1615 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1615 target RNA, herein designated GAM TARGET RNA. GAM1615 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a pro-

tein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25062] GAM1615 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1615 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1615 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1615 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1615 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25063] The complementary binding of GAM1615 RNA, herein designated GAM RNA, to target binding sites on GAM1615 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1615 target RNA, herein designated GAM TARGET RNA, into GAM1615 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25064] It is appreciated that GAM1615 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1615 target genes. The mRNA of each one of this plurality of GAM1615 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1615 RNA, herein designated GAM RNA, and which when bound by GAM1615 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1615 target proteins.

[25065] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1615 gene, herein designated GAM GENE, on one or more GAM1615 target gene, herein designated GAM TAR-

GET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25066] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1615 correlate with, and may be deduced from, the identity of the target genes which GAM1615 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25067] Nucleotide sequences of the GAM1615 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1615 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1615 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1615 are further described hereinbelow with reference to Table Table1.

[25068] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1615 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25069] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1616 (GAM1616) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25070] GAM1616 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1616 was detected is described hereinabove with reference to Figs. 2-8.

[25071] GAM1616 gene, herein designated GAM GENE, and GAM1616 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25072] GAM1616 gene, herein designated GAM GENE, encodes a GAM1616 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1616 precursor RNA, herein

designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1616 precursor RNA is designated SEQ ID:1589, and is provided hereinbelow with reference to the sequence listing part.

[25073] GAM1616 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25074] An enzyme complex designated DICER COMPLEX, dices the GAM1616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1616 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 89%) nucleotide sequence of GAM1616 RNA is designated SEQ ID:3265, and is provided hereinbelow with reference to the sequence listing part.

[25075] GAM1616 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1616 target RNA, herein designated GAM TARGET RNA. GAM1616 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25076] GAM1616 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1616 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1616 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target

binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1616 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1616 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25077] The complementary binding of GAM1616 RNA, herein designated GAM RNA, to target binding sites on GAM1616 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1616 target RNA, herein designated GAM TARGET RNA, into GAM1616 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25078] It is appreciated that GAM1616 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1616 target genes. The mRNA of each one of this plurality of GAM1616 target genes comprises one or more target binding sites, each having a nucleotide sequence

which is at least partly complementary to GAM1616 RNA, herein designated GAM RNA, and which when bound by GAM1616 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1616 target proteins.

[25079] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1616 gene, herein designated GAM GENE, on one or more GAM1616 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25080] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1616 correlate with, and may

be deduced from, the identity of the target genes which GAM1616 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25081] Nucleotide sequences of the GAM1616 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1616 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1616 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1616 are further described hereinbelow with reference to Table Table1.

[25082] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1616 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25083] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1617 (GAM1617) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25084] GAM1617 is a novel bioinformatically detected regulatory,

non protein coding, micro RNA (miRNA) gene. The method by which GAM1617 was detected is described hereinabove with reference to Figs. 2-8.

[25085] GAM1617 gene, herein designated GAM GENE, and GAM1617 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25086] GAM1617 gene, herein designated GAM GENE, encodes a GAM1617 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1617 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1617 precursor RNA is designated SEQ ID:1590, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1590 is located at position 4941128 relative to contig NT_004668.13, on chromosome 1.

[25087] GAM1617 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the

fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25088] An enzyme complex designated DICER COMPLEX, dices the GAM1617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1617 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1617 RNA is designated SEQ ID:3266, and is provided hereinbelow with reference to the sequence listing part.

[25089] GAM1617 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1617 target RNA, herein designated GAM TARGET RNA. GAM1617 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, desig-

nated 5UTR, PROTEIN CODING and 3UTR respectively.

[25090] GAM1617 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1617 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1617 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1617 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1617 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25091] The complementary binding of GAM1617 RNA, herein

designated GAM RNA, to target binding sites on GAM1617 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1617 target RNA, herein designated GAM TARGET RNA, into GAM1617 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25092] It is appreciated that GAM1617 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1617 target genes. The mRNA of each one of this plurality of GAM1617 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1617 RNA, herein designated GAM RNA, and which when bound by GAM1617 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1617 target proteins.

[25093] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1617 gene, herein designated GAM GENE, on one or more GAM1617 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA

genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25094] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1617 correlate with, and may be deduced from, the identity of the target genes which GAM1617 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25095] Nucleotide sequences of the GAM1617 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1617 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1617 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1617 are further described hereinbelow with reference to Table Table1.

[25096] Nucleotide sequences of target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1617 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25097] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1618 (GAM1618) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25098] GAM1618 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method by which GAM1618 was detected is described hereinabove with reference to Figs. 2-8.

[25099] GAM1618 gene, herein designated GAM GENE, and GAM1618 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25100] GAM1618 gene, herein designated GAM GENE, encodes a GAM1618 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1618 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a pro-

tein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1618 precursor RNA is designated SEQ ID:1591, and is provided hereinbelow with reference to the sequence listing part.

[25101] GAM1618 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25102] An enzyme complex designated DICER COMPLEX, dices the GAM1618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1618 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide se-

quence of GAM1618 RNA is designated SEQ ID:3267, and is provided hereinbelow with reference to the sequence listing part.

[25103] GAM1618 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1618 target RNA, herein designated GAM TARGET RNA. GAM1618 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25104] GAM1618 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1618 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1618 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration

only, and is not meant to be limiting GAM1618 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1618 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25105] The complementary binding of GAM1618 RNA, herein designated GAM RNA, to target binding sites on GAM1618 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1618 target RNA, herein designated GAM TARGET RNA, into GAM1618 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25106] It is appreciated that GAM1618 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1618 target genes. The mRNA of each one of this plurality of GAM1618 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1618 RNA,

herein designated GAM RNA, and which when bound by GAM1618 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1618 target proteins.

[25107] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1618 gene, herein designated GAM GENE, on one or more GAM1618 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., Perspective: Glimpses of a tiny RNA world, Science 294,779 (2001)).

[25108] It is yet further appreciated that specific functions, and accordingly utilities, of GAM1618 correlate with, and may be deduced from, the identity of the target genes which

GAM1618 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[25109] Nucleotide sequences of the GAM1618 precursor RNA, herein designated GAM PRECURSOR RNA, and of the diced GAM1618 RNA, herein designated GAM RNA, and a schematic representation of the secondary folding of GAM1618 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, of GAM1618 are further described hereinbelow with reference to Table Table1.

[25110] Nucleotide sequences of target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 8, found on, and schematic representation of the complementarity of each of these target binding sites to GAM1618 RNA, herein designated GAM RNA, are described hereinbelow with reference to Table Table2.

[25111] Fig. 8 further provides a conceptual description of another novel bioinformatically detected gene of the present invention, referred to here as Genomic Address Messenger 1619 (GAM1619) gene, which modulates expression of respective target genes thereof, the function and utility of which target genes is known in the art.

[25112] GAM1619 is a novel bioinformatically detected regulatory, non protein coding, micro RNA (miRNA) gene. The method

by which GAM1619 was detected is described hereinabove with reference to Figs. 2-8.

[25113] GAM1619 gene, herein designated GAM GENE, and GAM1619 target gene, herein designated GAM TARGET GENE, are human genes contained in the human genome.

[25114] GAM1619 gene, herein designated GAM GENE, encodes a GAM1619 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, GAM1619 precursor RNA, herein designated GAM PRECURSOR RNA, does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of GAM1619 precursor RNA is designated SEQ ID:1592, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1592 is located at position 3059501 relative to contig NT_011875.8, on chromosome Y.

[25115] GAM1619 precursor RNA, herein designated GAM PRECURSOR RNA, folds onto itself, forming GAM1619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional hairpin structure. As is well known in the art, this hairpin structure, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the

RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[25116] An enzyme complex designated DICER COMPLEX, dices the GAM1619 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, into GAM1619 RNA, herein designated GAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, dicing of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 89%) nucleotide sequence of GAM1619 RNA is designated SEQ ID:3268, and is provided hereinbelow with reference to the sequence listing part.

[25117] GAM1619 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, GAM1619 target RNA, herein designated GAM TARGET RNA. GAM1619 target RNA, herein designated GAM TARGET RNA, comprises three regions, as is typical of mRNA of a protein coding gene: a 5 untranslated region, a protein coding region and a 3 untranslated region, designated 5UTR, PROTEIN CODING and 3UTR respectively.

[25118] GAM1619 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in untranslated regions of GAM1619 target RNA, herein designated GAM TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of GAM1619 RNA, herein designated GAM RNA, is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 8 shows 3 such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of target binding sites shown in Fig. 8 is meant as an illustration only, and is not meant to be limiting GAM1619 RNA, herein designated GAM RNA, may have a different number of target binding sites in untranslated regions of a GAM1619 target RNA, herein designated GAM TARGET RNA. It is further appreciated that while Fig. 8 depicts target binding sites in the 3UTR region, this is meant as an example only these target binding sites may be located in the 3UTR region, the 5UTR region, or in both 3UTR and 5UTR regions.

[25119] The complementary binding of GAM1619 RNA, herein designated GAM RNA, to target binding sites on GAM1619

target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of GAM1619 target RNA, herein designated GAM TARGET RNA, into GAM1619 target protein, herein designated GAM TARGET PROTEIN. GAM target protein is therefore outlined by a broken line.

[25120] It is appreciated that GAM1619 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM1619 target genes. The mRNA of each one of this plurality of GAM1619 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM1619 RNA, herein designated GAM RNA, and which when bound by GAM1619 RNA, herein designated GAM RNA, causes inhibition of translation of respective one or more GAM1619 target proteins.

[25121] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 8 with specific reference to translational inhibition exerted by GAM1619 gene, herein designated GAM GENE, on one or more GAM1619 target gene, herein designated GAM TARGET GENE, is in fact common to other known miRNA genes. As mentioned hereinabove with reference to the